Notice of Award

RESEARCH PROJECT COOPERATIVE AGREEMENT **Federal Award Date:** 08/28/2020

Department of Health and Human Services
National Institutes of Health

NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES

Grant Number: 1U01AI151797-01 REVISED
FAIN: U01AI151797

Principal Investigator(s):
PETER DASZAK, PHD

Project Title: Understanding Risk of Zoonotic Virus Emergence in EID Hotspots of Southeast Asia

Aleksei Chmura
Authorized Organizational Representative
460 West 34th Street, Suite 1701
New York, NY 100012317

Award e-mailed to: [redacted] (b) (6)

Period Of Performance:
Budget Period: 06/17/2020 – 05/31/2021
Project Period: 06/17/2020 – 05/31/2025

Dear Business Official:

The National Institutes of Health hereby revises this award (see "Award Calculation" in Section I and "Terms and Conditions" in Section III) to ECOHEALTH ALLIANCE, INC. in support of the above referenced project. This award is pursuant to the authority of 42 USC 241 31 USC 6305 42 CFR 52 and is subject to the requirements of this statute and regulation and of other referenced, incorporated or attached terms and conditions.

Acceptance of this award including the "Terms and Conditions" is acknowledged by the grantee when funds are drawn down or otherwise obtained from the grant payment system.

Each publication, press release, or other document about research supported by an NIH award must include an acknowledgment of NIH award support and a disclaimer such as "Research reported in this publication was supported by the National Institute Of Allergy And Infectious Diseases of the National Institutes of Health under Award Number U01AI151797. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health." Prior to issuing a press release concerning the outcome of this research, please notify the NIH awarding IC in advance to allow for coordination.

Award recipients must promote objectivity in research by establishing standards that provide a reasonable expectation that the design, conduct and reporting of research funded under NIH awards will be free from bias resulting from an Investigator's Financial Conflict of Interest (FCOI), in accordance with the 2011 revised regulation at 42 CFR Part 50 Subpart F. The Institution shall submit all FCOI reports to the NIH through the eRA Commons FCOI Module. The regulation does not apply to Phase I Small Business Innovative Research (SBIR) and Small Business Technology Transfer (STTR) awards. Consult the NIH website http://grants.nih.gov/grants/policy/coi/ for a link to the regulation and additional important information.

If you have any questions about this award, please contact the individual(s) referenced in Section IV.

Sincerely yours,

NIH NGA R | Version: 56 - 12/26/2018 2:22:00 PM| Generated on: 8/29/2020 12:01:42 AM

Regina E. Kitsoulis
Grants Management Officer
NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES

Additional information follows

SECTION I – AWARD DATA – 1U01AI151797-01 REVISED

Award Calculation (U.S. Dollars)

Salaries and Wages	$272,938
Fringe Benefits	$96,627
Personnel Costs (Subtotal)	$369,565
Consultant Services	$15,000
Materials & Supplies	$7,918
Travel	$72,225
Other	$27,000
Subawards/Consortium/Contractual Costs	$857,689
Federal Direct Costs	$1,349,397
Federal F&A Costs	$197,347
Approved Budget	$1,546,744
Total Amount of Federal Funds Obligated (Federal Share)	$1,546,744
TOTAL FEDERAL AWARD AMOUNT	$1,546,744
AMOUNT OF THIS ACTION (FEDERAL SHARE)	$0

SUMMARY TOTALS FOR ALL YEARS		
YR	**THIS AWARD**	**CUMULATIVE TOTALS**
1	$1,546,744	$1,546,744
2	$1,505,568	$1,505,568
3	$1,504,400	$1,504,400
4	$1,503,220	$1,503,220
5	$1,502,037	$1,502,037

Recommended future year total cost support, subject to the availability of funds and satisfactory progress of the project

Fiscal Information:

CFDA Name: Allergy and Infectious Diseases Research
CFDA Number: 93.855
EIN: 1311726494A1
Document Number: UAI151797A
PMS Account Type: P (Subaccount)
Fiscal Year: 2020

IC	CAN	2020	2021	2022	2023	2024
AI	8472315	$1,546,744	$1,505,568	$1,504,400	$1,503,220	$1,502,037

Recommended future year total cost support, subject to the availability of funds and satisfactory progress of the project

NIH Administrative Data:
PCC: M32F B / **OC**: 41026 / **Released**: (b) (6) 08/28/2020
Award Processed: 08/29/2020 12:01:42 AM

SECTION II – PAYMENT/HOTLINE INFORMATION – 1U01AI151797-01 REVISED

For payment and HHS Office of Inspector General Hotline information, see the NIH Home Page at http://grants.nih.gov/grants/policy/awardconditions.htm

SECTION III – TERMS AND CONDITIONS – 1U01AI151797-01 REVISED

This award is based on the application submitted to, and as approved by, NIH on the above-titled project and is subject to the terms and conditions incorporated either directly or by reference in the following:

a. The grant program legislation and program regulation cited in this Notice of Award.
b. Conditions on activities and expenditure of funds in other statutory requirements, such as

those included in appropriations acts.

c. 45 CFR Part 75.
d. National Policy Requirements and all other requirements described in the NIH Grants Policy Statement, including addenda in effect as of the beginning date of the budget period.
e. Federal Award Performance Goals: As required by the periodic report in the RPPR or in the final progress report when applicable.
f. This award notice, INCLUDING THE TERMS AND CONDITIONS CITED BELOW.

(See NIH Home Page at http://grants.nih.gov/grants/policy/awardconditions.htm for certain references cited above.)

Research and Development (R&D): All awards issued by the National Institutes of Health (NIH) meet the definition of "Research and Development" at 45 CFR Part§ 75.2. As such, auditees should identify NIH awards as part of the R&D cluster on the Schedule of Expenditures of Federal Awards (SEFA). The auditor should test NIH awards for compliance as instructed in Part V, Clusters of Programs. NIH recognizes that some awards may have another classification for purposes of indirect costs. The auditor is not required to report the disconnect (i.e., the award is classified as R&D for Federal Audit Requirement purposes but non-research for indirect cost rate purposes), unless the auditee is charging indirect costs at a rate other than the rate(s) specified in the award document(s).

Carry over of an unobligated balance into the next budget period requires Grants Management Officer prior approval.

This award is subject to the requirements of 2 CFR Part 25 for institutions to receive a Dun & Bradstreet Universal Numbering System (DUNS) number and maintain an active registration in the System for Award Management (SAM). Should a consortium/subaward be issued under this award, a DUNS requirement must be included. See http://grants.nih.gov/grants/policy/awardconditions.htm for the full NIH award term implementing this requirement and other additional information.

This award has been assigned the Federal Award Identification Number (FAIN) U01AI151797. Recipients must document the assigned FAIN on each consortium/subaward issued under this award.

Based on the project period start date of this project, this award is likely subject to the Transparency Act subaward and executive compensation reporting requirement of 2 CFR Part 170. There are conditions that may exclude this award; see http://grants.nih.gov/grants/policy/awardconditions.htm for additional award applicability information.

In accordance with P.L. 110-161, compliance with the NIH Public Access Policy is now mandatory. For more information, see NOT-OD-08-033 and the Public Access website: http://publicaccess.nih.gov/.

In accordance with the regulatory requirements provided at 45 CFR 75.113 and Appendix XII to 45 CFR Part 75, recipients that have currently active Federal grants, cooperative agreements, and procurement contracts with cumulative total value greater than $10,000,000 must report and maintain information in the System for Award Management (SAM) about civil, criminal, and administrative proceedings in connection with the award or performance of a Federal award that reached final disposition within the most recent five-year period. The recipient must also make semiannual disclosures regarding such proceedings. Proceedings information will be made publicly available in the designated integrity and performance system (currently the Federal Awardee Performance and Integrity Information System (FAPIIS)). Full reporting requirements and procedures are found in Appendix XII to 45 CFR Part 75. This term does not apply to NIH fellowships.

Treatment of Program Income:

SECTION IV -- AI Special Terms and Conditions -- 1U01AI151797-01 REVISED

Clinical Trial Indicator: No
This award does not support any NIH-defined Clinical Trials. See the NIH Grants Policy Statement Section 1.2 for NIH definition of Clinical Trial.

REVISED AWARD:

Subaward Agreement Requirements: The ECOHEALTH ALLIANCE, INC. must provide NIAID with copies of all (existing and newly established) subaward agreements established under this award, including descriptions of the biosafety monitoring plans, within 30 days of establishment.

Federal Funding Accountability and Transparency Subaward Reporting System (FSRS) Requirements: This award is subject to the Transparency Act subaward reporting requirement of 2 CFR Part 170, which must be reported through the Federal Funding Accountability and Transparency Subaward Reporting System (FSRS). The ECOHEALTH ALLIANCE, INC. must provide NIAID with proof of documentation of timely entries of subaward information into the FSRS within 30 days of submitting to FSRS.

Supersedes previous Notice of Award dated **06/17/2020**. All other terms and conditions still apply to this award.

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This award does not include funds to support research subject to the *Department of Health and Human Services Framework for Guiding Funding Decisions about Proposed Research Involving Enhanced Potential Pandemic Pathogens* (DHHS P3CO Framework) Therefore:

- For Aim 1: Identify, characterize and rank spillover risk of high zoonotic potential viruses from wildlife, the building of chimeric SARS-like bat coronaviruses will be based on the SHC014 or the pangolin coronavirus molecular clones and the building of chimeric MERS-CoV will be based on the HKU5 strain. Prior to further altering the mutant viruses you must provide NIAID with a detailed description of the proposed alterations and supporting evidence for the anticipated phenotypic characteristics of each virus.
- Alternative approaches to those referenced above, including building chimeras based on SARS-CoV-1, SARS-CoV-2, and MERS-CoV, may be subject to the DHHS P3CO Framework and must be submitted to NIAID for review and approval prior to the work commencing.

If any of the experiments proposed for Aim 1 result in a virus with a phenotype of enhanced pathogenicity and/or transmissibility, enhanced growth by more than 10 fold when compared to wild type strains, or if the mice display significant increases in weight loss, viral titer, or mortality when compared to wild-type strains, the recipient must immediately stop the work and notify the NIAID Program Officer, Grants Management Specialist, and appropriate institutional biosafety committee. Policy changes regarding the classification of these experiments or components used in these experiments may be subject to immediate halting of experimentation. No NIH funding can be used to perform such experiments until these experiments have been approved by NIAID with a revised NOA.

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Dissemination of study data will be in accord with the Recipient's accepted genomic data sharing plan as stated on page(s) **373** of the application. Failure to adhere to the sharing plan as mutually agreed upon by the Recipient and the NIAID may result in Enforcement Actions as described in the NIH Grants Policy Statement.

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This award includes human subject research studies and must conform to the DHHS policies for the Protection of Human Subjects research, which are a term and condition of award. Human subjects research is covered by the 2018 Common Rule, and may not be initiated until the associated protocols have received IRB approval as specified in 45 CFR 46. Failure to comply

with the terms and conditions of award may result in the disallowance of costs and/or additional enforcement actions as outlined in Section 8.5 of the NIH Grants Policy Statement.

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The Research Performance Progress Report (RPPR), Section G.9 (Foreign component), includes reporting requirements for all research performed outside of the United States. Research conducted at the following site(s) must be reported in your RPPR:

Jeppesen Field Consulting Australia - AUSTRALIA
Conservation Medicine Ltd. - MALAYSIA
Duke-NUS Medical School - SINGAPORE
Chulalongkorn University - THAILAND

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This award may include collaborations with and/or between foreign organizations. Please be advised that short term travel visa expenses are an allowable expense on this grant, if justified as critical and necessary for the conduct of the project.

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This Notice of Award (NoA) includes funds for activity with **Conservation Medicine Ltd. - MALAYSIA** in the amount of **$224,997** (**$208,331** direct costs + **$16,666** F&A costs).

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This Notice of Award (NoA) includes funds for activity with **Duke-NUS Medical School - SINGAPORE** in the amount of **$108,000** (**$100,000** direct costs + **$8,000** F&A costs).

****

This Notice of Award (NoA) includes funds for activity with **Chulalongkorn University - THAILAND** in the amount of **$215,944** (**$199,948** direct costs + **$15,996** F&A costs).

****

This Notice of Award (NoA) includes funds for activity with **The University of North Carolina at Chapel Hill** in the amount of **$194,375** (**$125,000** direct costs + **$69,375** F&A costs).

****

This Notice of Award (NoA) includes funds for activity **The Henry M. Jackson Fdn. for the Adv'mt. of Mil. Med., Inc**. in the amount of **$114,373** (**$75,000** direct costs + **$39,373** F&A costs).

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In accordance with the NIAID Financial Management Plan, NIAID does not provide funds for inflationary increases. Committed future year (s) funding was adjusted accordingly. See: https://www.niaid.nih.gov/grants-contracts/financial-management-plan.

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This award is issued as a Cooperative Agreement, a financial assistance mechanism in which substantial NIH scientific and/or programmatic involvement is anticipated in the performance of the activity. This award is subject to the Terms and Conditions of Award as set forth in Section VI: Award Administrative Information of **RFA AI-19-028**, "**Emerging Infectious Diseases Research Centers**," posted date **3/5/2019**, which are hereby incorporated by reference as special terms and conditions of this award.

This RFA may be accessed at: http://grants.nih.gov/grants/guide/index.html

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This award is subject to the Clinical Terms of Award referenced in the NIH Guide for Grants and Contracts, July 8, 2002, NOT AI-02-032. These terms and conditions are hereby incorporated by reference, and can be accessed via the following World Wide Web address: https://www.niaid.nih.gov/grants-contracts/niaid-clinical-terms-award All submissions required by the NIAID Clinical Terms of Award must be forwarded electronically or by mail to the responsible NIAID Program Official identified on this Notice of Award.

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Select Agents:

Awardee of a project that at any time involves a restricted experiment with a select agent, is responsible for notifying and receiving prior approval from the NIAID. Please be advised that changes in the use of a Select Agent will be considered a change in scope and require NIH awarding office prior approval. The approval is necessary for new select agent experiments as well as changes in on-going experiments that would require change in the biosafety plan and/or biosafety containment level. An approval to conduct a restricted experiment granted to an individual cannot be assumed an approval to other individuals who conduct the same restricted experiment as defined in the Select Agents Regulation 42 CFR Part 73, Section 13.b (http://www.selectagents.gov/Regulations.html).

Highly Pathogenic Agent:
NIAID defines a Highly Pathogenic Agent as an infectious Agent or Toxin that may warrant a biocontainment safety level of BSL3 or higher according to the current edition of the CDC/NIH Biosafety in Microbiological and Biomedical Laboratories (BMBL) (http://www.cdc.gov/OD/ohs/biosfty/bmbl5/bmbl5toc.htm). Research funded under this grant must adhere to the BMBL, including using the BMBL-recommended biocontainment level at a minimum. If your Institutional Biosafety Committee (or equivalent body) or designated institutional biosafety official recommend a higher biocontainment level, the highest recommended containment level must be used.
When submitting future Progress Reports indicate at the beginning of the report:

> If no research with a Highly Pathogenic Agent or Select Agent has been performed or is planned to be performed under this grant.
>
> If your IBC or equivalent body or official has determined, for example, by conducting a risk assessment, that the work being planned or performed under this grant may be conducted at a biocontainment safety level that is lower than BSL3.
>
> If the work involves Select Agents and/or Highly Pathogenic Agents, also address the following points:
>
>> Any changes in the use of the Agent(s) or Toxin(s) including its restricted experiments that have resulted in a change in the required biocontainment level, and any resultant change in location, if applicable, as determined by your IBC or equivalent body or official.
>>
>> If work with a new or additional Agent(s)/Toxin(s) is proposed in the upcoming project period, provide:
>>
>>> o A list of the new and/or additional Agent(s) that will be studied;
>>> o A description of the work that will be done with the Agent(s), and whether or not the work is a restricted experiment;
>>> o The title and location for each biocontainment resource/facility, including the name of the organization that operates the facility, and the biocontainment level at which the work will be conducted, with documentation of approval by your IBC or equivalent body or official. It is important to note if the work is being done in a new location.

STAFF CONTACTS

The Grants Management Specialist is responsible for the negotiation, award and administration of this project and for interpretation of Grants Administration policies and provisions. The Program Official is responsible for the scientific, programmatic and technical aspects of this project. These individuals work together in overall project administration. Prior approval requests (signed by an Authorized Organizational Representative) should be submitted in writing to the Grants Management Specialist. Requests may be made via e-mail.

Grants Management Specialist: Shaun W Gratton
Email: (b) (6) **Phone**: (b) (6) **Fax**: 301-493-0597

Program Official: Jean Lois Patterson
Email: (b) (6) **Phone**: (b) (6)

SPREADSHEET SUMMARY
GRANT NUMBER: 1U01AI151797-01 REVISED

INSTITUTION: ECOHEALTH ALLIANCE, INC.

Budget	Year 1	Year 2	Year 3	Year 4	Year 5
Salaries and Wages	$272,938	$272,938	$272,938	$272,938	$272,938
Fringe Benefits	$96,627	$96,628	$96,628	$96,628	$96,628
Personnel Costs (Subtotal)	$369,565	$369,566	$369,566	$369,566	$369,566
Consultant Services	$15,000	$15,000	$15,000	$15,000	$15,000
Materials & Supplies	$7,918	$7,918	$7,918	$7,918	$7,918
Travel	$72,225	$72,225	$72,225	$72,225	$72,225
Other	$27,000	$27,000	$27,000	$27,000	$27,000
Subawards/Consortium/Contractual Costs	$857,689	$856,512	$855,344	$854,164	$852,981
TOTAL FEDERAL DC	$1,349,397	$1,348,221	$1,347,053	$1,345,873	$1,344,690
TOTAL FEDERAL F&A	$197,347	$157,347	$157,347	$157,347	$157,347
TOTAL COST	$1,546,744	$1,505,568	$1,504,400	$1,503,220	$1,502,037

Facilities and Administrative Costs	Year 1	Year 2	Year 3	Year 4	Year 5
F&A Cost Rate 1	32%	32%	32%	32%	32%
F&A Cost Base 1	$616,708	$491,709	$491,709	$491,709	$491,709
F&A Costs 1	$197,347	$157,347	$157,347	$157,347	$157,347

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PI: **DASZAK, PETER**	Title: Understanding Risk of Zoonotic Virus Emergence in EID Hotspots of Southeast Asia	
Received: 06/28/2019	FOA: AI19-028 Clinical Trial:Not Allowed	Council: 01/2020
Competition ID: FORMS-E	FOA Title: Emerging Infectious Diseases Research Centers (U01 Clinical Trial Not Allowed)	
1 U01 AI151797-01	Dual:	Accession Number: 4323726
IPF: 4415701	Organization: ECOHEALTH ALLIANCE, INC.	
Former Number:	Department:	
IRG/SRG: ZAI1 EC-M (J2)	AIDS: N	Expedited: N
Subtotal Direct Costs (excludes consortium F&A) Year 1: 1,050,579 Year 2: 1,050,579 Year 3: 1,050,579 Year 4: 1,050,579 Year 5: 1,050,579	Animals: Y Humans: Y Clinical Trial: N Current HS Code: (b) (4) HESC: N Special Topics: Genomic Data Sharing	New Investigator: N Early Stage Investigator: N
Senior/Key Personnel:	*Organization:*	*Role Category:*
PETER DASZAK	EcoHealth Alliance	PD/PI
Kevin Olival	EcoHealth Alliance	Co-Investigator
Ralph Baric	University of North Carolina	Co-Investigator
Linfa Wang	Duke-NUS Medical School	Co-Investigator
Hongying Li	EcoHealth Alliance	Other (Specify)-Epidemiologist
Thiravat Hemachudha	Chulalongkorn University Hospital	Co-Investigator
Timothy William	Gleneagles Hospital	Co-Investigator
Helen Lasimbang	Hospital Universiti Malaysia Sabah	Co-Investigator
Heng Gee Lee	Queen Elizabeth State Hospital	Other (Specify)-Senior Clinician
Giri Shan Rajahram	Queen Elizabeth State Hospital	Other (Specify)-Infectious Disease Epidemiologist
Jayaseelan Sekaran	Lintang Clinic, Kuala Kangsar District Health Office	Co-Investigator
Cheng Siang Tan	Unversiti Malaysia Sarawak	Co-Investigator
Anwarali Khan Faisal Ali	Unversiti Malaysia Sarawak	Other (Specify)-Zoologist and Biotechnician
Nadia Diyana Hamzah	Bario Clinic, Rural Area Service Ministry of Health Malaysia	Other (Specify)-Medical Officer and Clinician
Ahmed Kamruddin	Universiti Malaysia Sabah	Co-Investigator

Danielle Anderson	Duke NUS	Co-Investigator
Supaporn Wacharapluesadee	Chulalongkorn University Hospital	Co-Investigator
Tom Hughes	Conservation Medicine Ltd.	Co-Investigator
Eric Laing	Uniformed Services University	Co-Investigator
Christopher Broder	Uniformed Services University	Co-Investigator
Gerald Keusch	BU NEIDL	Co-Investigator
Ronald Corley	BU NEIDL	Co-Investigator
Amy Sims	University of North Carolina at Chapel Hill	Co-Investigator
Alice Latinne	EcoHealth Alliance	Other (Specify)-Bioinformatician
Kendra Phelps	EcoHealth Alliance	Other (Specify)-Field Scientist
Emma Mendelsohn	EcoHealth Alliance	Other (Specify)-Data Scientist
Patrick Dawson	EcoHealth Alliance	Other (Specify)-Epidemiologist
Stephanie Martinez	EcoHealth Alliance	Other (Specify)-Epidemiologist
Aleksei Chmura	EcoHealth Alliance	Other (Specify)-Senior Program Manager
Tsin Wen Yeo	Lee Kong Chian School of Medicine	Consultant
Andrew Hickey	Thailand MOPH-CDC	Consultant
Hume Field	Jeppesen Field Consulting	Consultant
Carloz Zambrana-Torrelio	EcoHealth Alliance	Co-Investigator
Pasin Hemachudha	Chulalongkorn University Hospital	Other (Specify)-Immunologist and Clinician
Ingrid Ting Pao Lin	Hospital Miri	Co-Investigator

APPLICATION FOR FEDERAL ASSISTANCE
SF 424 (R&R)

3. DATE RECEIVED BY STATE | **State Application Identifier**

1. TYPE OF SUBMISSION*

○ Pre-application ● Application ○ Changed/Corrected Application

4.a. Federal Identifier

b. Agency Routing Number

2. DATE SUBMITTED | **Application Identifier**

c. Previous Grants.gov Tracking Number

5. APPLICANT INFORMATION **Organizational DUNS*:** 0770900660000

Legal Name*: EcoHealth Alliance
Department:
Division:
Street1*: 460 West 34th Street, Suite 1701
Street2:
City*: New York
County:
State*: NY: New York
Province:
Country*: USA: UNITED STATES
ZIP / Postal Code*: 10001-2317

Person to be contacted on matters involving this application
Prefix: Dr. First Name*: Peter Middle Name: Last Name*: Daszak Suffix:
Position/Title: President
Street1*: 460 West 34th Street, Suite 1701
Street2:
City*: New York
County:
State*: NY: New York
Province:
Country*: USA: UNITED STATES
ZIP / Postal Code*: 10001-2317
Phone Number*: (b) (6) Fax Number: 2123804465 Email: (b) (6)

6. EMPLOYER IDENTIFICATION NUMBER *(EIN) or (TIN)** 311726494

7. TYPE OF APPLICANT* M: Nonprofit with 501C3 IRS Status (Other than Institution of Higher Education)

Other (Specify)*

Small Business Organization Type ○ Women Owned ○ Socially and Economically Disadvantaged

8. TYPE OF APPLICATION*

● New ○ Resubmission
○ Renewal ○ Continuation ○ Revision

If Revision, mark appropriate box(es).
○ A. Increase Award ○ B. Decrease Award ○ C. Increase Duration
○ D. Decrease Duration ○ E. Other *(specify)* :

Is this application being submitted to other agencies?* ○Yes ●No What other Agencies?

9. NAME OF FEDERAL AGENCY*
National Institutes of Health

10. CATALOG OF FEDERAL DOMESTIC ASSISTANCE NUMBER
TITLE:

11. DESCRIPTIVE TITLE OF APPLICANT'S PROJECT*
Understanding Risk of Zoonotic Virus Emergence in EID Hotspots of Southeast Asia

12. PROPOSED PROJECT
Start Date* Ending Date*
03/01/2020 02/28/2025

13. CONGRESSIONAL DISTRICTS OF APPLICANT
NY-010

SF 424 (R&R) APPLICATION FOR FEDERAL ASSISTANCE

14. PROJECT DIRECTOR/PRINCIPAL INVESTIGATOR CONTACT INFORMATION

Prefix: Dr. First Name*: PETER Middle Name: Last Name*: DASZAK Suffix:

Position/Title: President
Organization Name*: EcoHealth Alliance
Department:
Division:
Street1*: 460 West 34th Street, Suite 1701
Street2:
City*: New York
County:
State*: NY: New York
Province:
Country*: USA: UNITED STATES
ZIP / Postal Code*: 10001-2317
Phone Number*: (b) (6) Fax Number: 212-380-4465 Email*: (b) (6)

15. ESTIMATED PROJECT FUNDING

a. Total Federal Funds Requested*	$7,573,721.35
b. Total Non-Federal Funds*	$0.00
c. Total Federal & Non-Federal Funds*	$7,573,721.35
d. Estimated Program Income*	$0.00

16.IS APPLICATION SUBJECT TO REVIEW BY STATE EXECUTIVE ORDER 12372 PROCESS?*

a. YES ○ THIS PREAPPLICATION/APPLICATION WAS MADE AVAILABLE TO THE STATE EXECUTIVE ORDER 12372 PROCESS FOR REVIEW ON.

DATE:

b. NO ● PROGRAM IS NOT COVERED BY E.O. 12372; OR

○ PROGRAM HAS NOT BEEN SELECTED BY STATE FOR REVIEW

17. By signing this application, I certify (1) to the statements contained in the list of certifications* and (2) that the statements herein are true, complete and accurate to the best of my knowledge. I also provide the required assurances * and agree to comply with any resulting terms if I accept an award. I am aware that any false, fictitious, or fraudulent statements or claims may subject me to criminal, civil, or administrative penalties. (U.S. Code, Title 18, Section 1001)

● I agree*

** The list of certifications and assurances, or an Internet site where you may obtain this list, is contained in the announcement or agency specific instructions*

18. SFLLL or OTHER EXPLANATORY DOCUMENTATION File Name:

19. AUTHORIZED REPRESENTATIVE

Prefix: Dr. First Name*: Aleksei Middle Name: Last Name*: Chmura Suffix:

Position/Title*: Authorized Organizational Representative
Organization Name*: EcoHealth Alliance
Department:
Division:
Street1*: 460 West 34th Street, Suite 1701
Street2:
City*: New York
County:
State*: NY: New York
Province:
Country*: USA: UNITED STATES
ZIP / Postal Code*: 10001-2317
Phone Number*: (b) (6) Fax Number: 2123804465 Email*: (b) (6)

Signature of Authorized Representative*
Aleksei Chmura

Date Signed*
06/28/2019

20. PRE-APPLICATION File Name:

21. COVER LETTER ATTACHMENT File Name:Cover_Letter_EIDRC_2019_SEA_FINAL.pdf

424 R&R and PHS-398 Specific
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OMB Number: 4040-0010
Expiration Date: 10/31/2019

Project/Performance Site Location(s)

Project/Performance Site Primary Location

❍ I am submitting an application as an individual, and not on behalf of a company, state, local or tribal government, academia, or other type of organization.

Organization Name:	ECOHEALTH ALLIANCE, INC.
Duns Number:	0770900660000
Street1*:	460 W 34TH ST.
Street2:	SUITE 1701
City*:	NEW YORK
County:	
State*:	NY: New York
Province:	
Country*:	USA: UNITED STATES
Zip / Postal Code*:	10001-2320
Project/Performance Site Congressional District*:	NY-010

Project/Performance Site Location 1

❍ I am submitting an application as an individual, and not on behalf of a company, state, local or tribal government, academia, or other type of organization.

Organization Name:	Conservation Medicine Ltd
DUNS Number:	5344092560000
Street1*:	13H Villamas Condo
Street2:	Villamas Jalan Villamas
City*:	Sungai Buloh
County	
State*:	
Province:	
Country*:	MYS: MALAYSIA
Zip / Postal Code*:	
Project/Performance Site Congressional District*:	

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 Received Date: 2019-06-28T16:02:40.000-04:00

Project/Performance Site Location 2

❍ I am submitting an application as an individual, and not on behalf of a company, state, local or tribal government, academia, or other type of organization.

Organization Name: Duke-NUS Medical School
DUNS Number: 5951922530000
Street1*: 8 College Road
Street2
City*: Singapore
County.
State*:
Province:
Country*: SGP: SINGAPORE
Zip / Postal Code*: 169857
Project/Performance Site Congressional District*:

Project/Performance Site Location 3

❍ I am submitting an application as an individual, and not on behalf of a company, state, local or tribal government, academia, or other type of organization.

Organization Name: National Emerging Infectious Diseases Laboratories
DUNS Number: 0771630590000
Street1*: 620 Albany St.
Street2:
City*: Boston
County.
State*: MA: Massachusetts
Province:
Country*: USA: UNITED STATES
Zip / Postal Code*: 02118-2516
Project/Performance Site Congressional District*: MA-007

Project/Performance Site Location 4

❍ I am submitting an application as an individual, and not on behalf of a company, state, local or tribal government, academia, or other type of organization.

Organization Name: University of North Carolina, Chapel Hill
DUNS Number: 6081952770000
Street1*: 135 Dauer Drive
Street2·
City*: Chapel Hill
County:
State*: NC: North Carolina
Province:
Country*: USA: UNITED STATES
Zip / Postal Code*: 27599-7400
Project/Performance Site Congressional District*: NC-004

Project/Performance Site Location 5

❍ I am submitting an application as an individual, and not on behalf of a company, state, local or tribal government, academia, or other type of organization.

Organization Name:	Uniformed Services University
DUNS Number:	1446765660000
Street1*:	4301 Jones Bridge Rd
Street2	
City*:	Bethesda
County.	
State*:	MD: Maryland
Province:	
Country*:	USA: UNITED STATES
Zip / Postal Code*:	20814-4799
Project/Performance Site Congressional District*:	MD-008

Project/Performance Site Location 6

❍ I am submitting an application as an individual, and not on behalf of a company, state, local or tribal government, academia, or other type of organization.

Organization Name:	Chulalongkorn University
DUNS Number:	6598088360000
Street1*:	254 Phayathai Road
Street2.	
City*:	Pathumwan, Bangkok
County.	
State*:	
Province:	
Country*:	THA: THAILAND
Zip / Postal Code*:	10330
Project/Performance Site Congressional District*:	

Additional Location(s) File Name:

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED Other Project Information

1. Are Human Subjects Involved?* ● **Yes** ○ **No**

1.a. If YES to Human Subjects

Is the Project Exempt from Federal regulations? ○ Yes ● No

If YES, check appropriate exemption number: _ 1 _ 2 _ 3 _ 4 _ 5 _ 6 _ 7 _ 8

If NO, is the IRB review Pending? ● **Yes** ○ **No**

IRB Approval Date: 03-01-2020

Human Subject Assurance Number 00022431

2. Are Vertebrate Animals Used?* ● **Yes** ○ **No**

2.a If YES to Vertebrate Animals

Is the IACUC review Pending? ● Yes ○ No

IACUC Approval Date:

Animal Welfare Assurance Number None

3. Is proprietary/privileged information included in the application?* ○ **Yes** ● **No**

4.a. Does this project have an actual or potential impact - positive or negative - on the environment?* ○ **Yes** ● **No**

4.b. If yes, please explain:

4.c. If this project has an actual or potential impact on the environment, has an exemption been authorized or an environmental assessment (EA) or environmental impact statement (EIS) been performed? ○ Yes ○ No

4.d If yes, please explain.

5. Is the research performance site designated, or eligible to be designated, as a historic place?* ○ **Yes** ● **No**

5.a. If yes, please explain:

6. Does this project involve activities outside the United States or partnership with international collaborators?* ● **Yes** ○ **No**

6.a. If yes, identify countries: Thailand, Malaysia, Singapore

6.b. Optional Explanation

	Filename
7. Project Summary/Abstract*	Project_Summary EIDRC SEA_Daszak.pdf
8. Project Narrative*	Project_Narrative_EIDRC_RFA-AI-19-028 pdf
9. Bibliography & References Cited	EIDRC SEA_Bibliography FINAL.pdf
10.Facilities & Other Resources	Facilities_EIDRC_2019_SEA_FINAL.pdf
11.Equipment	Major Equipment_FINAL.pdf

PROJECT SUMMARY/ABSTRACT

Southeast Asia is one of the world's highest-risk EID hotspots, the origin of the SARS pandemic, Nipah virus, and repeated outbreaks of influenza. This is driven by high diversity of wildlife and rapidly expanding demography that brings human and wildlife populations closer. This proposal will launch the **E**merging **I**nfectious **D**iseases - **S**outh **E**ast **A**sia **R**esearch **C**ollaboration **H**ub **(EID-SEARCH)**, a collaboration among leaders in emerging disease research in the USA, Thailand, Singapore and the 3 major Malaysian administrative regions. These researchers have networks that span >50 clinics, laboratories and research institutions across almost all SE Asian countries and will use the EID-SEARCH as an early warning system for outbreaks involving exchange of information, reagents, samples and technology, and a collaborative power-house for fundamental and translational research. The EID-SEARCH will also act as **a significant asset to scale-up and deploy resources in the case of an outbreak in the region.** This EIDRC will conduct research to: **1)** Identify, characterize and rank spillover risk of high zoonotic potential viruses from wildlife, by analyzing previously-archived wildlife samples, conducting targeted wildlife surveillance, and using serology & PCR assays to identify novel viruses. These will be characterized to assess risk of spillover to people, and a series of *in vitro* (receptor binding, cell culture) and *in vivo* (humanized mouse and collaborative cross models) assays used to assess their potential to infect people and cause disease; **2)** Collect samples and questionnaire data from human communities that live in EID hotspots and have high cultural and behavioral risk of animal exposure (e.g. wildlife hunting, bat guano collection). These will be tested with serological assays to identify evidence of novel virus spillover, and analyzed against metadata to identify key risk pathways for transmission; **3)** Identify and characterize viral etiology of 'cryptic' outbreaks in clinical cohorts. We will conduct syndromic surveillance at clinics serving the populations in Aim 2, enroll patients with undiagnosed illness and symptoms consistent with emerging viral pathogens, and test samples with molecular and follow-up serological assays to identify causal links between these syndromes and novel viruses.

This research will advance our understanding of the risk of novel viral emergence in a uniquely important region. **It will also strengthen in-country research capacity** by linking local infectious disease scientists **with an international collaborative network that has proven capacity to conduct this work and produce significant findings.** The large body of high impact collaborative research from this EIDRC leadership team provides proof-of-concept that EID-SEARCH has the background, collaborative network, experience, and skillset to act as a **unique early warning system for novel EIDs of any etiology threatening to emerge in this hottest of the EID hotspots.**

PROJECT NARRATIVE

This proposed EID Research Center (EID-SEARCH) brings leaders in emerging disease research from the US, Thailand, Singapore and the 3 major Malaysian administrative regions together to build an early warning system to safeguard against pandemic disease threats. This team will identify novel viruses from Southeast Asian wildlife, characterize their capacity to infect and cause illness in people, and use serological assays of samples from people in rural communities with high wildlife contact to identify the background rate of exposure, and risk factors that drive this. They will conduct in-depth surveillance of clinical cohorts at hospitals serving these communities to examine if 'cryptic' outbreaks are caused by these novel agents, and to build significant capacity to rapidly detect and respond should there be a major outbreak of a virus in the region.

Facilities and Other Resources

EcoHealth Alliance, New York, USA (Drs. Daszak and Olival)
EcoHealth Alliance is a New York-based 501(c) 3 non-profit institution that conducts scientific research on emerging zoonoses and global health capacity building. EcoHealth Alliance New York headquarters has (b) (4) square feet of office space including a meeting room and basic laboratory – freezer storage and light microscopy. The scientific staff (34 core scientists, 100+ field staff) is supported by a core admin staff of 18 who are available for work on this project and funded through private donor and federal support. EcoHealth Alliance does not support diagnostic facilities at its core headquarters and works in partnership with a network of leading diagnostic labs both in the USA and around the world.

EcoHealth Alliance is the headquarters of a global network of over 70 partners that provides exceptional leverage for the core scientists. This network includes staff from: academic institutions at leading national universities; intergovernmental agencies (WHO, OIE, FAO, DIVERSITAS, IUCN); infectious disease surveillance laboratories including BSL-3 and -4 laboratories; national government agency offices and labs; locally-based wildlife conservation organizations in Asia, Africa and Latin America. EcoHealth Alliance is the headquarters of: The Consortium for Conservation Medicine (CCM); the journal EcoHealth; an NSF Research Coordination Network (EcoHealthNET); the IUCN Wildlife Health Specialist Group; and the OIE Wildlife Health Network. EcoHealth Alliance is a voting member of the IUCN and a partner in Columbia University's Earth Institute Center for Environmental Sustainability (EICES) and all senior scientific staff members are Adjunct Faculty at Columbia University's Department of Ecology, Evolution, and Environmental Biology or at the Mailman School of Public Health.

Information Technology Access
EcoHealth Alliance is equipped with fiber optic Internet access and video conferencing facilities to facilitate easy communication between collaborators. EcoHealth Alliance employees have around-the-clock access to servers, VPNs, encryption software, IT support, and all necessary software including Git and Github (Hosted software revision/audit service), Sublime and Vim text editors, Vagrant and Oracle Virtualbox virtual machines, Google Apps (Hosted email and collaboration web-based software), Ansible (Server provisioning software framework), Python, NodeJS, and R programming languages, Meteor (Javascript framework), Bash shell scripts, Jenkins (Continuous Integration server), Microsoft Office and Adobe CS6 running on both Apple Mac OS X, Ubuntu linux, and Windows Operating Systems. EcoHealth Alliance has a dedicated quad-core Linux server and another dedicated dual quad-core Mac Pro Server - each with 4TB hard drives. Either server individually or in combination may be used for intensive computational modeling and/or database processing by all the grantees. Access to the cloud and supercomputing services (Amazon) is provided by core funding to EcoHealth Alliance.

Biological Sample Storage and Access
Regarding this proposal, EcoHealth Alliance will serve as the central location for project coordination, as well as data management and analysis. No biological samples, however, will be stored at the institution. All samples collected as a result of project activities will be stored at the laboratories of partner institutions (listed within this document) that are equipped with BSL-2, BSL-3 or BSL-4 level facilities. Further details regarding these laboratory facilities are included within the facility descriptions below.

University of North Carolina, Chapel Hill, USA (Drs. Baric and Sims)
The Department of Epidemiology is internationally recognized as a leader in epidemiologic research and training. The Department offers research training in most specialized areas including cancer, cardiovascular diseases, environmental and occupational health, health services/clinical epidemiology, reproductive health and infectious diseases. For the fiscal year 2018, the Department was awarded in excess of $24 million in sponsored funding (research, training and public service) and ranks in the top five largest units at the University of North Carolina at Chapel Hill in the area of sponsored research awards. The Department's current faculty consists of 67 regular full-time faculty and 146 adjunct faculty members. The Department has 209 graduate students enrolled, including 11 in the MPH program, 20 in the MSCR program and 178 in the Ph.D. program.

The Department of Epidemiology is headquartered in the four-story McGavran-Greenberg Building adjacent to Rosenau Hall across the street from the School of Medicine. The epidemiology administrative and office space occupies (b) (4) sq. ft. and provides additional classroom space. Most of the department's research staff occupies a research annex consisting of approximately (b) (4) square feet of contiguous rental space in a commercial office building that is a 10-m nute walk from McGavran/Greenberg Hall.

Information Technology Access

The Department of Epidemiogy is equipped high speed internet access and has several IBM and Apple Pentium II/III computers with accompanying software. The university has an Information Technology Services department that dedicated to delivering reliable, secure and satisfying information technology capabilities and experiences to the University.

Biological Sample Storage and Access

Dr. Baric has three laboratories of (b) (4) sq. ft. equipped as BL2 space for the molecular biology, virology, immunology and recombinant DNA techniques proposed in the application in Hooker Research Center. Equipment includes gel electrophoresis equipment, power supplies, thermal cyclers, a programmable heat block, heat blocks, water baths, CO2 incubators (2), several 70oC freezers, one 140oC freezer, refrigerators, DNA documentation system, DNA sequencing and computer assisted sequence analysis programs, several microfuges, two Nikon microscopes w th photographic and fluorescent capabilities, several class 2 environmental hoods, refrigerated water baths, several IBM and Apple Pentium II/III computers with accompanying software, three thermocyclers, a fume hood, Nuclisens reader, hybridization oven, real time thermocyclers, three fluorescent inverted scopes with computer software (Olympus IX51), and a spectrophotometer. A Roche Light Cycler 480II is available for real time measurements. The laboratory has an ELISA plate reader, an illuminometer, 200 cages for animal maintenance and breeding in Seal-Safe housing, Bio Rad low pressure chromatography system, ELISA plate washer, spectrophotometers, and other equipment that is routinely used in characterizing antibody-protein interactions.

The Baric laboratory contains an additional (b) (4) square feet of newly renovated or new BSL3 facilities with enhanced features including 1) shower in/shower out facility, 2) dual anteroom access, 3) Hepa filtered exhaust, 4) redundant exhaust fans, 4) Card key access, alarm system to Public Health/Campus Police, Lab controlled combination lock, and 5) Techniplast SealsafeTM Hepa filtered animal housing for rodents (mice (~300 cages). PAPR and tyvek suits are worn at all times in the BSL3 facility. The BL3 facilities are in an adjacent, attached building (b) (4) or in (b) (4), the latter space is directly adjacent to Dr. Baric s BSL2 laboratory resources. Each facility is equipped with sterile hoods (BSCIIA), four CO2 incubators, gel electrophoresis equipment, thermal cyclers and power supplies, and related equipment necessary for virus cultivation and molecu ar genetic research. The facilities each house a -70C freezer, an inverted Nikon fluorescent microscope with an assortment of filters, magnifications and digital camera, an ELISA plate reader and illuminometer. Both facility contain rodent-sized Seal-Safe systems (~192 cages) for maintaining animals in a Hepa-filtered Air in/out environment, exhausted into the BSL3 Hepa-filtered exhaust system. An 8 chamber Buxco plethysmography system which allows for repetitive, noninvasive measures of the number of breaths, tidal volume, airway responsiveness, enhanced pause, respiratory gases, etc. from live control and infected mice in a contained system is available in the main BSL3 laboratory in (b) (4) (http://www.buxco.com/FinePointe.aspx?Page=FinePointe).

The Department of Epidemiology provides cold-room, autoclave, centralized dishwashing and a darkroom with an automated developer. The campus has central facilities for DNA oligonucleotide synthesis, histopathology, DNA sequencing, EM, light and confocal microscopy, automated PCR genotyping and Taqman facilities, and Fluorescent activated cell sorter facilities (FAC). As a member of the Department of Microbiology and Immunology and UNC Cancer center, our laboratory has access to these facilities and receives discounts. The University provides a variety of core services including: sequencing and deep sequencing cores, genomics cores, oligonucleotide synthesis cores, hybridoma cores, transgenic cores, structural biology cores, etc. typical of any world class research institution. Campus wide core facilities are available for oligonucleotide synthesis, Sanger and 454 sequencing, RNAseq, pathology and histology services, and Flow Cytometry. Approximately, 40,000 cages are available for CC RIX production in the (b) (4) on UNC Campus.

Duke-NUS Medical School, Singapore (Drs. Wang and Anderson)
The laboratory of One Health Approach to EID at Duke-NUS Medical School Singapore is headed by Professor Lin-Fa Wang. The lab consists of 8 post-doctoral fellows, 4 research assistants and 3 MD-PhD students. Professor Wang is Director, Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore. His proven track record in the field includes identifying the bat origin of SARS-CoV, and pioneering work on Henipaviruses. His work has shifted from identifying the bat-origin of pathogens to understanding basic bat biology and the mechanisms by which they can endure sustained virus infection. Professor Wang currently heads and administers a Singapore National Research Foundation grant entitled "Learning from bats".

Assistant Professor Danielle Anderson is the scientific director of the ABSL3 facility at Duke-NUS and is an expert in RNA virus replication She has extensive experience in molecular biology, high throughput screening and animal models. Assistant Professor Anderson has performed both human and bat siRNA screens and personally implemented and transferred the siRNA screening protocols from the RNAi facility at Duke University, USA, to Duke-NUS in order to establish capacity in Singapore. Additionally, Assistant Professor Anderson has established pathogenesis models in Singapore, using different species (non-human primates, ferrets and bats) and inoculation routes (such as mosquito inoculation), and has performed animal trials in both ABSL2 and ABSL3 containment facilities.

Information Technology Access
Duke-NUS is supported by the National University of Singapore's dedicated IT department, NUS Information Technology, that employs over 200 staff providing reliable, high-performance IT infrastructure and services for NUS. Duke-NUS is well-equipped with high speed internet access and computers with relevant software.

Biological Sample Storage and Access
The Duke-NUS Animal Biosafety Level 3 Facility consists of three laboratories with support space occupying a gross floor area of (b)(4) square meters. The facility is fully equipped to conduct ABSL3 experiments ranging from in vitro experiments to large animal studies. The facility consists of three laboratories, one lab for in vitro and molecular work, one lab for housing small animals in isolator cages and one lab for large animals (non-human primates, ferrets, bats). The laboratory where the non-human primates are housed is equipped with Air Pressure Resistant doors to allow housing of large animals in open cage housing, and is the first of this kind in Singapore. The facility also contains of support areas including shower rooms, autoclaves, tissue digester and effluent decontamination system.

Duke-NUS Genome Biology Facility: This facility is setup to cater to the needs of researchers who are interested in using high end genomics technology such as microarray and next generation sequencing. The goal of the facility is to enhance biomedical research through genomic technology. Duke-NUS Genome Biology Facility is constantly upgrading to newer technology to provide researchers with more flexibility to choose the technology and platforms that best suit their projects. The core facilities and services includes: Human Genome U133 Plus 2.0 array and Gene Chip Mouse Genome 430 2.0 array expression profiling services, HumanHT-12 v4 and MouseWG-6 v2 Expression profiling services, HumanMethylation27 assay profiling service, Full RNA-Seq service, sequencing service, total RNA quality assessment service and Agilent Unrestricted Human Microarray miRNA v14 Rev.2 expression profiling service.

Uniformed Services University, Bethesda, USA (Drs. Broder and Laing)
Uniformed Services University (USU) is the medical school at which approximately half of the physicians in the Armed Services receive their graduate training. Research at USU is supported primarily by extramural grants, as in other medical schools. Dr. Broder is a tenured Professor in the Department of Microbiology and Immunology and is also the Department Chair, which includes 12 full-time Faculty members. The overall focus of the Department is mechanisms of infectious diseases and the host response/immunology. Faculty interests and active research programs at USU are diverse, with many nationally- and internationally-known investigators. Dr. Broder has had and is currently involved in active collaborations within the University, in areas of viral immunology and vaccine and antiviral therapeutics and animal model development (with Dr. Joseph Mattapallil and Dr. Brian Schaefer). USU is also physically located directly across from the main NIH campus in Bethesda, Maryland. The overall broad scientific environment at both USU and the NIH is highly conducive to productive collaborations. Dr. Broder often uses these resources to his advantage, both for his

research objectives and interests, but also in his role as Chair and as the former Director of the Emerging Infectious Diseases Graduate Program (for the Ph.D.) because he has activity recruited adjunct faculty appointments within the EID graduate program for both on and off-campus scientists interested in participating in graduate education and graduate student training. Dr. Broder submits such appointments requests through the Office of Dean of the Medical School (USU). The USU/EID program can accept 5 fully supported student positions per academic year, for 3 years, at which time the student's mentor begins support, and there is no tuition or fees associated with the EID program. The PI has an office separate from, but across from the laboratory. Two full-time administrative assistants and two full-time program managers are available to provide support within the department. Overall, the available technical resources (and University support for continually improving technical resources) is exceptional.

Information Technology Access

USU is equipped with a pentium computer, scanners and two laser jet printers in the PI's office and 9 windows based computers in the laboratories/offices are connected by a central server to each other and to the Internet. A variety of USU-supported software programs are available, including EndNote, Microsoft Office, Adobe Creative Cloud, Geneious 9.15 and Graph Pad Prism 6.0. The University also has an equipment repair service, central duplicating service, audiovisual service, and microcomputer support service. The University Learning Resource Center is a high quality medical and scientific library with additional microcomputers and support. A wide variety of scientific journals are available in print and via remote computer access.

Biological Sample Storage and Access

The PI's laboratories are divided into 3 rooms totaling (b) (4) sf, and are equipped with eight CO2 incubators for tissue culture, 4 inverted and 1 bright field microscopes, high speed and ultracentrifuges, four biological safety cabinets, 2 -20°C, 3 -80°C freezers, 4 liquid nitrogen freezers 6 refrigerator/freezers, 4 PCR machines, 2 ELISA plate reader, and various small equipment items (gel electrophoresis, circulating adjustable water baths, heat blocks). 2 complete GE-ATKA low pressure chromatography systems, with integrated UV detectors, fraction collectors, and pump systems, and gradient fractionator apparatus. A central autoclave/glassware washroom serves the Department of Microbiology and Immunology and is maintained through extramural grant support.

Animal: Animals if applicable are maintained in the University's laboratory animal facilities under the supervision of a full-time veterinarian. These facilities are a modern AAALC accredited, central animal tract of about (b) (4) sq. ft. The animal care and use program is managed by the Department of Laboratory Animal Medicine which is directed by a veterinarian who is an ACLAM Diplomat and staffed with one other veterinarian, a graduate animal husbandryman, and about 30 technicians.

National Emerging Infectious Diseases Laboratories (NEIDL), Boston, USA (Drs. Keusch and Corley)

The National Emerging Infectious Diseases Laboratories (NEIDL) is housed on the Boston University Medical Campus within close proximity to the School of Medicine, School of Dental Medicine and School of Public Health and their associated research facilities, and Boston Medical Center, the principal teaching hospital for the medical school. The Medical Campus also houses major Core facilities and includes an extensive Animal Science Center which includes animal facilities for BSL-2 and BSL-1 animal work. In addition to Basic Sciences and Clinical Departments, the Medical Campus also includes the Center for Regenerative Medicine, the Center for Network Systems Biology, and the Clinical and Translational Science Center. The Boston University Medical Campus is a short shuttle bus ride from the Boston University Campus on the Charles River. The BU campus includes the School of Engineering and its Biomedical Engineering Department and its Biologic Design ("synthetic biology") group, and the Hariri Institute for Computing and Computational Science. Major research programs in the Department of Chemistry and the Department of Biology are also of importance to the goals of the NEIDL, as is the Bioinformatics Graduate Program which is managed from the Charles River Campus. Boston University is a highly interactive and collaborative environment which is supported by the University administration to ensure that artificial barriers to success are removed and do not hamper innovation in research. Office spaces for faculty and staff are integrated throughout the NEIDL. Most faculty have offices in administrative spaces adjacent to the BSL-2 laboratories. Administrative support is provided and is supported by the administrative infrastructure of the University. All offices are accessible in an environment secured via proximity card and iris scan access.

Information Technology Access

All laboratories are serviced by the Boston Jniversity IS&T group, with the exception of those services that are uniquely required for work within the NEIDL and are managed by the IT Core staff dedicated to the NEIDL. This includes building automation systems and select agent inventory control which are managed in a safe and secure network environment. Computational resources for individual faculty and staff are augmented by the BU Shared Computing Cluster which is maintained by BU and its consortium in Holyoke, MA, site of the LEED Platinum certified MA Green High Performance Computing Center (MGHPCC). Two pairs of 10 Gigabit Ethernet network connections between the MGHPCC and the BU campus connect the two locations. The system currently includes over 2600 shared processors, over 5100 buy-in processors, a combined 244 GPUs, and petabytes of redundantly backed up storage

Facility security: The Public Safety Core supports the NEIDL's mission by providing a safe and secure environment with particular attention to risks, threats and vulnerabilities. Public Safety personnel are well trained in the intricacies of a secure site, criminal applications and a significant amount of training pertaining to safety, facilities, emergency preparedness and response, biosafety incidents, animal rights activism and coordinated notification and response of external local, state and federal responders. The Public Safety Core monitors and audits all areas of access, and manages personnel suitability on a continual basis to ensure regulations are adhered to, as well as 24/7 management of the environment with police-academy-trained officers. Core managerial staff have developed a comprehensive set of Public Safety Standard Operating Procedures, consistent with BUMC-wide policies and procedures, which meet and/or exceed all applicable federal, state, and local regulations (NIH BMBL, OSHA, CDC, NRC, MWRA, DEP, BFD, etc). In addition, they manage the process of background checks (CORI) and drug screening for staff in order to ensure that recruitments are consistent with security requirements.

Interfacing with other support offices at Boston University: The operational core services offered in the NEIDL benefit from the additional infrastructure on the Boston University Campus, which not only contribute significant expertise but also provide services that we do not need to duplicate. For example, the IT services in the NEIDL are supported by a large BU Information Services and Technology Team that insures expert IT services are provided, and we have in house IT experts who are also trained to work within the containment facilities Similarly, our Environmental Health & Safety core is supported by a larger EH&S group within the University, and Emergency Response is supported by a University wide ER group which has long experience working with local, state, and national responders. The Community Relations Services are integrated with BU campus-wide services which include the Office of Government and Community Affairs, while our Occupational Medicine Program is supplemented by a larger Research Occupational Health Program at the University.

Biological Sample Storage and Access

The National Emerging Infectious Diseases Laboratories (NEIDL) is designed to provide safe working conditions for handling pathogens at every biosafety level, including biosafety level 2 (BSL-2; (b)(4) sq.ft.), BSL-3 (b)(4) sq.ft.) and BSL-4 (b)(4) sq.ft). This includes laboratories and animal facilities for infectious diseases research at all containment levels. BSL-2 spaces include imbedded cell culture and pathogen propagation suites as well as BSL-2+ laboratory suites that can be upgraded to BSL-3 as needed. Support spaces includes shared rooms for instrumentation, chemical storage, cold rooms and dark rooms. The BSL-3 facilities include 5 independent suites that integrate into a central corridor from which 8 animal suites, each with its own procedure space, can be accessed. The BSL-4 facilities include 6 laboratory suites and 7 independent animal study spaces, each with its own procedure space for support of animal related experiments on emerging infectious diseases Laboratory spaces are accessed by approved personnel and controlled through proximity card and biometric access.

Full-length cDNA clone laboratory (BSL-2): The NEIDL has dedicated laboratory space with secured access to conduct work with full-length cDNA clones of filoviruses and henipaviruses. This laboratory is equipped for all contemporary cloning work including growth of transformed bacteria. The full-length cDNA work at the NEIDL has been approved by NIH, Boston Public Health Commission, and BU IBC.

Animal: The Laboratory Animal Science Center (ASC) at Boston University has been an AAALAC accredited animal care program since 1971. Animals are housed in a state-of-the-art facility run by licensed veterinarians supported by a large technical staff. All individuals involved in animal research are trained in proper animal

handling, dissection, anesthesia and euthanasia techniques as described and approved by the Institutional Animal Care and Use Committee (IACUC) protocol(s). The Animal Services component of the NEIDL are integrated into the larger Animal Sciences Center, under the direction of the Attending Veterinarian.

Animal study rooms in the NEIDL are designed for use with multiple species of animals and can each accommodate 900 mice (in microisolators), 216 guinea pigs (in microisolators), 72 ferrets (in specially designed isolator housing) and 12-16 non-human primates.

Insectaries: The NEIDL includes spaces for the integration of insectaries into the containment laboratories. There is a functioning insectary for mosquito transmission studies at ACL-2 and ACL-3. The insectary has 4 dedicated rooms that permit the isolation of infection studies from the areas designed for rearing mosquitoes, and integrates with the necessary animal facilities. A 3 room suite for vector transmission studies using ticks can be activated in the future.

Transport of select agents: All biohazards that are shipped or received for these approved projects are mandated to meet the standards of the High Hazard Materials Management policy, which states that BUMC will meet or exceed all applicable shipping regulations under the requirements of the U.S. Department of Transportation (DOT) and the International Air Transportation Authority (IATA). The BUMC Office of Environmental Health and Safety and Public Safety have responsibility for managing the transportation process for select agents and have contracted with appropriate transportation vendors which utilize screened personnel and GPS tracking systems and which can provide an all-inclusive chain of custody document for each shipment.

Thai Red Cross Emerging Infectious Diseases Health Science Centre (TRC-EID), Faculty of Medicine, Chulalongkorn University Hospital, Thailand (Drs. Hemachudha and Wacharapluesadee)

TRC-EID is a Bangkok-based non-profit institution that conducts scientific research on emerging zoonoses and regional laboratory capacity building. TRC-EID has (b) (4) square feet of office space, including a meeting room, and fully equipped laboratory. The medical doctors (3) and scientific staff (17 core scientists/field staff) is supported by a core admin staff of 3 and one IT staff who are available for work on this project. TRC-EID supports diagnostic facilities at its laboratories for both infectious and non-infectious diseases.

TRC-EID has worked with over 20 partners. This network includes staff from: academic institutions at leading national universities; intergovernmental agencies (WHO, OIE, FAO, BTRP/DTRA); infectious disease surveillance laboratories; national government agency offices and labs; locally-based wildlife conservation organizations. TRC-EID is the government's reference laboratory for all emerging infectious diseases and s a WHO Collaborating Centre for Research and Training on Viral Zoonoses, responsible for capacity building and strengthening laboratories in the region.

Information Technology Access

Thai Red Cross Emerging Infectious Diseases - Health Science Centre (TRC-EID) have necessary software including Bioinformatic tools (Blast Standalone, SAMTOOL, GATK, AliVIEW, RaxML, FigTREE, MAFFT, Guppy, Megan, PoreChop, MEGA), Database (MySQL, MongoDB) Web, jQuery, Node.js, Express js React, API, PHP, Ruby, Python, Java, C#, HTML5, Bootstrap, CSS, Responsive, Cloud, Linux Command, PACS (sample management system), Virtualbox virtual machines, R programming languages, Perl scripts, Bash shell scripts, Open source software, Microsoft Office running on both Apple Mac OS X, Ubuntu, Linux, and Windows Operating Systems. TRC-EID has a dedicated 16-core Ram 64GB Linux server with 4TB hard drives, dual quad-core Mac Pro Server with 2TB hard drives and another dedicated iMac Pro (Retina 4K, 21.5-inch, 2017) Processor 3.6GHz quad-core Intel Core i7 (Turbo Boost up to 4.2GHz) Ra, 16GB with 512GB hard drives. TRC-EID also has HPC Linux server CPU: 4 x 26cores Intel Xeon = 104 cores 2.1GHz with 52 TB HHD and 2x3.84TB SSD with GPU 2x Tesla v100 (CUDA core = 5120 cores/GPU, Tenser core = 640 cores/GPU). TRC-EID has a dedicated 10/100/1000 of LAN (Local Area Network), 2.4G / 5G Gigabit Wi-Fi 802.11ac.

Biological Sample Storage and Access

All samples collected as a result of project activities will be stored at TRC-EID. TRC-EID will be responsible for data management and analysis. TRC-EID is equipped with BSL-2 and BSL-3 level facilities.

Conservation Medicine Ltd, Kuala Lumpur, Malaysia. (Mr. Hughes, Ms. Lee, Mr. Lee)
Conservation Medicine Ltd. (CM), was incorporated in 2014 in Kuala Lumpur, Malaysia, and is run as a non-profit directed by Mr. Tom Hughes who has worked with EcoHealth Alliance (EHA) since 2005. CM employs a Lab Coordinator (Mei Ho Lee) and Field Manager (Jimmy Lee), who have worked together with EHA since 2009 to implement field and lab projects including activities under the USAID Emerging Pandemic Threats: PREDICT program and the USAID Infectious Disease Emergence and Economics of Altered Landscapes (IDEEAL) project. CM employs; 1 Administrative Assistant to help coordinate the logistics of projects, assist with data entry and communicate with partners; 5 rangers who have worked together with EHA since April 2017 and a Veterinarian who joined the team in November 2017 to carry out field work in PM and Sabah with our government partners; a lab manger to run the Wildlife Health, Genetic and Forensic Laboratory (WHGFL) established in collaboration with Sabah Wildlife Department (SWD) and 3 lab techs who conduct disease testing at our government partner laboratories.

Information Technology Access
CM is equipped with office space, laptop computers, internet, mobile phones, GPS units, and three 4WD vehicle fully equipped for field transportation to remote field sites (two in Peninsular Malaysia and one in Sabah). CM maintains wildlife capture equipment and supplies for biological sample collection from humans and animals and liquid nitrogen dry shippers for ensuring cold chain during transport of biological samples from field to lab for both PM and Sabah. CM has supplies of personal protective equipment for all field and lab staff, including PAPRs and N95 respirators, gloves and disposable coveralls. CM maintains close communication with Ministry of Health and the National Public Health Laboratory (NPHL), Department of Wildlife and National Parks (DWNP), Faculty of Veterinary Medicine Universiti Putra Malaysia (FVMUPM), Department of Veterinary Services, SWD, Sabah State Health Department, Kota Kinabalu Public Health Laboratory (KKPHL) and Universiti Malaysia Sabah on behalf of EHA, and CM staff work closely with government partners to implement PREDICT, IDEEAL and DTRA field and lab activities.

Biological Sample Storage and Access
CM helped establish and manages the SWD WHGFL (certified as a BSL- 2 laboratory according to the US standard for laboratory specifications) that has all the equipment necessary to store samples, run extractions, PCR and analysis on biological samples for disease surveillance. The lab is used to conduct health checks on rescued and relocated wildlife before being released into new areas or sanctuaries, to screen samples for the PREDICT and Deep Forest Project and for genetic research and forensic investigations. CM also helped establish the new molecular zoonosis laboratories (certified as a BSL- 2 laboratory according to the US standard for laboratory specifications), at DWNP's National Wildlife Forensic Laboratory. The lab is used to screen samples for the PREDICT & DTRA projects. In addition CM also has access to NPHL and KKPHL for screening human samples and the Virology lab at FVMUPM for screening Livestock samples.

Borneo Medical and Health Research Centre (BMHRC), Universiti Malaysia Sabah, (Dr. Kamruddin & Dr. Lasimbang)
Borneo Medical and Health Research Centre (BMHRC) is a centre of excellence that conducts teaching and scientific researches on communicable diseases, outbreak investigations, and ethnomedicine. BMHRC has offices space including a meeting room and seven laboratories which including preparation lab, parasitology lab, cell culture lab, bacteriology lab, natural product lab, virology lab, and molecular biology lab. BMHRC is supported by an administration staff, medical lab technologist, and research assistants who are available to work on projects. BMHRC leading research centre in Sabah that is internationally recognized for its excellent research on tropical endemic diseases and improving human health.

BMHRC has a global network of 10 research partners which are the Ministry of Health, Malaysia, Sabah State Health Department, Kota Kinabalu City Hall, Nagasaki University, Zunyi Medical University, National University of Singapore,Adtec Corporation, Oita University, Tottori Nursing College, and EcoHealth Alliance.

Information Technology Access
BMHRC equipped with LAN and wireless internet access. BMHRC users also have around-the-clock access to servers, VPN, encryption software, IT support, and all necessary software. Software such as Oracle Virtualbox virtual machine, Google Apps, Node JS, R programming languages, Bash shell script, Microsoft Office and Open Office can be accessed at the Centre. BMHRC dedicated ion torrent performance computer with 11 TB

hard drive, 49 GB of RAM, and dual Xeon processor with 24 cores. BMHRC has also Ubuntu Linux and Window Operating System.

Biological Sample Storage and Access
BMHRC has a laboratory equipment facility such as light microscopes, incubators, shaking incubator, magnifying lamp, -80°C freezer, refrigerator for reagents (4°C), refrigerated centrifuge, thermal cyclers, next generation sequencer (ion torrent), water bath, laminar air flow, digital droplet PCR, flow cytometer, and autoclave machine.

Queen Elizabeth Hospital (QEH), Kota Kinabalu, Sabah, Malaysia (DrsHeng Gee Lee and Giri Shan Rajahram)
The Infectious Diseases (ID) Unit and Clinical Research Centre (CRC), Queen Elizabeth Hospital conduct scientific researches on infectious diseases. The ID Unit consists of a twenty bedded ward and an infectious disease clinic. The unit is headed by an ID Consultant together with a Medical Specialist and six Medical Officers. The CRC staffs consist of two Medical Officers, 1 pharmacist, 2 research officers, 2 registered nurses, 1 administration assistant, and 1 operation assistant.

Information Technology Access
CRC QEH is equipped with internet access and video conferencing facilities to facilitate communication between collaborators. CRC QEH has important software including Microsoft Office and Stata 12 running on Windows Operating Systems.

Biological Sample Storage and Access
The CRC office space includes a meeting room and basic laboratory which contains a -86°C freezer, centrifuges x 2, refrigerated centrifuge x1, -20°C freezer x 1, a household fridge, pharmaceutical refrigerator x 2 (4-8 °C) and a portable incubator.

Sabah State Ministry of Health and Infectious Diseases Society of Kota Kinabalu, (A/Prof Yeo Tsin Wen)
The Sabah State Ministry of Health is responsible for the clinical care for the Malaysian State of Sabah which an estimated population of 3.5 million. Hospital care is provided by 14 Hospitals (2 Tertiary and 12 District Hospitals) and outpatient care through an extensive network of outpatient polyclinics. These facilities are located throughout the State including several in near proximity to primary and secondary rainforest with a high degree of biodiversity. These facilities can be selected for the clinical studies depending on the areas assessed to be at high risk for viral zoonotic crossover.
There is also a Clinical Research Centre (CRC) attached to the Sabah Ministry of Health which will assist in the conduct of clinical studies in these facilities, including ensuring it is done according to good clinical practice, (GCP).

The Infectious Diseases Society of Kota Kinabalu (IDSKK) is a non-governmental organization who in collaboration with the Sabah Ministry of Health conducts clinical infectious diseases research of relevance to Sabah.

Information Technology Access
The Sabah State Ministry of Health and Infectious Diseases Society of Kota Kinabalu both are equipped with high-speed internet access that allows for communication across international partners. The administrative office at IDSKK has Microsoft Office access and also access to clinical data management platforms such as REDCAP.

Biological Sample Storage and Access
IDSKK currently has 6 administrative and 4 laboratory staff and is based in Kota Kinabalu. The laboratory in Kota Kinabalu has a BSL-2 biosafety hood for sample processing, ultra-low freezers and liquid nitrogen freezers, multiple centrifuges, microscopes and PCR machines. Outside of Kota Kinabalu, it also has biosafety hoods, ultra-low/liquid nitrogen freezers and centrifuges which are mobile and can be located at selected health facilities within the state. The mobility was demonstrated in several collaborative studies funded by Australian and European funders where the laboratory facilities were relocated several times. The logistical

chain with the main laboratory in Kota Kinabalu was also demonstrated during these projects with samples transported back from various district hospitals using transport provided by the Sabah Ministry of Health and local means.

Nanyang Technological University (NTU) - Lee Kong Chian School of Medicine, Singapore (A/Prof Yeo Tsin Wen)

Nanyang Technological University, Lee Kong Chian School of Medicine currently employed about 400 staffs, which includes researchers and faculty members. It occupies two buildings, Experimental Medicine Building and Clinical Sciences Building, in which they are situated in Nanyang Technological University, 59 Nanyang Drive Singapore 636921 and at Novena, 11 Mandalay Road, Singapore 308232 respectively. The information technology available is similar to that detailed above for EcoHealth Alliance.

Information Technology Access

Nanyang Technological University, Lee Kong Chian School of Medicine is equipped Internet access and video conferencing facilities to facilitate easy communication between collaborators. The University provides IT and AV assistance through its Information Technology department.

Biological Sample Storage and Access

NTU has various facilities integrated in the school relevant for this study. They are namely multiple BLS-2 level facilities, dedicated samples processing rooms for viral and pathogens and multiple sequencers (Illumina Mi-SEQ and Oxford Nanopore Platforms) with bioinformatics support. The University also has a biobank facility that aims to provide a facility to aid researchers to store biological specimens for future clinical research purposes. The biobank currently holds several ultra-low freezers and liquid nitrogen freezer at Experimental Medicine Building and Clinical Sciences Building. These will all be available for the study if required for sample processing, sample storage and sequencing.

Other core facilities available for use include Flow Cytometry Facility, histology core facility and medical imaging.

Major Equipment

EcoHealth Alliance, New York, USA (Drs. Daszak and Olival)
EcoHealth Alliance is equipped with fiber optic Internet access and video conferencing facilities to facilitate easy communication between collaborators. EcoHealth Alliance employees have around-the-clock access to servers, VPNs, encryption software, IT support, and all necessary software including Git and Github (Hosted software revision/audit service), Sublime and Vim text editors, Vagrant and Oracle Virtualbox virtual machines, Google Apps (Hosted email and collaboration web based software), Ansible (Server provisioning software framework), Python, NodeJS, and R programming languages, Meteor (Javascript framework), Bash shell scripts, Jenkins (Continuous Integration server), Microsoft Office and Adobe CS6 running on both Apple Mac OS X, Ubuntu Linux, and Windows Operating Systems. EcoHealth Alliance has a dedicated quad-core Linux server and another dedicated dual quad-core Mac Pro Server - each with 4TB hard drives. Either server individually or in combination may be used for intensive computational modeling and/or database processing by all the grantees. Access to the cloud and supercomputing services (Amazon) is provided by core funding to EcoHealth Alliance.

University of North Carolina, Chapel Hill, USA (Drs. Baric and Sims)
BSL2 Facility. Equipment includes gel electrophoresis equipment, power supplies, thermal cyclers, a programmable heat block, heat blocks, water baths, CO_2 incubators (2), several -70°C freezers, one -140°C freezer, refrigerators, DNA documentation system, DNA sequencing and computer assisted sequence analysis programs, several microfuges, two Nikon microscopes with photographic and fluorescent capabilities, several class 2 environmental hoods, refrigerated water baths, several IBM and Apple Pentium II/III computers with accompanying software, three thermocyclers, a fume hood, Nuclisens reader, hybridization oven, real time thermocyclers, three fluorescent inverted scopes with computer software (Olympus IX51), and a spectrophotometer. A Roche Light Cycler 480II is available for real time measurements. The laboratory has an ELISA plate reader, an illuminometer, 200 cages for animal maintenance and breeding in Seal-Safe housing, Bio Rad low pressure chromatography system, ELISA plate washer, spectrophotometers, and other equipment that is routinely used in characterizing antibody-protein interactions.

BSL 3 Facility. The BL3 facilities are in an adjacent, attached building [redacted] (b) (4) and in [redacted] (b) (4), the latter space is directly adjacent to Dr. Baric's BSL2 laboratory resources. Each facility is equipped with sterile hoods (BSCIIA), four CO_2 incubators, gel electrophoresis equipment, thermal cyclers and power supplies, and related equipment necessary for virus cultivation and molecular genetic research. The facilities each house a -70C freezer, an inverted Nikon fluorescent microscope with an assortment of filters, magnifications and digital camera, an ELISA plate reader and illuminometer. Both facility contain rodent-sized Seal- Safe systems (~192 cages) for maintaining animals in a Hepa-filtered Air in/out environment, exhausted into the BSL3 Hepa-filtered exhaust system. An 8 chamber Buxco plethysmography system which allows for repetitive, noninvasive measures of the number of breaths, tidal volume, airway responsiveness, enhanced pause, respiratory gases, etc. from live control and infected mice in a contained system is available in the main BSL3 laboratory in [redacted] (b) (4).

Duke-NUS Medical School, Singapore (Drs. Wang and Anderson)
Laboratory of One Health Approach to EID: It is fully equipped with 2 biological safety cabinets, cell culture incubators, RT-PCR, freezers, centrifuges that are required to conduct the experiments described in the proposal.

Duke-NUS Emerging Infectious Diseases Research Programme: The Emerging Infectious Diseases Signature Research Program provides common equipment for PIs for their research in emerging infections. The list of equipment is exhaustive, including but not limited to the following: Bio-Rad Bioplex 200, Cell Disrupter, Centrifuges, Cytospin, Electroporation system, ELISA reader, FPLC, Freezers, Gel Documentation system, incubators, microplate reader, microplate washer, inverted fluorescence microscope, upright fluorescence microscope, Real-Time PCR, refrigerator, pH meter, protein crystallography system, PryoMark Q96D, Rotor Gene Q, QIAxtractor, Nanodrop, Speedvac system, 96 well thermocyclers, vacuum pump motor, vacuum aspiration system, Qiacube, Beckman Coulter Counter, Luminex, bacteria shaker incubators.

Duke-NUS Institutional shared resources: The shared equipment provided by Duke-NUS for use by any researcher in Duke-NUS includes but are not limited to: Applied Biosystems HT7900 RT-PCR, Beckman Coulter AcT Diff Automated Cell Counter, Beckman FC500 Flow Cytometer, Scintillation Counter, Biorad Benchmark Plus Microplate Reader, Biorad CFX96RT PCR, FACS analyser, Spectrophotometer, ImageQuant, Confocal Microscope, Nanodrop, Fluorescent Microscope, Stereozoom microscope, Cellomics high throughput microscope and ABSL3 containment facilities.

Uniformed Services University, Bethesda, USA (Drs. Broder and Laing)

The Biostatistics Consulting Center (BCC), a service of the Department of Preventive Medicine and Biometrics, provides statistical consulting to USUHS scientific investigators. We routinely consult with Cara Olsen, Research Assistant Professor (the full-time Biostatistics Consultant of the BCC), regarding proper design of experiments for statistical testing and for statistical analysis of the resulting data.

The USU Translational Imaging Facility (TIF) houses state-of-the art equipment for live animal imaging, including a Siemens Inveon SPECT/PET/CT Scanner, a Bruker Biospec 70/20 USR Magnetic Resonance Imaging system, and a Bruker In-Vivo Xtreme II bioluminescence and X-ray imaging system.

The USU Biomedical Instrumentation Center (BIC) houses core equipment for use by investigators throughout the University. Instrumentation is available either free or on a fee-for-service basis, depending on which instruments have annual service contracts (which are paid largely through per-hour use fees). The BIC Flow Cytometry Core includes two Becton-Dickinson (10- and 13-parameter) LSRII FACS analyzers, one 15-parameter FACSAria FACS sorter, and one Amnis Image Stream X Mark II imaging flow cytometer, as well as off-line analysis workstations.

The BIC Imaging Core houses three confocal microscopes, including a Zeiss 700 inverted system with 405/458/488/514/561/633 laser excitation; a Zess 710NLO inverted system with 405/458/488/514/561/633 conventional lasers and a Coherent Ultra2 Ti-Sapphire laser for multiphoton excitation, continuously tunable over the range of 690 to 1080 nm; and a Zeiss AxioExaminer-Z1 upright microscope equipped with a direct-coupled Coherent Chameleon tunable infrared laser for ex vivo and in vivo mutliphoton imaging projects. A Becker-Hickl two-detector FLIM system (for FRET analyses) is connected to the inverted Zeiss 710NLO system. Recently, the BIC has also acquired a Zeiss Elyra PS.1 super-resolution microscope, which is capable of 4-parameter SR-SIM (super-resolution structured illumination) imaging, 3-parameter PALM (Photoactivation localization microscopy) and dSTORM (direct stochastic optical reconstruction microscopy), as well as 3D-PALM/dSTORM. The BIC also houses a Leica AF6000 system, consisting of an inverted microscope equipped with a fully motorized 3-axis stage plus atmosphere and temperature control, allowing extended term (days) live cell analyses. Additionally, there is a stereology system consisting of a Zeiss AxioImager.M2 upright microscope connected to MicroBrightField's Stereo Investigator software package. The facility also includes several additional wide-field fluorescence microscopes, and three offline data analysis stations with software packages including: Zeiss Zen software and full Physiology package; Media Cybernetics' 3D Constructor, Image Pro Analyzer, Autodeblur, and Autovisualize; Metamorph Basic. The Imaging Core also includes a transmission electron microscope (Philips CM100 transmission EM) and an ultramicrotome (Leica EM UC6 with EM FC6 cryo attachment).

The BIC Genomics core includes an ABI 3900 DNA synthesizer, an ABI3500xl Genetic Analyzer (for sequencing), a RochLightCycler 480 for real-time PCR, and Systec Mediaprep and Plate Pourer instrument. There is also an integrated Fuji FLA-5000/LAS-3000 imaging system for many applications that involve fluorescence and chemiluminescence imaging of gels and blots. The BIC Proteomics Core includes two Agilent 1100 HPLCs, an AB SCIEX Voyager DSTR MALDI-TOF mass spectrometer, and an AB SCIEX Q-TOF tandem mass spectrometer.

The BIC Structural Biology Core includes a Rigaku HighFlux HomeLab X-ray diffraction system, with a MicroMax-007 HF microfocus rotating anode generator, an R-AXIS Imaging Plate detector, and an X-stream 2000 cryogenic system. Other available BIC instruments and services include histopathology and PET/CT instrumentation for small animal research.

National Emerging Infectious Diseases Laboratories (NEIDL), Boston, USA (Drs. Keusch and Corley)
The NEIDL has much of the major instrumentation necessary to carry out modern virology and microbiology, molecular biology, and immunologically related research. Included are imaging facilities containing a Leica Confocal Microscope, Zeiss 200M with conventional and oil immersion (100x, 63x) lenses and climate-controlled stage and time lapse, mosaic and optical sectioning capacities, a Nikon Ti2-E microscope (equipped with high quality objectives including 100x oil immersion lambda NA 1.45 lens and a Photometrics sCMOS camera), and Biotek Cytation high throughput imaging system with an automated plate loader and Autoquant software, EVOS fluorescent cell imager, and other standard compound and inverted microscopes. For immunological analysis, dedicated flow cytometer analyzers are available (BD LSRFortessa, LSR II), Biorad Bioplex 200 ianalyzers, automated ELISPOT readers, Beckman L90K ultracentrifuges at every biocontainment level, as well as superspeed, micro and tissue culture centrifuges, various plate readers (Tecan M200 and M100), Odyssey CLx infrared imager, ELISA readers, etc.

For nucleic acid analysis the NEIDL has real time PCRs (BioRad qRT-CFX-96, Quantstudio 6) as well as conventional PCR machines, gel box and purification systems, gel documentation systems and all essential molecular biology equipment. For RNA work, dedicated laboratory preparation stations are available, and there is access to Qiagen QiaCubes for automated RNA preparation, sequencers (Illumina MiSeq, MinION nanopore sequencer with two dedicated computers that allow parallel run-and-analysis), and nanodrop and a BioAnalyzer for nucleic acid analysis and RNA quality determination.

For work with animals, instrumentation includes clinical chemistry and hematology systems (Drew Scientific Hemavet 950 FS multi-species automated hematology system, Abaxis Vetscan VS2 and Clinical Chemistry Analyzers, Abaxis Piccolo Xpress Chemistry Analyzer, Abaxis VSpro for coagulopathies. The NEIDL also houses a Bruker 4.7T MRI, CT scan and IVIS scan instrumentation for live animal monitoring. An extensive aerobiology suite with instrumentation allows aerosol delivery of pathogens or therapeutics to animals from mice to non-human primates. Class III glovebox biosafety cabinet and animal transfer modules are in the facility as well.

Thai Red Cross Emerging Infectious Diseases Health Science Centre (TRC-EID), Faculty of Medicine, Chulalongkorn University Hospital, Thailand (Drs. Hemachudha and Wacharapluesadee)
TRC-EID has 28 deep freezers (-80°C), 10 -20°C refrigerators, and 11 standard refrigerators, and our own electric generator for backup. The laboratory is fully equipped with biosafety cabinet class IIs, centrifuges, conventional PCR systems, real-time PCR systems (including fast real-time systems), extraction machines, gel documentation system, dehumidifiers, electrophoresis and NGS (Illumina MiSeq). TRC-EID also has biosafety level III biological glovebox which increases efficiency in working with highly dangerous pathogens without delay. Further, TRC-EID has access to shared facilities with Chula Medical Research Center, Faculty of Medicine, Chulalongkorn University.

Conservation Medicine Ltd, Kuala Lumpur, Malaysia. (Mr. Hughes, Ms. Lee, Mr. Lee)
Conservation Medicine is equipped with office space, laptop computers, internet, mobile phones, GPS units, and three 4WD vehicle fully equipped for field transportation to remote field sites (two in Peninsular Malaysia and one in Sabah). CM maintains wildlife capture equipment and supplies for biological sample collection from humans and animals and liquid nitrogen dry shippers for ensuring cold chain during transport of biological samples from field to lab for both PM and Sabah. CM has supplies of personal protective equipment for all field and lab staff, including PAPRs and N95 respirators, gloves and disposable coveralls. CM maintains close communication with Ministry of Health and the National Public Health Laboratory (NPHL), Department of Wildlife and National Parks (DWNP), Faculty of Veterinary Medicine Universiti Putra Malaysia (FVMUPM), Department of Veterinary Services, SWD, Sabah State Health Department, Kota Kinabalu Public Health Laboratory (KKPHL) and Universiti Malaysia Sabah on behalf of EHA, and CM staff work closely with government partners to implement PREDICT, IDEEAL and DTRA field and lab activities.

Borneo Medical and Health Research Centre (BMHRC), Universiti Malaysia Sabah, (Dr. Kamruddin & Dr. Lasimbang)
Borneo Medical and Health Research Centre (BMHRC) is equipped with LAN and wireless Internet access and meeting room facility to facilitate easy communication between collaborators. BMHRC users have around-the-clock access to servers, VPN, encryption software, IT support, and all necessary software. BMHRC also has ion

torrent, high performance computer with 11 TB hard drive, 49 GB RAM, and dual Xeon processor with 24 cores. Along with other equipment or software, BMHRC has complete virtue Ubuntu 16.04 with support bioinformatic and the tools such as Oracle Virtualbox virtual machine, Google Apps, NodeJS, R programming languages, Bash shell script, Microsoft Office and Open Office. Ubuntu Linux and window operating system also provided by core funding to BMHRC.

BMHRC has a laboratory equipment facility such as light microscopes, incubators, shaking incubator, magnifying lamp, -80°C freezer, refrigerator for reagents (4°C), refrigerated centrifuge, thermal cyclers, next generation sequencer (ion torrent), water bath, laminar air flow, digital droplet PCR, flow cytometer, and autoclave machine.

Queen Elizabeth Hospital (QEH), Kota Kinabalu, Sabah, Malaysia (DrsHeng Gee Lee and Giri Shan Rajahram)

The QEH Clinical Research Centre (CRC) is equipped with Internet access and video conferencing facilities to facilitate communication between collaborators. QEH CRC has important software including Microsoft Office, Adobe, and Stata 12 running on Windows Operating Systems. CRC QEH is also equipped with office space, computers, internet, and phones. QEH has supplies of personal protective equipment for lab staff, including N95 respirators, gloves and disposable coveralls.

Sabah State Ministry of Health and Infectious Diseases Society of Kota Kinabalu, (A/Prof Yeo Tsin Wen)

The equipment located in Kota Kinabalu which will be available for the proposed studies include a dedicated research laboratory with the following: a BSL-2 biosafety hood for sample processing, multiple high speed/ normal centrifuges, microscopes, PCR machines, ultra-low freezers and liquid nitrogen freezers. It also has a high speed internet access and dedicated laboratory computers for sample database documentation and record keeping. There is 4 laboratory staff based in Kota Kinabalu who are also rostered to attend to the freezers in case of any power outages or other emergencies.

Outside of Kota Kinabalu, there are additional biosafety hoods, ultra-low/liquid nitrogen freezers and centrifuges which are mobile and can be located at selected health facilities within the state which will be adequate for sample processing and storage for the clinical studies proposed for this project.

For shipment of the samples within the state of Sabah, there liquid nitrogen dry shippers for transport of samples from selected district hospitals or health facilities to the main laboratory in Kota Kinabalu. For overseas shipments, there are also liquid nitrogen dry shippers or commercial couriers available.

Technological University (NTU) - Lee Kong Chian School of Medicine, Singapore (A/Prof Yeo Tsin Wen)

The laboratories in Lee Kong Chian School of Medicine from both schools are equipped with a number of core equipment that are to be shared among the many researchers in the school. Big core equipment includes at least 2 biosafety cabinets on each floor of the 2 buildings, CO2 incubators from Nuaire and ESCO, drying ovens, electroporator, 1 flow cytometer, a number of gel doc system, high pressure homogenizer, a number of incubators from Incucell and Thermo Scientific, water purification system from MilliQ and 2 X-ray film proccessor. The laboratories are also equipped with transilluminators, spectrophotometers, sonicators, QRT PCR and PCR machines and 1 stereomicroscope from Leica.

Common equipment includes a number of autoclaves and cell counters, Bio-Plex multiplex array system, Cobas biochemistry and immunoassay analyser, a number of gyratory rocker, sufficient number of ice machines, a few of Eppendorf vacuum concentrator, quite a number of tissue culture microscopes from Leica for IVD phase contrast, 3 TS100 inverted brightfield and phase contrast from Nikon, 1 TS100 inverted brightfield without phase contrast. Water baths, tube rollers, shaking incubators, centrifuges (high speed, swing bucket and ultracentrifuge), orbital shakers and rotators are provided sufficiently to keep up with the use from each Principal Investigators in Lee Kong Chian School of Medicine.

Specialized equipment includes Histology equipment that includes equipment from Leica: 1 Flattening table, 1 Histology Water Bath, Microsystem – Automated Vacuum Tissue Processor, Tissue Embedding Instrumentation, Cryostat, Motorised Rotary Microtome. We have a few specialized microscopes and they include wide-field

fluorescent upright microscope from Leica, an upright Axio Z2 confocal microscope with LSM 800 2-PMT from Carl Zeiss, Inverted Axio Observer, Z1 confocal microscope with LSM 800 2-GaAsp detector from Carl Zeiss, Ti-E inverted spinning disk confocal system from Nikon as well as a high modality total internal refection microscope from Nikon.

OMB Number: 4040-0001
Expiration Date: 10/31/2019

RESEARCH & RELATED Senior/Key Person Profile (Expanded)

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Attach Biographical Sketch*: File Name: Biosketch_(Daszak,Peter)_EIDRC_RFA-AI-19-2018_(PI-Daszak) v03.pdf

Attach Current & Pending Support: File Name:

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 Received Date: 2019-06-28T16:02:40.000-04:00

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Attach Biographical Sketch*: File Name: Biosketch_(Olival.Kevin)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v03_FINAL.pdf

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Project Role*: Co-Investigator Other Project Role Category:

Degree Type: PHD Degree Year: 1983

Attach Biographical Sketch*: File Name: Biosketch_(Baric,Ralph)_EIDRC_RFA-AI-19-2018_(PI-Daszak)_v03.pdf

Attach Current & Pending Support: File Name:

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Credential, e.g., agency login: (b) (6)

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: PHD Degree Year: 1986

Attach Biographical Sketch*: File Name: Biosketch_(Wang,Linfa)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v03.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Danielle Middle Name Last Name*: Anderson Suffix:

Position/Title*:
Organization Name*: Duke NUS
Department:
Division:
Street1*: 8 College Road
Street2:
City*: Singapore
County:
State*:
Province:
Country*: SGP: SINGAPORE
Zip / Postal Code*: 169857

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login:

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: PHD Degree Year: 2007

Attach Biographical Sketch*: File Name: Biosketch_(Anderson,_Dani)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Supaporn Middle Name Last Name*: Wacharapluesadee Suffix:

Position/Title*:
Organization Name*: Chulalongkorn University Hospital
Department:
Division:
Street1*: 1873 Rama IV Road
Street2:
City*: Bangkok
County:
State*:
Province:
Country*: THA: THAILAND
Zip / Postal Code*: 10330

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login:

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: PHD Degree Year: 2006

Attach Biographical Sketch*: File Name: Biosketch_(Wacharapluesadee,Supaporn)_EIDRC_RFA-AI_19-028_(PI-Daszak)_v02.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Mr. First Name*: Tom Middle Name Last Name*: Hughes Suffix:

Position/Title*:
Organization Name*: Conservation Medicine Ltd.
Department:
Division:
Street1*: 13H Villamas Condo
Street2:
City*: Selangor
County:
State*:
Province:
Country*: MYS: MALAYSIA
Zip / Postal Code*: 47000

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login:

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: Post Grad Diploma Degree Year: 2009

Attach Biographical Sketch*: File Name: Biosketch_(Hughes,Tom)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Christopher Middle Name Last Name*: Broder Suffix:

Position/Title*:
Organization Name*: Uniformed Services University
Department:
Division:
Street1*: 4301 Jones Bridge Road
Street2:
City*: Bethesda
County:
State*: MD: Maryland
Province:
Country*: USA: UNITED STATES
Zip / Postal Code*: 20814-4799

Phone Number*: [redacted] (b) (6) Fax Number:

E-Mail*: c[redacted] (b) (6)

Credential, e.g., agency login:

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: PHD Degree Year: 1989

Attach Biographical Sketch*: File Name: Biosketch_(Broder,Chris)_EIDRC_RFA-AI-19-028_(PI-Daszak).pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Eric Middle Name Last Name*: Laing Suffix:

Position/Title*:
Organization Name*: Uniformed Services University
Department:
Division:
Street1*: 4301 Jones Bridge Road
Street2:
City*: Bethesda
County:
State*: MD: Maryland
Province:
Country*: USA: UNITED STATES
Zip / Postal Code*: 20814-4799

Phone Number*: [redacted] (b) (6) Fax Number:

E-Mail*: [redacted] (b) (6)

Credential, e.g., agency login:

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: PHD Degree Year: 2016

Attach Biographical Sketch*: File Name: Biosketch_(Laing,Eric)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Gerald Middle Name Last Name*: Keusch Suffix:

Position/Title*:
Organization Name*: BU NEIDL
Department:
Division:
Street1*: 620 Albany Street
Street2:
City*: Boston
County:
State*: MA: Massachusetts
Province:
Country*: USA: UNITED STATES
Zip / Postal Code*: 02118-2516

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login:

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: MD Degree Year: 1963

Attach Biographical Sketch*: File Name: Biosketch_(Keusch,Gerald)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf

Attach Current & Pending Support: File Name.

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Ronald Middle Name Last Name*: Corley Suffix:

Position/Title*:
Organization Name*: BU NEIDL
Department:
Division:
Street1*: 620 Albany Street
Street2:
City*: Boston
County:
State*: MA: Massachusetts
Province:
Country*: USA: UNITED STATES
Zip / Postal Code*: 02118-2516

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login:

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: PHD Degree Year: 1975

Attach Biographical Sketch*: File Name: Biosketch_(Corley,Ron)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v03.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Amy Middle Name Last Name*: Sims Suffix:

Position/Title*:
Organization Name*: University of North Carolina at Chapel Hill
Department:
Division:
Street1*: 2107 McGavran-Greenberg Hall
Street2:
City*: Chapel Hill
County:
State*: NC: North Carolina
Province:
Country*: USA: UNITED STATES
Zip / Postal Code*: 27599-7400

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login:

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: PHD Degree Year: 2001

Attach Biographical Sketch*: File Name: Biosketch_(Sims,Amy)_EIDRC_RFA-AI-19-2018_(PI-Daszak)_v03.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Alice Middle Name Last Name*: Latinne Suffix:

Position/Title*:
Organization Name*: EcoHealth Alliance
Department:
Division:
Street1*: 460 W. 34th Street
Street2: Suite 1701
City*: New York
County:
State*: NY: New York
Province:
Country*: USA: UNITED STATES
Zip / Postal Code*: 10001-2317

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login:

Project Role*: Other (Specify) Other Project Role Category: Bioinformatician

Degree Type: PHD Degree Year: 2012

Attach Biographical Sketch*: File Name: Biosketch_(Latinne,Alice)_EIDRC_RFA-AI-19-2018_(PI-Daszak)_v03.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Kendra Middle Name Last Name*: Phelps Suffix:

Position/Title*:
Organization Name*: EcoHealth Alliance
Department:
Division:
Street1*: 460 W. 34th Street
Street2: Suite 1701
City*: New York
County:
State*: NY: New York
Province:
Country*: USA: UNITED STATES
Zip / Postal Code*: 10001-2317

Phone Number*: [redacted] (b) (6) Fax Number:

E-Mail*: [redacted] (b) (6)

Credential, e.g., agency login:

Project Role*: Other (Specify) Other Project Role Category: Field Scientist

Degree Type: PHD Degree Year: 2016

Attach Biographical Sketch*: File Name: Biosketch_(Phelps,Kendra)_EIDRC_RFA-AI-19-028_(PI-Daszak).pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Ms. First Name*: Emma Middle Name Last Name*: Mendelsohn Suffix:

Position/Title*:
Organization Name*: EcoHealth Alliance
Department:
Division:
Street1*: 460 W. 34th Street
Street2: Suite 1701
City*: New York
County:
State*: NY: New York
Province:
Country*: USA: UNITED STATES
Zip / Postal Code*: 10001-2317

Phone Number*: [redacted] (b) (6) Fax Number:

E-Mail*: [redacted] (b) (6)

Credential, e.g., agency login:

Project Role*: Other (Specify) Other Project Role Category: Data Scientist

Degree Type: MEM Degree Year: 2015

Attach Biographical Sketch*: File Name: Biosketch_(Mendelsohn,Emma)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Patrick Middle Name Last Name*: Dawson Suffix:

Position/Title*:
Organization Name*: EcoHealth Alliance
Department:
Division:
Street1*: 460 W. 34th Street
Street2: Suite 1701
City*: New York
County:
State*: NY: New York
Province:
Country*: USA: UNITED STATES
Zip / Postal Code*: 10001-2317

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login:

Project Role*: Other (Specify) Other Project Role Category: Epidemiologist

Degree Type: PHD Degree Year: 2019

Attach Biographical Sketch*: File Name: Biosketch_(Dawson,Patrick)_EIDRC_RFA_AI-19-028_(PI-Daszak)_v02.pdf

Attach Current & Pending Support: File Name.

PROFILE - Senior/Key Person

Prefix: Ms. First Name*: Stephanie Middle Name Last Name*: Martinez Suffix:

Position/Title*:
Organization Name*: EcoHealth Alliance
Department:
Division:
Street1*: 460 W. 34th Street
Street2: Suite 1701
City*: New York
County:
State*: NY: New York
Province:
Country*: USA: UNITED STATES
Zip / Postal Code*: 10001-2317

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login:

Project Role*: Other (Specify) Other Project Role Category: Epidemiologist

Degree Type: MPH Degree Year: 2017

Attach Biographical Sketch*: File Name: Biosketch_(Martinez,Stephanie)_EIDRC_RFA-AI-19-2018_(PI-Daszak) v03.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Aleksei Middle Name Last Name*: Chmura Suffix:

Position/Title*:
Organization Name*: EcoHealth Alliance
Department:
Division:
Street1*: 460 W. 34th Street
Street2: Suite 1701
City*: New York
County:
State*: NY: New York
Province:
Country*: USA: UNITED STATES
Zip / Postal Code*: 10001-2317

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login:

Project Role*: Other (Specify) Other Project Role Category: Senior Program Manager

Degree Type: PHD Degree Year: 2018

Attach Biographical Sketch*: File Name: Biosketch_(Chmura,Aleksei)_EIDRC_RFA-AI-19-028_(PI-Daszak).pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Ms. First Name*: Hongying Middle Name Last Name*: Li Suffix:

Position/Title*:
Organization Name*: EcoHealth Alliance
Department:
Division:
Street1*: 460 W. 34th Street
Street2: Suite 1701
City*: New York
County:
State*: NY: New York
Province:
Country*: USA: UNITED STATES
Zip / Postal Code*: 10001-2317

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login:

Project Role*: Other (Specify) Other Project Role Category: Epidemiologist

Degree Type: MPH Degree Year: 2015

Attach Biographical Sketch*: File Name: Biosketch_(Li,Hongying)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Thiravat Middle Name Last Name*: Hemachudha Suffix:

Position/Title*:
Organization Name*: Chulalongkorn University Hospital
Department:
Division:
Street1*: 1873 Rama IV Road
Street2:
City*: Bangkok
County:
State*:
Province:
Country*: THA: THAILAND
Zip / Postal Code*: 10330

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login:

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: MD Degree Year: 1981

Attach Biographical Sketch*: File Name: Biosketch_(Hemachudha,Thiravat)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v05.pdf

Attach Current & Pending Support: File Name.

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Timothy Middle Name Last Name*: William Suffix:

Position/Title*: Head
Organization Name*: Gleneagles Hospital
Department: Infectious Disease Unit
Division:
Street1*: Riverson at Sembulan
Street2:
City*: Kota Kinabalu
County:
State*:
Province:
Country*: MYS: MALAYSIA
Zip / Postal Code*:

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login:

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: FRCP Degree Year: 2013

Attach Biographical Sketch*: File Name: Biosketch_(William,Timothy)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Helen Middle Name B Last Name*: Lasimbang Suffix:

Position/Title*: CEO
Organization Name*: Hospital Universiti Malaysia Sabah
Department:
Division:
Street1*: Hospital Universiti Malaysia Sabah
Street2:
City*: Kota Kinabalu
County:
State*:
Province:
Country*: MYS: MALAYSIA
Zip / Postal Code*:

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login:

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: MBBS Degree Year: 1991

Attach Biographical Sketch*: File Name: Biosketch_(Lasimbang,Helen_Benedict)_EIDRC_RFA-AI-19-2018)_(PI-Daszak)_v02.pdf

Attach Current & Pending Support: File Name.

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Heng Middle Name Last Name*: Gee Lee Suffix:

Position/Title*:
Organization Name*: Queen Elizabeth State Hospital
Department:
Division:
Street1*: 13a, Jalan Penampang
Street2:
City*: Kota Kinabalu
County:
State*:
Province:
Country*: MYS: MALAYSIA
Zip / Postal Code*:

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login:

Project Role*: Other (Specify) Other Project Role Category: Senior Clinician

Degree Type: MRCP Degree Year: 2011

Attach Biographical Sketch*: File Name: Biosketch_(Lee,Heng_Gee)_EIDRC_RFA-AI-19-028_(PI-Daszak) v02.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Giri Shan Middle Name Last Name*: Rajahram Suffix:

Position/Title*:
Organization Name*: Queen Elizabeth State Hospital
Department:
Division:
Street1*: 13a, Jalan Penampang
Street2:
City*: Kota Kinabalu
County:
State*:
Province:
Country*: MYS: MALAYSIA
Zip / Postal Code*:

Phone Number* (b) (6) Fax Number:

E-Mail* (b) (6)

Credential, e.g., agency login:

Project Role*: Other (Specify) Other Project Role Category: Infectious Disease Epidemiologist

Degree Type: MRCP Degree Year: 2011

Attach Biographical Sketch*: File Name: Biosketch_(Rajahram,Giri_Shan)_EIDRC_RFA-AI_19-028_(PI-Daszak)_v02.pdf

Attach Current & Pending Support: File Name.

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Jayaseelan Middle Name Last Name*: Sekaran Suffix:

Position/Title*:
Organization Name*: Lintang Clinic, Kuala Kangsar District Health Office
Department:
Division:
Street1*: 31100 Sg. Siput
Street2:
City*: Kuala Kangsar
County:
State*:
Province:
Country*: MYS: MALAYSIA
Zip / Postal Code*:

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login:

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: Degree Year:

Attach Biographical Sketch*: File Name: Biosketch_(Sekaran,_Jayaseelan)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Cheng Siang Middle Name Last Name*: Tan Suffix:

Position/Title*:
Organization Name*: Universiti Malaysia Sarawak
Department:
Division:
Street1*: Jalan Datuk Mohammad Musa
Street2:
City*: Kota Samarahan
County:
State*:
Province:
Country*: MYS: MALAYSIA
Zip / Postal Code*:

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login:

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: PHD Degree Year: 2012

Attach Biographical Sketch*: File Name: Biosketch_(Tan,Cheng_Siang)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf

Attach Current & Pending Support: File Name.

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Anwarali Khan Middle Name Last Name*: Faisal Ali Suffix:

Position/Title*:
Organization Name*: Universiti Malaysia Sarawak
Department:
Division:
Street1*: Jalan Datuk Mohammad Musa
Street2:
City*: Kota Samarahan
County:
State*:
Province:
Country*: MYS: MALAYSIA
Zip / Postal Code*:

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login:

Project Role*: Other (Specify) Other Project Role Category: Zoologist and Biotechnician

Degree Type: PHD Degree Year: 2013

Attach Biographical Sketch*: File Name: Biosketch_(Anwarali_Khan,Faisal)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Nadia Diyana Middle Name Last Name*: Hamzah Suffix:

Position/Title*:
Organization Name*: Bario Clinic, Rural Area Service Ministry of Health Malaysia
Department:
Division:
Street1*: Dataran Tinggi Kelabit Baram
Street2:
City*: Bario
County:
State*:
Province:
Country*: MYS: MALAYSIA
Zip / Postal Code*:

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login:

Project Role*: Other (Specify) Other Project Role Category: Medical Officer and Clinician

Degree Type: MD Degree Year: 2015

Attach Biographical Sketch*: File Name: Biosketch_(Hamzah,_Nadia)_EIDRC_RFA-AI-19-2018_(PI-Daszak)_v02.pdf

Attach Current & Pending Support: File Name.

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Ahmed Middle Name Last Name*: Kamruddin Suffix:

Position/Title*:
Organization Name*: Universiti Malaysia Sabah
Department:
Division:
Street1*: Jalan UMS
Street2:
City*: Kota Kinabalu
County:
State*:
Province:
Country*: MYS: MALAYSIA
Zip / Postal Code*:

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login:

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: PHD Degree Year: 1992

Attach Biographical Sketch*: File Name: Biosketch_(Kamruddin,Ahmed)_EIDRC_RFA-AI-19-2018_(PI-Daszak)_v02.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Tsin Wen Middle Name Last Name*: Yeo Suffix:

Position/Title*:
Organization Name*: Lee Kong Chian School of Medicine
Department:
Division:
Street1*: 59 Nanyang Dr
Street2:
City*: Singapore
County:
State*:
Province:
Country*: SGP: SINGAPORE
Zip / Postal Code*: 636921

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login:

Project Role*: Consultant Other Project Role Category:

Degree Type: PHD Degree Year: 2008

Attach Biographical Sketch*: File Name: Biosketch_(Yeo,Tsin_Wen)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf

Attach Current & Pending Support: File Name.

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Andrew Middle Name Last Name*: Hickey Suffix:

Position/Title*:
Organization Name*: Thailand MOPH-CDC
Department:
Division:
Street1*: Tivanon Road
Street2:
City*: Nonthaburi
County:
State*:
Province:
Country*: THA: THAILAND
Zip / Postal Code*: 11000

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login:

Project Role*: Consultant Other Project Role Category:

Degree Type: PHD Degree Year: 2010

Attach Biographical Sketch*: File Name: Biosketch_(Hickey,Andrew)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Hume Middle Name Last Name*: Field Suffix:

Position/Title*:
Organization Name*: Jeppesen Field Consulting
Department:
Division:
Street1*: 19 Counihan Street
Street2:
City*: Brisbane
County:
State*:
Province:
Country*: AUS: AUSTRALIA
Zip / Postal Code*: 4160

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login:

Project Role*: Consultant Other Project Role Category:

Degree Type: PHD Degree Year: 2005

Attach Biographical Sketch*: File Name: Biosketch_(Field,Hume)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Carloz Middle Name Last Name*: Zambrana-Torrelio Suffix:

Position/Title*: Associate Vice President
Organization Name*: EcoHealth Alliance
Department:
Division:
Street1*: 460 West 34th Street
Street2: Suite 1701
City*: New York
County:
State*: NY: New York
Province:
Country*: USA: UNITED STATES
Zip / Postal Code*: 10001-2317

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login:

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: PHD Degree Year: 2017

Attach Biographical Sketch*: File Name: Biosketch_(Zambrana-T,Carlos) _EIDRC_RFA-AI-19-028_(PI-Daszak).pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Pasin Middle Name Last Name*: Hemachudha Suffix:

Position/Title*:
Organization Name*: Chulalongkorn University Hospital
Department:
Division:
Street1*: 1873 Rama IV Road
Street2:
City*: Bangkok
County:
State*:
Province:
Country*: THA: THAILAND
Zip / Postal Code*: 10330

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login:

Project Role*: Other (Specify) Other Project Role Category: Immunologist and Clinician

Degree Type: MD Degree Year: 2017

Attach Biographical Sketch*: File Name: Biosketch_(Hemachudha,Pasin)_FINAL_USETHISONE.pdf

Attach Current & Pending Support: File Name:

PROFILE - Senior/Key Person

Prefix: Dr. First Name*: Ingrid Ting Pao Middle Name Last Name*: Lin Suffix:

Position/Title*: Clinical Specialist
Organization Name*: Hospital Miri
Department: Medicine
Division:
Street1*: Jalan Cahaya
Street2:
City*: Sarawak
County:
State*:
Province:
Country*: MYS: MALAYSIA
Zip / Postal Code*:

Phone Number*: (b) (6) Fax Number:

E-Mail*: (b) (6)

Credential, e.g., agency login:

Project Role*: Co-Investigator Other Project Role Category:

Degree Type: MD Degree Year: 2009

Attach Biographical Sketch*: File Name: Biosketch_(Lin,_Ingrid_Ting_Pao)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf

Attach Current & Pending Support: File Name:

OMB No. 0925-0001 and 0925-0002 (Rev. 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

NAME: Daszak, Peter

eRA COMMONS USER NAME: (b) (6)

POSITION TITLE: President & Chief Scientist

EDUCATION/TRAINING:

INSTITUTION AND LOCATION	DEGREE	COMPLETION DATE	FIELD OF STUDY
Bangor University, UK	B.S. (hons)	07/1986	Zoology
University of East London, UK	Ph.D.	03/1993	Infectious Diseases

A. Personal Statement

I have 20+ year's NIH-funded research experience on emerging viral zoonoses, and the scientific skills to manage this proposed work that involves a large international collaboration on human and wildlife surveillance, and translational research. I am President and Chief Scientist of EcoHealth Alliance, a US-based 501 (c) 3 institution that conducts research on emerging zoonoses. My research background is focused on understanding the process of zoonotic disease emergence, particularly viral zoonoses. This includes identifying the bat origin of SARS-CoV and SADS-CoV, analyzing the causes of West Nile, Nipah and Hendra virus emergence and spread, publishing the first unbiased analysis of global emerging disease hotspots, and analyzing patterns of viral spillover into human populations in EID hotspots. I have been the PI on 5 multidisciplinary R01s, all with international collaborating organizations, including most on the current proposal. All of these used modeling, epidemiology, laboratory and field science to test hypotheses on the emergence of wildlife-origin viral zoonoses, including SARS-CoV, Nipah and Hendra virus, Avian influenza and bat-origin viruses. I have also led large contracts from USAID (institutional lead on $75 million PREDICT-1 and $138 million PREDICT-2; Chief-of-Party on $3 million IDEEAL), successfully managing teams of virologists, field biologists, mathematical modelers, veterinarians, epidemiologists, laboratorians and anthropologists.

1. Li W, Shi Z, Yu M, Ren W, Smith C, Epstein JH, Wang H, Crameri G, Hu Z, Zhang H, Zhang J, McEachern J, Field H, **Daszak P**, Eaton BT, Zhang S & Wang L-F (2005). Bats are natural reservoirs of SARS-like coronaviruses. **Science** 310: 676-679.
2. Jones KE, Patel NG, Levy MA, Storeygard A, Balk D, Gittleman JL, and **Daszak P*** (2008). Global trends in emerging infectious diseases. **Nature** 451:990-993
3. Olival KJ*, Hosseini PR, Zambrana-Torrelio C, Ross N, Bogich TL, **Daszak P*** (2017). Host and viral traits predict zoonotic spillover from mammals. **Nature** 546, 646–650.
4. Carroll D, **Daszak P***, Wolfe ND, Gao GF, Morel C, Morzaria S, Pablos-Méndez A, Tomori O, Mazet JAK (2018). The global virome project. **Science** 359: 872-874.

B. Positions and Honors

Positions and Employment

1993 -98 Senior Faculty Research Scientist, Kingston University UK
1998 Guest Researcher, Centers for Disease Control and Prevention (CDC)
1999 -01 Faculty Research Scientist, University of Georgia
2001 - Adjunct Faculty, Columbia University
2001 - 09 Executive Director, Consortium for Conservation Medicine, EcoHealth Alliance, New York
2009 - President & Chief Scientist, EcoHealth Alliance New York

Other Experience and Professional Membership

2003 - 7 NIH: ad hoc member, ZRG1 IDM-G 90 (2003-5) ZRG1 IRAP-Q (2005-7)
2004 - Editorial Board, *Conserv. Biol.*
2005 NIAID: Steering Committee, workshop on virus-host shifts & emergence of new pathogens
2010 - Editor-in-Chief, *EcoHealth*; Member of IOM Forum on Microbial Threats; External Advisory Board, DHS and Kansas State Univ. Ctr. of Excellence for Emerg. & Zoonotic Animal Diseases (CEEZAD)
2011 Steering Committeee, NIAID Workshop on Arboviruses
2014 - Member NRC Advisory Committee to advise the US Global Change Research Program (USGCRP)
2015 - Member of Supervisory Board, One Health Platform; Editorial Board *One Health*
2016 - Member, WHO Expert group on Public Health Emergency Disease Prioritization
2016 - Member, Core Steering Committee & Co-Chair, Science & Technol WG, Global Virome Project
2017 External Review Committee, CSIRO Health & Biosecurity Business Unit
2017 - Chair, Forum on Microbial Threats, National Academies of Science, Engineering & Medicine

Honors

1999 Meritorious service award, CDC
2000 CSIRO silver medal for collaborative research
2002 Honored by the naming of a new species of centipede, *Cryptops daszaki* (J Nat Hist 36: 76-106)
2003 6th Annual Lecturer, Medicine & Humanities, Texas A&M
2007 Finalist, Director's Pioneer Award
2008 Presidential Lecturer, University of Montana
2012 Elected member of the Cosmos Club, Washington DC
2013 Honored by the naming of a new parasite species, *Isospora daszaki* (Parasit Res 111:1463-1466)
2013 Hsu-Li Distinguished Lectureship in International Epidemiology, Univ. Iowa
2015 Robert Leader Endowed Lecture in Food Safety, Michigan State Univ.
2018 - Member, National Academy of Medicine (NAM), USA.

C. Contribution to Science

1. **Research on the bat origins of emerging viruses.** Numerous high impact emerging viruses appear to have bat reservoirs (e.g. SARS-CoV, EBOV, NiV, HeV, MERS-CoV, SADS-CoV). As PI on five R01s on bat-origin viruses, my work has helped demonstrate the bat origin of SARS- and SADS-CoV, analyze the drivers of bat viral emergence and risk factors for spillover. Collaborating with virologists in China, we have isolated and characterized SARSr-CoVs from bats that use the same human host cell receptor (ACE-2) as SARS-CoV. This work provides critical reagents and resources that have helped advance understanding of virus-host binding and may contribute to vaccine development. My other work identified factors leading to the emergence of NiV from *Pteropus* bats in Malaysia and Bangladesh; a likely bat origin for MERS-CoV; and proof that bats harbor a significantly higher proportion of zoonoses than all other mammalian groups.

   a. Ge X-Y, Li J-L, Yang X-L, Chmura AA, Zhu G, Epstein JH, Mazet JK, Hu B, Zhang W, Peng C, Zhang Y-J, Luo C-M, Tan B, Wang N, Zhu Y, Crameri G, Zhang S-Y, Wang L-F, **Daszak P***, Shi Z-L* (2013). Isolation and characterization of a bat SARS-like Coronavirus that uses the ACE2 receptor. **Nature** 503: 535-538.

   b. Memish ZA, Mishra N, Olival KJ, Fagbo SF, Kapoor V, Epstein JH, Al Hakeem R, Durosinloun A, Al Asmari M, Islam A, Kapoor A, Briese T, **Daszak P**, Al Rabeeah A, Lipkin WI. (2013). Middle East respiratory syndrome coronavirus in bats, Saudi Arabia. **EID** 19(11): 1819-1823.

   c. Zhou P, Fan H, Lan T, Yang X-L, Shi W-F, Zhang W, Zhu Y, Zhang Y-W, Xie Q-M, Mani S, Zheng X-S, Li B, Li J-M, Guo H, Pei G-Q, An X-P, Chen J-W, Zhou L, Mai K-J, Wu Z-X, Li D, Anderson DE, Zhang L-B, Li S-Y, Mi Z-Q, He T-T, Cong F, Fuo P-J, Huang R, Luo Y, Liu X-L, Chen J, Huang Y, Sun Q, Zhang X-L-L, Wang Y-Y, Xing S-Z, Chen Y-S, Sun Y, Li J, **Daszak P***, Wang L-F*, Shi Z-L*, Tong Y-G*,

Ma J-Y* (2018). Fatal Swine Acute Diarrhea Syndrome caused by an HKU2-related Coronavirus of Bat Origin. **Nature** 556: 255-258.

d. Nikolay B, Salje H, Hossain MJ, Khan AKMD, Sazzad HMS, Rahman M, **Daszak P**, Ströher U, Pulliam JRC, Kilpatrick AM, Nichol ST, Klena JD, Sultana S, Afroj S, Luby SP, Cauchemez S & Gurley ES. (2019). Transmission of Nipah Virus - 14 Years of Investigations in Bangladesh. **New England Journal of Medicine** 380:1804-1814

2. **Analyzing the process of disease emergence.** Emerging infectious diseases are a significant threat to global health. However, their emergence is sporadic, and involves a complex process that is hard to predict. In the early 2000s I started to use analytical approaches to identify predictable patterns in the process of disease emergence. By collating a database of all known prior EID events, identifying their point origins, and correcting for reporting biases, I published the first ever predictive 'hotspots' maps of where future disease emergence is most likely. I have continued this line of research, publishing spatial analyses of the drivers of disease spread, and outlining strategies to predict pandemic emergence.

   a. Kilpatrick AM, Chmura AA, Gibbons DW, Fleischer RC, Marra PP & **Daszak P** (2006). Predicting the global spread of H5N1 avian influenza. **PNAS** 103: 19368-19373.

   b. Morse SS, Mazet JAK, Woolhouse M, Parrish CR, Carroll D, Karesh WB, Zambrana-Torrelio C, Lipkin WI, **Daszak P*** (2012). Prediction and prevention of the next pandemic zoonosis. **Lancet** 380:1956-1965.

   c. **Daszak P***, Zambrana-Torellio C, Bogich TL, Fernandez M, Epstein JH, Murray KA, Hamilton H (2013). Interdisciplinary approaches to understanding disease emergence: The past, present and future drivers of Nipah virus emergence. **PNAS** 110: 3681-3688

   d. Allen T, Murray KA, Zambrana-Torrelio C, Morse SS, Rondinini C, Di Marco M, Breit N, Olival KJ, **Daszak P*** (2017). Global hotspots and correlates of emerging zoonotic diseases. **Nature Comm** 8: 1124

3. **Studies of wildlife disease ecology to understand emerging zoonoses.** The majority of EIDs are zoonotic, with the majority of these originating in wildlife. I reviewed this field in a paper in *Science* in 2000 and in a more recent paper in *Nature* on the links among biodiversity and health. During the last two decades, I have led collaborative research programs on how the ecology of specific wildlife-origin zoonoses can help explain patterns of risk to people. This includes my role as PI on 4 R01s, as institutional lead for USAID-EPT-PREDICT, and Chief of Party for USAID-IDEEAL. This work includes estimations of the diversity of yet-to-be discovered viruses which forms the rationale for the Global Virome Project.

   a. **Daszak P***, Cunningham AA, Hyatt AD (2000). Emerging infectious diseases of wildlife - threats to biodiversity and human health. **Science** 287: 443-449

   b. Keesing F, Belden LK, **Daszak P**, Dobson A, Harvell CD, Holt RD, Hudson P, Jolles A, Jones KE, Mitchell CE, Myers SS, Bogich T & Ostfeld RS. (2010). Impacts of biodiversity on the emergence and transmission of infectious diseases. **Nature** 468:647-652.

   c. Anthony SJ, Epstein JH, Murray KA, Navarrete-Macias I, Zambrana-Torrelio CM, Solovyov A, Ojeda-Flores R, Arrigo NC, Islam A, Ali Khan S, Hosseini P, Bogich TL, Olival KJ, Sanchez-Leon MD, Karesh W, Goldstein T, Luby SP, Morse SS, Mazet JAK, **Daszak P***, Lipkin WI. (2013). A strategy to estimate unknown viral diversity in mammals. **MBio** 4(5): e00598-13.

   d. Mandl JN, Ahmed R, Barreiro LB, **Daszak P**, Epstein JH, Virgin HW, Feinberg MB. (2015). Reservoir host immune responses to emerging zoonotic viruses. **Cell** 160: 20-35

4. **National and international leadership in infectious disease research.** I have tried to use my research to promote multidisciplinary collaboration among medical doctors, veterinarians and ecologists. In addition

to primary data and analysis papers, I have published editorials, reviews, book chapters to highlight these linkages, including 5 Policy Forums and editorials in *Science*. I have served as a member of the NASEM Forum on Microbial Threats for over 10 years, and now Chair, where I help set the agenda on EID threats. I am a new and active member of the National Academy of Medicine, and represent the health sciences on the NRC Committee to Advise the US Global Change Research Program. I have served on advisory and review boards at CSIRO, Australia and on the Australian Biosecurity CRC, and on all annual meetings of the WHO R&D Blueprint Pathogen Prioritization Committee. I have managed meetings among senior leadership of the US NSF and NSF-China to promote US-China collaboration, and am an active member of a series of One Health editorial boards and international organization boards, as well as a Commissioner of *The Lancet Commission on One Health*.

a. Womack JE, Anderson LC, Bull LS, Capen CS, Cheville NF, **Daszak P**, Dodds WJ, Doyle MP, Franz DR, Shadduck JA, Shaw DH, Swayne DE, Tolwani RJ (2005). Critical needs for research in veterinary science. ***National Academies Press***, 222 pp.

b. Rodríguez JP, Taber AB, **Daszak P**, Sukumar R, Valladares-Padua C, Padua S, Aguirre LF, Medellin R, Acosta M, Aguirre AA, Bonacic C, Bordino P, Bruschini J, Buchori D, Gonzálalez S, Mathew T, Mendez M, Mugijca L, Pacheco LF, Dobson AP, Pearl M (2007). Policy Forum: The globalization of conservation: A view from the South. **Science** 317: 755-756.

c. Smith KF*, Behrens M, Schloegel LM, Marano N, Burgiel S & **Daszak P*** (2009). Reducing the risks of the wildlife trade. **Science** 324: 594-595.

d. **Daszak P** (2012). Anatomy of a pandemic. **Lancet** 380: 1883-1884. Lead article as Guest Editor for a ***Lancet Series*** on Zoonoses.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

USAID Emerging Pandemic Threats Mazet (PI) 10/01/14 – 09/30/19
PREDICT-2
The goal is to conduct surveillance for novel pathogens in wildlife, livestock and people; characterize human risk behavior; analyze EID risk; and design interventions in >20 countries
Role: PI on Subcontract

2R01 AI110964 Daszak (PI) 06/01/19 – 05/31/24
Understanding the Risk of Bat Coronavirus Emergence
The goal of this work is to characterize the virological, behavioral and demographic factors that present a high risk of future emergence of SARSr-CoVs in people in southern China, and identify any clinical outcomes.
Role: PI

Completed Research Support (last 3 years only) out of 14 prior awards

1R01 AI110964 Daszak (PI) 06/01/14 – 05/31/19
Understanding the Risk of Bat Coronavirus Emergence
The goal was to conduct ecological and virological studies on bat-origin SARSr-CoVs in China, behavioral risk surveys and testing in people, to identify risk of future spillover of these viruses.
Role: PI

USAID 1414374 (RDMA, Thailand) Daszak (CoP) 10/01/13 - 03/30/19
Infectious Disease Emergence and Economics of Altered Landscapes (IDEEAL)
Cooperative agreement to analyze how land use change affects economics of disease risk in SE Asia.
Role: Chief of Party

NSF DEB 1414374 Perrings (PI) 10/15/14 - 04/14/18
US-UK Collab: Risks of Animal and Plant Infectious Diseases through Trade (RAPID Trade)
The goal is to analyze and model how policy changes to trade affect emerging disease risk globally.
Role: Co-Investigator

HDTRA1 Allen (PI) 04/15/15 - 04/14/17
Global Rapid Identification of undiagnosed EID Events
The goal was to design software for the DoD biosurveillance ecosystem to diagnose novel EID events.
Role: Co-Investigator

1R01GM100471 (NIGMS) Perrings (PI) 09/15/11-06/30/15
MASpread: Modeling Anthropogenic Effects in the Spread of Infectious Disease
The goal was to analyze the social decisions involved in disease spread through trade.
Role: Co-Investigator

NSF Daszak (PI) 07/01/10-06/30/15
EcoHealthNet - a Research Coordination Network
Funding for student exchange and workshops to fuse veterinary science, ecology and human medical sciences
Role: PI

OMB No. 0925-0001 and 0925-0002 (Rev. 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Olival, Kevin James

eRA COMMONS USER NAME: (b) (6)

POSITION TITLE: Vice President for Research

EDUCATION/TRAINING:

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Colorado State University, Fort Collins, CO	B.S	05/1997	Biology
Columbia University, New York, NY	M.A	10/2003	Conservation Biology
Columbia University, New York, NY	Ph.D.	05/2008	Ecology & Evolution
American Museum of Natural History, New York	Post Doctoral	08/2009	Molecular Parasitology
NIH Fogarty US Global Health Fellow, New York	Post Doctoral	08/2011	International Emerging Infectious Diseases

A. Personal Statement

The goal of our proposal is to establish an Emerging Infectious Disease Research Center in Southeast Asia to better understand the risk of zoonotic viral emergence, and to strengthen regional capacity to identify, characterize, and rapidly respond to novel infectious diseases threats. I have 17 years of experience managing zoonotic disease surveillance projects, primarily in Southeast Asia, and leading cutting-edge research on pathogen discovery, disease ecology, and modeling the risk of viral spillover that are strongly complementary to our project's aims. As a PhD student and then NIH-Fogarty Global Health Post-Doc Fellow, I investigated the ecology of Nipah virus in Malaysia and Bangladesh, respectively, using phylogeographic approaches to integrate wildlife host and virus data. Over the last 10 years, I have served as the global lead for USAID-PREDICT activities in Thailand and Indonesia managing all human and animal surveillance, and coordinated training and other project activities in Malaysia, Myanmar, Bangladesh, and India. I have managed field-based disease investigations around the world, leading to the following significant discoveries: the wildlife origin of Ebola Reston in the Philippines, first evidence of Ebola Zaire infection in Asian wildlife, MERS-CoV in Saudi Arabian bats, and the first isolation of Nipah virus from the large flying fox in Malaysia. I currently serve as the Modeling & Analytics coordinator under the USAID PREDICT-2 project, leading a team analyzing combined human, animal, and laboratory surveillance data to predict and prevent zoonoses. As part of this effort, I developed a new approach that combines phylogenetic, ecological, and life-history traits to predict viral diversity, host/reservoir range, and spillover potential, leading to a recent first author paper in *Nature*.

1. Rahman SA, Hassan SS, **Olival KJ**, Mohamed M, Chang L-Y, Hassan L, Saad NM, Shohaimi SA, Mamat ZC, Naim MS, Epstein JH, Suri AS, Field HE, Daszak P and HERG (2010). Characterization of Nipah virus from Naturally Infected *Pteropus vampyrus* Bats, Malaysia. **EID** 16(12): 1990-1993.
2. **Olival KJ***, Islam A, Yu M, Anthony SJ, Epstein JH, Khan SA, Khan SU, Crameri G, Wang LF, Lipkin WI, Luby SP, and Daszak P (2013). Ebolavirus Antibodies in Fruit Bats, Bangladesh **EID** 19(2): 270-273.

3. Memish ZA, Mishra N, **Olival KJ**, Fagbo SF, Kapoor V, Epstein JH, AlHakeem R, Al Asmari M, Islam A, Kapoor A, Briese T, Daszak P, Al Rabeeah AA, Lipkin WI (2013). Middle East Respiratory Syndrome Coronavirus in Bats, Saudi Arabia. **EID** 19(11): 1819-1823.
4. **Olival KJ***, Hosseini P, Zambra-Torrellio C, Ross N, Bogich T, Daszak P* (2017). Host and viral traits predict zoonotic spillover from mammals. **Nature** 546(7660): 646-650.

*corresponding author

B. Positions and Honors

Positions and Employment

1999 -02 Research Associate, Kewalo Marine Laboratory, University of Hawaii
2003 -07 US Environmental Protection Agency STAR Fellow
2006 -13 Instructor, Columbia University Secondary School Summer Program
2010 -12 NIH Fogarty US Global Health Post-Doc Fellow
2012 -15 Senior Research Scientist, EcoHealth Alliance
2015 -17 Associate Vice President for Research, EcoHealth Alliance
2009 - Visiting Scientist, American Museum of Natural History
2009 - Adjunct Faculty, Earth Institute Center for Environmental Sustainability, Columbia University
2017 - Vice President for Research, EcoHealth Alliance

Other Experience and Professional Memberships

1998 -00 Member, American Association for the Advancement of Science
2000 -02 Mentor, NSF Undergraduate Mentoring in Environmental Biology (UMEB), University of Hawaii
2003 -05 Member, American Society of Mammalogists
2005 -06 Member, New York Academy of Sciences
2011 - Scientific Steering Committee Member, Southeast Asian Bat Conservation Research Unit
2011 - Scientific Advisory Board Member, Lubee Bat Conservancy, FL
2011 - Scientific Advisor, Bat Conservation International
2011 - Review Editor, EcoHealth
2015 - US White-Nose Syndrome Stakeholder Committee and Communications Committee Member
2017 - DoD DTRA: Steering Committee Member, Bat One Health Research Network
2017 - Founder, Western Asia Bat Research Network

Honors

1993 -97 Colorado State University Distinguished Scholar Award
2003 NSF Graduate Student Fellowship, Honorable Mention
2005 -07 Bat Conservation International Student Award and Scholarship
2004 -07 US EPA STAR Fellowship Award
2008 PhD Dissertation *with Distinction*, Columbia University
2013 Plenary Speaker, 11th Annual ASM Biodefense and EID Research Meeting
2013 -14 Institute of Medicine, Forum on Microbial Threats. Invited speaker, briefings on MERS-CoV and Emerging Viral Diseases
2016 Plenary Speaker, NYC Medtech conference – Global Virome Project
2017 -18 Three papers awarded the InCites Highly Cited Paper™ designation (top 1% in field) for Immunology and Microbiology
2019 Keynote Speaker, World-Wide Human Geography Data Working Group, Harvard University, MA
2019 Keynote Speaker, 18th International Bat Research Conference, Phuket, Thailand

C. Contribution to Science

1. **Characterizing viral diversity in people and wildlife.** A large body of my research has focused on the discovery and characterization of viruses in wildlife populations to better anticipate viral emergence. This includes over 10 studies in South and Southeast Asia, generating sequence data for 100s of novel viral strains. These include: molecular evidence for MERS-related coronaviruses circulating in bats at guano mining sites in Thailand; Ebola Reston sequences from multiple bat species in the Philippines captured near pig farms where outbreaks first occurred; and novel virus discovery using metagenomic approaches in Saudi Arabian bats collected at the site of the first human MERS-CoV case. Lastly, follow-up human viral surveillance in guano miner populations from Thailand yielded a full-genome sequence of HKU-1 coronavirus. Most of these research studies were conducted and published jointly with in-country colleagues on the current proposal.

   a. Wacharapluesadee S, Sintunawa C, Kaewpom T, Khongnomnan K, **Olival KJ**, Epstein JH, Rodpan A, Sangsri P, Intarut N, Chindampom A, Suksawa K, Hemachudha T (2013). Group C Betacoronavirus in Bat Guano Fertilizer, Thailand. **EID** 19(8): 1349-1352.

   b. Jayme S, Yu M, Jong Cd, **Olival KJ**, Tagtag A, Hughes T, Foord A, Marsh G, Crameri G, Epstein JH, Santos I, Catbagan D, Lim M, Benigno C, Wang L, Daszak P, Field H, Newman S (2015). Molecular evidence of Ebola Reston virus infection in Philippine bats. **Virology Journal** 12(1): 107.

   c. Mishra N, Fagbo S, Alagaili AN, Nitido A, Williams SH, Ng J, Lee B, Durosinlorun A, Garcia JA, Jain K, Kapoor V, Epstein JH, Briese T, Memish Z, **Olival KJ**, Lipkin WI (2019). A viral metagenomic survey identifies known and novel mammalian viruses in bats from Saudi Arabia. **PLOS ONE** 14(4): e0214227.

   d. Joyjinda Y, Rodpan A, Chartpituck P, Suthum K, Yaemsakul S, Cheun-Arom T, Bunprakob S, **Olival KJ**, Stokes MM, Hemachudha T, Wacharapluesadee S (2019). First complete genome sequence of Human Coronavirus HKU1 (HCoV-HKU1) from a non-ill bat guano miner, Thailand. **Microbiol Resour Announc** 8:e01457-18.

2. **Analyses to better target zoonotic disease surveillance.** For the last 5 years, I have led the development of new strategies to better target the geographic regions, transmission pathways, host species, and sample types to make zoonotic surveillance more effective [redacted] (b) (4) [redacted] Previous work includes the first use of species accumulation curves to estimate viral diversity from longitudinal surveillance data in wildlife (Bangladesh bats); two meta-analyses using pathogen-specific transmission and host range data from all known zoonotic EIDs to refine disease surveillance targets; and analysis of data from 100 viral discovery studies in bats to optimize surveillance.

   a. Anthony SJ, Epstein JH, Murray KA, Navarrete-Macias I, Zambrana-Torrelio CM, Solovyov A, Ojeda-Flores R, Arrigo NC, Islam A, Khan SA, Hosseini P, Bogich TL, **Olival KJ**, Sanchez-Leon MD, Karesh WB, Goldstein T, Luby SP, Morse SS, Mazet JAK, Daszak P, Lipkin WI (2013). A Strategy To Estimate Unknown Viral Diversity in Mammals. **Mbio** 4(5): e00598-13.

   b. Levinson J, Bogich TL, **Olival KJ**, Epstein JH, Johnson CK, Karesh WB, and Daszak P (2013). Targeting surveillance for zoonotic virus discovery. **EID** 19(5): 743-747.

   c. Loh EH, Bogich TL, **Olival KJ**, Johnson CK, Mazet JAK, Karesh W, Daszak P (2015). Targeting emergence pathways for zoonotic disease surveillance and control. **Vector Borne and Zoonotic Diseases** 15(7):432-437.

   d. Young CC and **Olival KJ*** (2016). Optimizing Viral Discovery in Bats. **PLOS ONE** 11(2) e0149237.

3. **Modeling global disease emergence and spillover risk.** I have used my applied ecology background to develop new models that help explain zoonotic spillover and disease circulation. This includes studies of the environmental drivers of bat virus spillover to humans, cross-species transmission among bat species, spatial analysis of emerging zoonotic disease hotspots, and novel phylo-factorization approaches to estimating viral host range. These models explicitly use data from PCR- and serology-based field studies, combined with an understanding of wildlife biology, ecology, and host phylogenetics and evolution, to assess the environmental and demographic drivers of disease transmission -- bridging the gap between field investigations and transmission risk.

   a. Brierley L, Vonhof MJ, **Olival KJ**, Daszak P, Jones KE (2016). Quantifying global drivers of zoonotic bat viruses: a process-based perspective. **American Naturalist** 187(2): E53-64.

   b. Willoughby AR, Phelps K, PREDICT Consortium, **Olival KJ*** (2017). A Comparative Analysis of Viral Richness and Viral Sharing in Cave-Roosting Bats. **Diversity** 9(3): 35.

   c. Allen T, Murray KA, Zambrana-Torrelio C, Morse SS, Rondinini C, Di Marco M, Breit N, **Olival KJ**, Daszak P (2017). Global hotspots and correlates of emerging zoonotic diseases. **Nature Comm** 8(1124): 1-10.

   d. Washburne A, Crowley DE, Becker DJ, **Olival KJ**, Taylor M, Munster VJ, Plowright RK (2018). Taxonomic patterns in the zoonotic potential of mammalian viruses. **PeerJ** 6:e5979.

4. **Elucidating host-vector-pathogen interactions using evolutionary biology.** I started using evolutionary and phylogenetic tools to improve the understanding of host and vector disease biology during my PhD dissertation. I continued this through my NIH post-doctoral fellowship research on Nipah virus dynamics using host phylogeographic analyses of *Pteropus* spp. fruit bats and their associated bat fly vectors. Other examples include DNA barcoding analysis of mosquito bloodmeals to understand bunyavirus vertebrate host range; co-phylogenetic mapping of bacterial pathogens in bats and rodents to identify host-switching events; and analyzing patterns of coronavirus diversification in bat communities in Eastern Thailand.

   a. Murdock C, **Olival KJ**, and Perkins SL (2010). Feeding preference of snow-melt mosquitoes (Culicidae: *Culiseta* and *Ochelerotatus*) show a link between cervid amplifying hosts for Jamestown Canyon Virus (Bunyaviridae: Orthobunyavirus) and humans. **Journal of Medical Entomology**. 47(2): 226-229.

   b. **Olival KJ***, Dick CW, Simmons NB, Morales JC, Melnick DJ, Dittmar K, Perkins SL, Daszak P, DeSalle R (2013). Lack of population genetic structure and host specificity in the bat fly, *Cyclopodia horsfieldi*, across species of Pteropus bats in Southeast Asia. **Parasites & Vectors**. 8(6): e231.

   c. Lei BR, **Olival KJ*** (2014). Contrasting Patterns in Mammal-Bacteria Coevolution: *Bartonella* and *Leptospira* in Bats and Rodents. **PLOS NTD**. 8(3): e2738.

   d. Wacharapluesadee S, Duengkae P, Rodpan A, Kaewpom T, Maneeorn P, Kanchanasaka B, Yinsakmongkon S, Sittidetboripat N, Chareesaen C, Khlangsap N, Pidthong A, Leadprathom K, Ghai S, Epstein JH, Daszak P, **Olival KJ**, Blair PJ, Callahan MV, Hemachudha T (2015). Diversity of Coronavirus in Bats from Eastern Thailand. **Virology Journal** 12:57.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

HDTRA11710064 Olival (PI) 10/02/17-10/01/22
Understanding the Risk of Bat-Borne Zoonotic Disease Emergence in Western Asia
The goal of this project is to characterize pathogen diversity, strengthen zoonotic disease surveillance capacity, and test key hypotheses about the risk of bat-borne zoonotic disease emergence in Western Asia.

Role: PI

USAID Emerging Pandemic Threat Mazet (PI) 10/01/14-09/30/19
PREDICT 2
The goal of this project is to create and implement a global virus surveillance system in animals and humans and analyze spillover risk.
Role: Modeling and Analytics Coordinator; Country lead for Indonesia and Thailand.

Completed Research Support

R01 AI110964 Daszak (PI) 06/01/14-05/31/19
Understanding Risk of Bat Coronaviruses
The goal of this study is to analyze the risk of coronavirus spillover from bats to humans in Southern China
Role: co-PI

OMB No. 0925-0001 and 0925-0002 (Rev. 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Baric, Ralph Steven

eRA COMMONS USER NAME (credential, e.g., agency login): [redacted] (b) (6)

POSITION TITLE Professor, Kenan Distinguished Professor

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
N.C. State University, Raleigh, NC	B.S.	1977	Zoology
N.C. State University, Raleigh, NC	Ph.D.	1982	Microbiology
University of Southern CA, School of Med., Los Angeles, CA	Post-Doc	1986	Microbiology

A. Personal Statement

We use systems genetic, biochemical, molecular and immunologic approaches to study the molecular mechanisms regulating viral evolution, virus immunity, virus-host interactions, virus pathogenesis and vaccine mediated protective immunity primarily using coronaviruses (SARS-CoV, MERS-CoV), noroviruses (GII.4 and related strains) and flaviviruses (Dengue, Zikv) as models. Additional studies have focused on the pathogenesis of influenza and Ebola viruses. My major contributions include publications describing: **a**) emerging coronavirus, Dengue 1-4 and Zikv reverse genetic platforms, **b**) the identification of human host susceptibility alleles that regulate norovirus infection and pathogenesis, **c**) the identification of host susceptibility alleles that regulate SARS-CoV and Ebola virus pathogenesis and immunity using the Collaborative Cross Genetic Reference Population, **d**) the development of platform strategies and animal models to identify and culture emerging, pre-epidemic human viruses from outbreak samples or in silico sequences, **e**) the functional mapping of human monoclonal antibodies and their epitopes against all of the viruses described above, **f**) pioneering approaches in structure guided immunogen design to develop bivalent vaccine and immune diagnostic viruses and VLPs to all three virus families noted above, **e**) the mapping and characterization of the primary targets of polyclonal neutralizing antibodies following infection and vaccination, **g**) the design and testing of broadly cross protective coronavirus, norovirus and dengue virus vaccines, **h**) the identification novel antivirals targeting the emerging human, contemporary and prepandemic threat viruses and **i**) structure-function studies of viral genes involved in replication, pathogenesis, innate immune evasion and cross species transmission. We also helped to demonstrate the existence of the first proof-reading enzyme in an RNA virus. I have extensively collaborated with Dr Daszak and his team in the past including joint publications and grants. I have considerable experience managing large cooperative centers and program project grants and also study human DENV vaccine outcomes and human norovirus challenge studies.

1. Lindesmith L, Moe C, Marionneau S, Ruvoen N, Jiang X, Lindblad L, Stewart P, LePendu J, **Baric R** (2003). Human susceptibility and resistance to Norwalk virus infection. **Nat Med** 9(5):548-53.

2. Graham RL, Becker MM, Eckerle LD, Bolles M, Denison MR, **Baric RS**. 2012. A live, impaired-fidelity coronavirus vaccine protects in an aged, immunocompromised mouse model of lethal disease. **Nat Med** 6;18(12):1820-6.

3. Menachery VD, Yount BL, Debbink K, Agnihothram S, Gralinski LE, Plante JA, Graham RL, Scobey T, Ge S-Y, Donaldson EF, Randell SH, Lanzavecchia A, Marasco WA, Shi Z-L, **Baric RS** (2015). Novel

platform identifies threat posed by a SARS-like cluster of circulating bat coronavirus. **Nature Med** 21(12):1508-13.

4. Cockrell AS, Yount BL, Scobey T, Jensen K, Douglas M, Beall A, Tang XC, Marasco WA, Heise MT, **Baric RS** (2016). A mouse model for MERS coronavirus-induced acute respiratory distress syndrome. **Nat Microbiol** 28;2:16226.

B. Position and Honors

Positions and Employment

1986 -1992	Assistant Professor, Department of Parasitology and Laboratory Practice and Department of Epidemiology, University of North Carolina (UNC), Chapel Hill, NC
1992 -2001	Associate Professor, Departments of Epidemiology and Microbiology & Immunology, UNC Chapel Hill
2001 -	Professor, Departments of Epidemiology and Microbiology and Immunology, UNC Chapel Hill

Other Experience and Professional Membership

2005 -09	Permanent Member, NIH VirB Study Section
2005 -15	Review Board, J. Virology
2006 -07	Acting Chair and Chair, Division T RNA Viruses, American Society of Microbiology
2007 -08	Associate Editor, Plos Pathogens
2008	Nat'l Acad Sci: Working Group: Gene Sequence Methods for Classification of Select Agents
2008 -17	Senior Editor, Plos Pathogens
2014	National Academy of Sciences: Working Group on Risks and Benefits of Gain of Function Research
2015	MERS-CoV Stakeholders Workshop, Organizer and Invited panelist, NIH
2015	Natl. Acad. Of Sciences "China-U.S. Workshop on the Challenges of Emerging Infections, Laboratory Safety, and Global Health Security" September 28-30 in Beijing, China
2017	Natl. Acad. Of Sciences "China-U.S. Workshop on the Challenges of Emerging Infections, Laboratory Safety, and Global Health Security" Jan 16-18th in Galveston-Texas.
2018	Natl. Acad. Of Sciences "China-U.S. Workshop on the Challenges of Emerging Infections, Laboratory Safety, and Global Health Security" Jan 6-10th in Harbin China.

Honors

1984 -86	Harvey Weaver Scholar, National Multiple Sclerosis Society
1984 -87	Established Investigator: American Heart Association
2003	Finalist/Runner-up, World Technology Award
2011	Innovation/Inspiration Award for Faculty Research, UNC Gillins School of Public Health
2019	Kenan Distinguished Professor

C. Contributions to Science

1. **Contributions to Virology:** My group studies coronavirus, norovirus and flavivirus immunology, molecular biology, virus-host interactions, genetics, pathogenesis, vaccine and therapeutic design, using traditional and new technologies like structure guided immunogen design, synthetic genome design, and systems genetics. We developed new approaches to identify and recover prepandemic viruses.
   a. Yount B, Curtis K, Fritz L, Hensley L, Jahrling P, Prentice E, Denison M, Geisbert T, **Baric RS** (2003). Reverse Genetics with a full-length infectious cDNA for the SARS Coronavirus. **Proc Natl Acad Sci USA** 100(22):12995-13000.
   b. Lindesmith LC, Donaldson EF, Lobue AD, Cannon JL, Zheng DP, Vinje J, **Baric RS** (2008). Mechanisms of GII.4 NoV persistence in humans. **PLoS Med** 5(2):e31.
   c. Sheahan TP, Sims AC, Graham RL, Menachery VD, Gralinski LE, Case JB, Leist SR, Pyrc K, Feng JY, Trantcheva I, Bannister R, Park Y, Babusis D, Clarke MO, Mackman RL, Spahn JE, Palmiotti CA, Siegel D, Ray AS, Cihlar T, Jordan R, Denison MR, **Baric RS** (2017). Broad-spectrum antiviral GS-5734 inhibits both epidemic and zoonotic CoV. **Sci Transl Med** 28;9(396).

d. Menachery VD, Yount BL Jr, (+15 other authors) and **Baric RS** (2016). SARS-like WIV1-CoV poised for human emergence. **Proc Natl Acad Sci USA** 113:3048-3053.

2. **Viral Immunity**. New diagnostic metrics are needed to identify precise correlates of protective immunity at the molecular level. Our group has pioneered the use of structure-guided immunogen design, coupled with reverse genetic strategies, to transfer complex conformational immunogen epitopes between viruses (or viral proteins), using noroviruses and dengue/zikv virus as model platforms.
   a. Lindesmith LC, Ferris MT, Mullan CW, Ferreira J, Debbink K, Swanstrom J, Richardson C,Goodwin RR, Baehner F, Mendelman PM, Bargatze RF, **Baric RS** (2015). Broad blockade antibody responses in human volunteers after immunization with a multivalent norovirus VLP candidate vaccine: immunological analyses from a phase I clinical trial. **PLoS Med** 24;12(3):e1001807.
   b. Gallichotte EN, Baric TJ, Yount BL Jr, Widman DG, Durbin A, Whitehead S, **Baric RS**, de Silva AM (2018). Human dengue virus serotype 2 neutralizing antibodies target two distinct quaternary epitopes. **PLoS Pathog** 26;14(2):e1006934.
   c. Gallichotte EN, Baric TJ, Nivarthi U, Delacruz MJ, Graham R, Widman DG, Yount BL, Durbin AP, Whitehead SS, de Silva AM, **Baric RS** (2018). Genetic Variation between Dengue Virus Type 4 Strains Impacts Human Antibody Binding and Neutralization. **Cell Rep** 30;25(5):1214-1224.
   d. Lindesmith LC, McDaniel JR, Changela A, Verardi R, Kerr SA, Costantini V, Brewer-Jensen PD, Mallory ML, Voss WN, Boutz DR, Blazeck JJ, Ippolito GC, Vinje J, Kwong PD, Georgiou G, **Baric RS**. Sera Antibody Repertoire Analyses Reveal Mechanisms of Broad and Pandemic Strain Neutralizing Responses after Human Norovirus Vaccination. Immunity. 2019 Jun 18;50(6):1530-1541.e8.

3. **Virus Molecular Genetics/Immunity**. My group has pioneered strategies for performing reverse genetic analyses in coronaviruses and flaviviruses, including recently emerged strains like SARS-CoV, MERS-CoV, PEDV, conventional human and model coronaviruses like MHV and HCoV NL63, and several bat coronaviruses. We have also built full length infectious cDNA clones for DENV1-4 serotypes, several Zikv strains, as well as panels of isogenic DENV serotypes encoding genotype distinct E glycoproteins. We demonstrated that coronaviruses and influenza viruses regulate host expression, by epigenetics.
   a. Douglas G, Widman DG, Ellen Young E, Yount BL, Plante K, Carbaugh D, Gallichotte EN, Peck KM, Plante J, Swanstrom J, Heise MT, Lazear HM, **Baric RS** (2017). A reverse genetics platform that spans the Zika virus family tree. **MBio** 7;8(2). pii: e02014-16.
   b. Swanstrom JA, Plante JA, Plante KS, Young EF, McGowan E, Gallichotte EN, Widman DG, Heise MT, de Silva AM, **Baric R** (2016). Dengue Virus Envelope Dimer Epitope Monoclonal Antibodies Isolated from Dengue Patients Are Protective against Zika Virus. **MBio** 19;7(4). pii: e01123-16.
   c. Lindesmith LC, Beltramello M, Donaldson EF, Corti D, Swanstrom J, Debbink K, Lanzavecchia A, **Baric RS** (2012). Immunogenetic mechanisms driving norovirus GII.4 antigenic variation. **PLoS Pathog** 8(5):e1002705.
   d. Menachery VD, Eisfeld AJ, (+23 other authors) and Baric RS. Pathogenic influenza viruses and coronaviruses utilize similar and contrasting approaches to control interferon-stimulated gene responses. **Mbio** 5:e01174-14, 2014.

4. **Host Susceptibility/Innate Immune Antagonism.** Coronaviruses, noroviruses and DENV are major causes of human morbidity and mortality worldwide. We have used the Collaborative Cross Mice to identify host susceptibility alleles that regulate SARS-CoV and EBoV pathogenesis, and demonstrated common epigenetic control mechanisms that antagonize antigen presentation after infection.
   a. Gralinski LE, Ferris MT, (+16 other authors) and **Baric RS** (2015). Genome Wide Identification of SARS-CoV Susceptibility Loci Using the Collaborative Cross. **PLoS Genet** 11:e1005504,
   b. Gralinski L, Menachery V, (+9 other authors) and **Baric RS** (2017). *Ticam2* contributes to SARS-CoV pathogenesis. **G3** 7;7(6):1653-1663.
   c. Rasmussen AL, Okumura A, (**Baric RS** + 18 others) and Katze MG (2014). Host genetic diversity enables Ebola hemorrhagic fever pathogenesis and resistance. **Science** 346:987-991, PMC4241145.

d. Menachery VD, Schäfer A, (+12 other authors), Sims AC, Kawaoka Y, **Baric RS** (2018). MERS-CoV and H5N1 influenza virus antagonize antigen presentation by altering the epigenetic landscape. **Proc Natl Acad Sci USA** 30;115(5):E1012-E1021.

5. **Pathogenesis and Intervention Studies**. Our group has studied the role of virus-host interactions in susceptibility, pathogenesis and vaccine design.
   a. Adams Waldorf KM, Nelson BR, Stencel-Baerenwald JE, Studholme C, Kapur RP, Armistead B, Walker CL, Merillat S, Vornhagen J, Tisoncik-Go J, Baldessari A, Coleman M, Dighe MK, Shaw DWW, Roby JA, Santana-Ufret V, Boldenow E, Li J, Gao X, Davis MA, Swanstrom JA, Jensen K, Widman DG, **Baric RS et al** (2018). Congenital Zika virus infection as a silent pathology with loss of neurogenic output in the fetal brain. **Nat Med** 24(3):368-374.
   b. Tang XC, Agnihothram SS, Jiao Y, Stanhope J, Graham RL, Peterson EC, Avnir Y, Tallarico AS, Sheehan J, Zhu Q, **Baric RS**, Marasco WA (2014). Identification of human neutralizing antibodies against MERS-CoV and their role in virus adaptive evolution. **PNAS USA** 13;111(19):E2018-26.
   c. de Alwis R, Smith SA, Olivarez NP, Messer WB, Huynh JP, Wahala WM, White LJ, Diamond MS, **Baric RS**, Crowe JE Jr, de Silva AM (2012). Identification of human neutralizing antibodies that bind to complex epitopes on dengue virions. **PNAS USA** 8;109(19):7439-44.
   d. Zhang S, Kostyuchenko VA, Ng TS, Lim XN, Ooi JS, Lambert S, Tan TY, Widman DG, Shi J, **Baric RS**, Lok SM (2016). Neutralization mechanism of a highly potent antibody against Zika virus. **Nat Commun** 24;7:13679.

Complete List of Publications in MyBibliography:
http://www.ncbi.nlm.nih.gov/sites/myncbi/ralph.baric.1/bibliography/40583903/public/?sort=date&direction=ascending. 328 total publications, >120 since 2014, overall H-index:86; 22625 total citations.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

U19 AI 142759 CETR Whitley (PI) 03/07/19-02/28/24
UAB/NIH/NIAID Antiviral Drug Discovery and Development Center Role: Baric Co-Director: Project 2.
The specific aims of the proposal will identify small molecule inhibitors of CoV replication and pathogenesis.

U19 AI109761 CETR Lipkin (PI) 03/01/14-02/28/19
(NCE) Columbia/NIH/NIAID Diagnostic and Prognostic Biomarkers for Viral Severe Lung Disease
The goal is to develop new platform technologies that use functional genomics as diagnostic and prognostic indicators of severe end stage lung disease following virus infection. Role: Project 1 Leader.

R01 AI110700 Baric/Li(MPIs) 04/20/15-03/31/20
NIH/NIAID Mechanisms of MERS-CoV Entry, Cross-species Transmission and Pathogenesis
The overall goal is to build a comprehensive understanding of the molecular mechanisms guiding group 2c CoV receptor recognition, entry and pathogenesis.

P01 AI106695 Harris (PI) 07/1/2015-6/30/20
NIH/NIAID Protective immunity following dengue virus natural infections and vaccination
Project 2: Aravinda deSilva and Ralph S. Baric (Co-PI). The goal of these studies is to identify natural correlates of protective immunity following natural infection and or vaccination.

R01 AI125198 de Silva (PI) 05/01/16-04/30/21
NIH/NIAID Preclinical assays to predict dengue vaccine efficacy
We use samples from DENV tetravalent vaccine clinical trials to identify mechanisms and correlates of protective immunity or breakthrough infections in vaccines. Role: Co-investigator

R01 AI 089728 Fang Li (PI) 07/01/16-06/30/21
NIH/NIAID Receptor recognition and cell entry of coronaviruses
The program studies receptor usage and cell entry mechanisms of emerging coronaviruses, focused on PEDV, MHV and SARS-like Coronaviruses. Role: Co-Investigator

U19 AI00625 Baric/Heise (MPIs) 9/01/17-8/31/22
NIH/NIAID Systems Immunogenetics of Biodefense Pathogens in the Collaborative Cross

We use the Collaborative Cross (CC) to identify genes and gene interactions which regulate the induction, kinetics, and magnitude of the innate, inflammatory and adaptive immune response after infection.

R01 1AI132178 Baric/Sheahan (PI) 08/15/17-8/14/22
NIH/NIAID Broad-spectrum antiviral GS-5734 to treat MERS-CoV and related emerging CoV.
The goal of this proposal is to obtain GS-5734 preclinical data for IND development and translational studies, all designed to move the therapeutic into human trials.

Not Assigned Baric (PI) 07/01/16-12/30/19
(b) (4) Breadth of Blockade Antibody Responses Following Norovirus Vaccination.
(b) (4) and UNC will collaborate to evaluate the breadth of the antibody blockade response following norovirus vaccination of about 14,000 samples in various human volunteer populations.

R01 AI108197 Baric/Denison (MPIs) 05/01/18-04/30/23
NIH/NIAID Determinants of Coronavirus Fidelity in Replication and Pathogenesis
We test if nsp14 functions in maintaining high replication fidelity and antagonizes innate immunity.

R21 AI135682 Baric/Georgiou (MPIs) 04/01/18-03/30/20
NIH/NIAID Molecular Analysis of Serum Antibody Constituents in Zika Virus Infection.
The goal of this application is to identify antibodies that make up the serologic repertoire after Zikv infection of naive and DENV preimmune individuals. Role: Co-investigator.

NIH R01AI127845 Becker-Dreps (PI) 09/01/16-08/31/21
NIH/NIAID Natural history, immunity, and transmission patterns of sapovirus in a Nicaraguan birth cohort
We study sapovirus gastroenteritis and immunity in early childhood development. We also study the potential impact of maternal immunity on infection. Role: Investigator.

R01 AI 107731 de Silva (PI) 03/01/19-02/27/24
NIH/NIAID Molecular Basis of Dengue Virus Neutralization by Human Antibodies
These studies proposed here are directly relevant to developing simple assays to predict the performance, safety and efficacy of the leading dengue vaccine candidates. Role: Co-Investigator.

48415 de Silva (PI) 06/30/16-12/31/19
(b) (4) UNC- (b) (4) study to characterize human antibody response to DENVax
The de Silva and Baric laboratories will jointly characterize the properties of neutralizing antibodies using competition assays with monoclonal antibodies and neutralization assays. Role: Investigator

D43 TW010923 Becker-Dreps/Meshnick (MPIs) 05/10/18-02/28/23
NIH/NIAID Nicaraguan Emerging and Endemic Diseases (NEED)
The goals of this program are to 1) train young Nicaraguan scientists in Infectious Disease Epidemiology at the UNC, 2) create a sustainable supply of scientists in Nicaragua and 3) foster professional growth and development among trainees and local faculty. Role: Investigator

R21 AI137887 Moorman/Heise (MPIs) 02/05/18-01/31/20
NIH/NIAID Molecular Characterization of Functional RNA Structures in the ZikV genome
The proposed studies will identify new viral virulence determinants that can be targeted to generate safer and more effective Zika virus vaccines and therapeutics. Role: Investigator

K24 AI141744 Becker-Dreps (PI) 12/06/18-11/30/23
NIH/NIAID. The Development of Norovirus Immunity in Early Childhood and Implications for Norovirus Vaccines. To acquire new research skills and carry out a research plan that will allow guidance of the development of pediatric norovirus vaccines. Role: Investigator.

U01AI149644 Baric (PI) 05/01/2019-4/30/2024
NIH/NIAID Respiratory Virus Vaccine and Adjuvant Exploration
To use systems genetic approaches to map susceptibility alleles that regulate vaccine and adjuvant performance in genetic reference models of outbred populations.

.OMB No. 0925-0001 and 0925-0002 (Rev. 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Wang, Linfa

eRA COMMONS USER NAME (credential, e.g., agency login): (b) (6)

POSITION TITLE: Professor and Programme Director

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
East China Normal University, Shanghai, China	B.S.	02/1982	Biology
University of California, Davis, USA	Ph.D.	06/1986	Molecular Biology

A. Personal Statement

My research group focuses on the investigation of emerging infectious diseases, especially those caused by zoonotic agents or with unknown etiology. Trained as a biochemist and molecular biologist, I have been working in the field of virology and infectious diseases for more than 25 years and played a key role in identification of animal links with several high-profile zoonotic agents, including Hendra virus in Australia, Nipah virus in Malaysia and SARS virus in China. In my current role as director of the Program in Emerging Infectious Diseases at Duke-NUS Medical School, I have initiated several major projects to develop cutting edge technological platforms for investigation of human infections of unknown etiology using both molecular and serological approaches. We have also started a new area of research into the interplay of immunity, inflammation, apoptosis, DNA damage repair and tumor suppression of bats as part of an ambitious goal to learn from bats on their ability to live long and co-exist with viruses largely free of clinical diseases. Over the years, I have established an extensive collaborative network with scientists all around the world, covering research and surveillance work into infections of human, animal and wildlife in a truly OneHealth approach. I have been invited by international organizations including WHO, FAO, OIE and CEPI for investigation of major disease outbreaks and for playing a consultation role in several committees in the area of zoonotic infections. My research experience and track record fit extremely well with the proposed project.

1. Li W, Shi Z, Yu M, Ren W, Smith C, Epstein JH, Wang H, Crameri G, Hu Z, Zhang H, Zhang J, McEachern J, Field H, Daszak P, Eaton BT, Zhang S Wang L-F (2005). Bats are natural reservoir of SARS-like coronaviruses. Science 310: 676-679.
2. Ge XY, Li JL, Yang XL, Chmura AA, Zhu G, Epstein JE, Mazet JK, Hu B, Zhang W, Peng C, Zhang YJ, Luo CM, Tan B, Wang N, Zhu Y, Crameri G, Zhang SY, Wang L-F, Daszak P, Shi Z (2013). Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor Nature 503: 535-8.
3. Zhang G, Cowled C, Shi, Z, Huang Z, Bishop-Lily KA, Fang X, Wynne JW, Xiong Z, Baker ML, Zhao W, Tachedjian M, Zhu Y, Zhou P, Jiang X, Ng J, Yang L, Wu L, Xiao J, Feng Y, Chen Y, Sun X, Zhang Y, Marsh GA, Crameri G, Broder CC, Frey KG, **Wang L-F**. and Wang, J (2013). Comparative Analysis of Bat Genomes Provides Insight into the Evolution of Flight and Immunity. **Science** 339: 456-60.
4. Zhou P, Fan H, Lan T, Yang XL, Shi WF, Zhang W, Zhu Y Zhang YW, Xie QM, Mani S, Zheng XS, Li B, Li JM, Guo H, Pei GQ, An XP, Chen JW, Zhou L, Mai KJ, Wu ZX, Li D, Anderson DE, Zhang LB, Li SY, Mi ZQ, He TT, Cong F, Guo PJ Huang R, Luo Y, Liu XL, Chen J, Huang Y, Sun Q, Zhang XL,

Wang YY, Xing SZ, Chen YS, Sun Y, Li J, Daszak P, **Wang L-F,** Shi ZL, Tong YG, Ma JY (2018). Fatal swine acute diarrhoea syndrome caused by an HKU2-related coronavirus of bat origin. **Nature** 556: 255-258.

B. Positions and Honors

Positions and Employment

1982 -86 Doctoral Candidate, Department of Biochemistry, University of California, Davis, USA
1986 -89 Post-doctoral Fellow, Department of Biochemistry, University of California, Davis, USA
1990 Senior Research Officer, Ctr for Molecular Bio. and Med., Monash University, Clayton, Australia
1990 -92 Research Scientist, CSIRO Australian Animal Health Laboratory (AAHL), Geelong, Australia
1992 -96 Senior Research Scientist, CSIRO AAHL, Geelong, Australia
1996 -04 Principal Research Scientist, CSIRO AAHL, Geelong, Australia
2004 -08 Senior Principal Research Scientist, CSIRO AAHL, Geelong, Australia
2008 - OCE Science Leader, CSIRO AAHL, Geelong, Australia
2012 - Professor and Director, Program in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore

Other Experience and Professional Membership

1996 - Editorial Board, Asia Pacific Journal of Molecular Biology and Biotechnology
2003 WHO SARS Scientific Research Advisory Committee
2005 - Honorary Professor, Wuhan Institute of Virology, Chinese Academy of Sciences
2006 - Editorial Board, Chinese Journal of Virology
2006 - Editorial Board, Zoonoses and Public Health
2006 -07 NH&MRC Grant Review Panel
2008 -15 Chair, ICTV Study Group, Paramyxoviridae
2009 - Honorary Professor, The University of Melbourne, Australia
2010 - Editorial Board, Frontiers in Virology
2012 - Editor-in-Chief, Virology Journal
2012 - Board of Directors, Singapore Eye Research Institute
2012 - Executive Committee, Australasian Society of Virology
2013 - WHO International Health Regulations Roster of Experts
2015 - Editorial Board, Scientific Reports

Honors

2006 CSIRO Award for Excellence in Partnership
2007 Finalist, Eureka Prize for Scientific Research
2008 CSIRO CEO Science Leader Award
2010 Elected fellow of the Australian Academy of Technological Sciences and Engineering
2011 Gardner Lecture Award, European Society of Clinical Virologist
2013 CSIRO Chairman's Medal for Research
2014 Winner, Eureka Prize for Infectious Disease Research

C. Contributions to Science

1. **Identification of bats as major reservoir of emerging zoonotic viruses.** I have used surveillance in wildlife, livestock and humans, coupled with experimental infections under BSL-2, -3, and -4, and laboratory assays to identify evidence that bats are the reservoir for a series of emerging viruses in people, including Hendra virus, Nipah virus, SARS-CoV, and others. This work has been one of the foundations for current interest in bats in EID research globally.

a. Chua KB, Crameri C, Hyatt A, Yu M, Tompang MR, Rosli J, McEachern J, Crameri S, Kumarasamy V, Eaton BT, **Wang L-F** (2007). A previously unknown reovirus of bat origin is associated with an acute respiratory disease in humans. **Proc. Natl. Acad. Sci. USA** 27: 11424-11429.

b. Mahalingam S, Herrero LJ, Playford G, Spann K, Herring B, Rolph R, Middleton D, McCall B, Field H, **Wang L-F** (2012). Hendra virus: an emerging paramyxovirus in Australia. **Lancet Infectious Diseases** 12: 799-807.

c. Zhou P, Fan H, Lan T, Yang X-L,Shi W-F, Zhang W, Zhu Y, Zhang Y-W, Xie Q-M, Mani S, Zheng X-S, Li B, Li J-M, Guo H, Pei G-Q, An X-P, Chein J-W, Zhou L, Mai K-J, Wu Z-X, Li D, Anderson DE, Zhang L-B, Li S-Y, Mi Z-Q, He T-T, Cong F, Guo P-J, Huang R, Luo Y, Liu X-L, Chen J, Huang Y, Sun Q, Zhang H-L, Wang Y-Y, Xing S-Z, Chen Y-S, Sun Y, Li J, Daszak P, **Wang L-F**, Shi ZL, Tong YG, Ma JY (2018). Fatal swine acute diarrhoea syndrome caused by an HKU2-related coronavirus of bat origin. **Nature** 556:255-258.

d. Yang XL, Tan CW, Anderson DE, Jiang RD, Li B, Zhang W, Zhu Y, Lim XF, Zhou P, Liu XL, Guan W, Zhang L, Li SY, Zhang YZ, **Wang L-F,** Shi ZL (2019). Characterization of a filovirus (Mengla virus) from Rousettus bats in China. **Nat Microbiol**. 4:390-395.

2. **Establishment of bats as a new mammalian model system to study virus-host interaction and evolutionary biology.** Working with collaborators around the world, my lab has amassed an unprecedented collection of serological, tissue and other samples from bat surveillance programs. I have used these to develop and disseminate primary and immortalized bat cell lines, and a host of reagents which my team and collaborators are using to test hypotheses about why bats are able to host so many distinct viruses. Current projects include bat genomics and proteomics; examining the bat MHC, using gene knockout technology to identify links between flight, viral resistance, and longevity.

   a. Wynne JW, Shiell BJ, Marsh G, Boyd V, Monaghan P, Zhou P, Klein R, Todd S, Mok L, Green D, Tachedjian M, Baker M, Matthews D, **Wang L-F** (2014). Proteomics informed by transcriptomics reveals Hendra virus sensitizes bat cells to TRAIL mediated apoptosis. **Genome Biology** 15: 532.

   b. Xie J, Li Y, Shen X, Goh G, Zhu Y, Cui J, **Wang L-F**, Shi ZL, Zhou P (2018). Dampened STING-Dependent Interferon Activation in Bats. **Cell Host Microbe** 23(3):297-301.e4.

   c. Ahn M, Anderson DE, Zhang Q, Tan CW, Lim BL, Luko K, Wen M, Chia WN, Mani S, Wang LC, Ng JHJ, Sobota RM, Dutertre C-A, Ginhoux F, Shi Z-L, Irving A, **Wang L-F** (2019). Dampened NLRP3-mediated inflammation in bats and implications for a special viral reservoir host. **Nat Microbiol.** 4:789-799.

3. **Application of both molecular and serological platforms to pathogen discovery.** My work at CSIRO AAHL, and now at Duke-NUS has focused on the development and use of PCR and serological assays to identify novel pathogens in wildlife, livestock and people, often under outbreak conditions. This includes the discovery of bats as a reservoir for SARS-CoV, using novel serological assays and PCR techniques I developed.

   a. Bossart KN, McEacherna JA, Hickey AC, Choudhry V, Dimitrov DS, Eaton BT, **Wang L-F** (2007). Neutralization assays for differential henipavirus serology using Bio-Plex Protein Array Systems. **J. Viol. Meth.** 142: 29-40.

   b. Kaku Y, Noguchi A, Marsh G, Barr JA, Okutani A, Hotta K, Bazarzeren B, Fukushi S, Broder CC, Yamada A, Inoue I, **Wang L-F** (2012). Second generation of pseudotype-based serum neutralization assay for Nipah virus antibodies: Sensitive and high-throughput analysis utilizing secreted alkaline phosphatise. **J. Virol. Meth.** 179: 226-232.

   c. Mani S, Tan CW, **Wang L-F**, Anderson DE (2018). Serological Cross Reactivity between Zika and Dengue Viruses in Experimentally Infected Monkeys. **Virol Sin.** 33:378-381.

d. Uehara A, Tan CW, Mani S, Chua KB, Leo YS, Anderson DE, **Wang L-F** (2018). Serological evidence of human infection by bat orthoreovirus in Singapore. **J Med Virol.** 91(4).

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

9016102060 Wang (PI) 29/09/16 - 28/09/19
Ministry of Defense, Singapore
Pathogen Finder
Role: PI

NRF2016NRF-NSFC002-013 Wang (PI) 01/01/17 - 31/12/19
National Research Foundation (NRF, Singapore)
Combating the next SARS-or MERS-like emerging infectious disease outbreak by active surveillance
Role: PI

R01 AI121378 Wang (Co-PI) 01/01/16 - 31/12/20
Investigating Febrile Deaths in Tanzania (INDITe)
NIH (Sub-award from Duke University)
Role: Co-PI

NRF2018NRF-NSFC003SB-002 Wang (PI) 01/04/19 - 31/03/22
National Research Foundation (NRF, Singapore)
Synthetic biology-driven smart virus sensors for prevention and control of emerging zoonotic viral diseases
Role: PI

Completed Research Support (last 3 years only)

NRF2012NRF-CRP001-056 Wang (PI) 01/11/13 - 31/10/18
National Research Foundation (NRF, Singapore)
Learning from bats: from genomics to controlling viral infection and combating cancer
Role: Leading PI

(b) (4)

Development of multiple serological platforms for differentiation of Zika and dengue virus infections
Role: PI

CDPHRG12NOV003 Wang (PI) 01/02/14 - 31/01/17
Ministry of Health, Singapore
Establishment of serological diagnostic capability for highly virulent zoonotic viral infections in Singapore
Role: PI

DP150102569 Moseley (PI) 01/01/15 - 31/12/18
Australia Research Council, Australia
Nucleolus targeting by negative strand RNA viruses
Role: Co-PI

OMB No 0925-0001 and 0925-0002 (Rev. 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

NAME: Anderson, Danielle Elizabeth

eRA COMMONS USER NAME (credential, e.g., agency login):

POSITION TITLE: Research Assistant Professor

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Deakin University, Australia	BSc (Hons)	12/2000	Biology
Curtain University of Technology, Australia	PhD	02/2007	Virology

A. Personal Statement

As a Research Assistant Professor in the Emerging Infectious Diseases (EID) program at Duke-NUS Medical School, my research aims to identify host factors important for paramyxovirus and coronavirus replication. I serve as Scientific Director of the Duke-NUS ABSL3 laboratory, which provides infrastructure, expertise and support for research with pathogens requiring high containment. I have a background in virology, with specific training and expertise in high throughput screening. In my current role, my vision for the Duke-NUS ABSL3 is to create a world class containment research lab with an impeccable safety record. A facility that not only Duke-NUS, but Singapore can be proud of, and that enhances the biomedical research activities in Singapore by providing the opportunity for *in vitro* and *in vivo* experimentation with BSL3 pathogens. I was involved in the design and accreditation process of commissioning the Duke-NUS ABSL3, so I am intimately familiar with capacities of the facility and the regulatory framework it is embedded in. In addition to my laboratory expertise, I have extensive experience in designing animal experiments with ferrets, non-human primates and bats. As I have trained and worked at BSL3 facilities in Singapore (Duke-NUS Medical School) and the USA (Duke University), and the BSL4 facility in China (Wuhan Institute of Virology), I believe that I have the necessary broad expertise and the international network to continue my research. The current application not only builds logically on my prior work and expertise in this field but is aligned with my future research program.

1. **DE Anderson***, K Pfeffermann*, SY Kim, B Sawatsky, J Pearson, M Kovtun, DL Corcoran, Y Krebs, K Sigmundsson, SF Jamison, ZZJ Yeo, LJ Rennick, L-F Wang, PJ Talbot, WPDuprex, MA Garcia-Blanco and V von Messling (*Authors contributed equally). Comparative Loss-of-Function Screens Reveal ABCE1 as an Essential Cellular Host Factor for Efficient Translation of *Paramyxoviridae* and *Pneumoviridae*. **mBio**. 10(3) e00826-19; DOI: 10.1128/mBio.00826-19, **2019**.
2. X-L Yang, CW Tan, **DE Anderson**, R-D Jiang, B Li, W Zhang, Y Zhu, XF Lim, P Zhou, X-L Liu, W Guan, L Zhang, S-Y Li, Y-Z Zhang, L-F Wang and Z-L Shi. Characterization of a filovirus (Měnglà virus) from *Rousettus* bats in China. **Nature Microbiology**. doi: 10.1038/s41564-019-0398-5, **2019**.
3. **DE Anderson***, A Islam*, G Crameri*, S Todd, A Islam, MSU Khan, A Foord, MZ Rahman, IH Mendenhall, SP Luby, ES Gurley, P Daszak, JH Epstein and L-F Wang (*Authors contributed equally). Isolation and full-genome characterization of multiple Nipah viruses from bats, Bangladesh. **Emerging infectious Diseases**. 25(1):166-170, **2019**.
4. P Zhou, H Fan, T Lan, X-L Yang, W-F Shi, W Zhang, Y Zhu, Y-W Zhang, Q-M Xie, S Mani, X-S Zheng, B Li, J-M Li, H Guo, G-Q Pei, X-P An, J-W Chen, Li Zhou, K-j Mai, Z-X Wu, D Li, **DE Anderson**, L-B Zhang, S-Y Li, Z-Q Mi, T-T He, F Cong, P-J Guo, R Huang, Y Luo, X-L Liu, J Chen, Y Huang, Q Sun, X-L-L Zhang, Y-Y Wang, S-Z Xing, Y-S Chen, Y Sun, J LI, P Daszak, L-F Wang, Z-L Shi, Y-G Tong, J-

Y Ma. Fatal Swine Disease Outbreak Caused by a Novel HKU2-related Coronavirus of Bat Origin. **Nature**. 556(7700), 255-258., **2018**.

B. Positions and Honors

Positions and employment

2001 -03 Research Technician, Dana-Farber Cancer Institute, Harvard Medical School, Boston, Massachusetts, USA.
2006 -07 Research Technician, CSIRO Australian Animal Health Laboratory, Geelong, Australia.
2007 -10 Postdoctoral Fellow, INRS-Institut Armand-Frappier / Université du Québec, Montréal, Canada.
2010 -10 Research Scientist, INRS-Institut Armand-Frappier / World Anti-Doping Agency. Vancouver 2010 Winter Olympic Games (Feb 12-28, 2010), Vancouver, Canada.
2012 -12 Visiting Scientist, Duke University Medical Center, Department of Molecular Genetics and Microbiology, RNAi Facility (May 9- July 27, 2012), Durham, USA
2011 -17 Senior Research Fellow, Duke Medical School / National University of Singapore, Singapore.
2017 - Research Assistant Professor, Scientific Director of ABSL3 Laboratory, Duke Medical School/National University of Singapore, Singapore.

Other Experience and Professional Membership

2012 -14 Committee Member, Duke-NUS Early Career Scientists Association
2014 -19 Editorial Board Member, Journal of General Virology
2017 - Committee Member, Duke-NUS ABSL3 Biosafety Committee
2017 - Committee Member, NUS Institutional Biosafety Committee
2017 - Committee Member, National Large Animal Research Facility (NLARF) User Committee

Honors

2003 CSIRO Postgraduate Scholarship
2007 Canadian Louis Pasteur Postdoctoral Fellowship
2008 Fondation J.-Louis Lévesque Postdoctoral Fellowship
2009 Fonds de la Recherche en Santé Québec (FRSQ) Postdoctoral Fellowship
2018 National Centre for Infectious Disease short-term fellowship

C. Contributions to Science

1. **Characterization of novel paramyxoviruses.** I received my PhD from Curtin University of Technology, Australia, for work undertaken at the Australian Animal Health Laboratory on the characterization of new paramyxoviruses.
   a. **DE Anderson,** EJ Dubovi, M Yu, L-F Wang and RW Renshaw. Genome characterization of Salem virus reveals its evolutionary intermediate status in the subfamily *Paramyxovirinae*. **Archives of Virology**, 157(10), 1989-93, 2012.
   b. L Lambeth*, M Yu*, **DE Anderson***, G Crameri, BT Eaton, L-F Wang. (*Authors contributed equally). Complete genome sequence of Nariva virus, a rodent paramyxovirus. **Archives of Virology**, 154(2), 199-207, 2009.
   c. **DE Magoffin,** JS Mackenzie and L-F Wang. Genetic analysis of J-virus and Beilong virus using minireplicons. **Virology** 364(1), 103-111, 2007.
   d. Z Li, M Yu, H Zhang, **DE Magoffin,** PJM Jack, A Hyatt, H-Y Wang, and L-F Wang. Beilong virus, a novel paramyxovirus with the largest genome of non-segmented negative-stranded RNA viruses. **Virology** 346(1), 219-228, 2006.
2. **Viral pathogenesis**. My post-doctoral studies at the INRS-Institut Armand-Frappier, University of Quebec, Canada, expanded my paramyxovirus research into the area of viral pathogenesis. I studied the pathogenesis of canine distemper virus in ferrets as a surrogate model for measles virus infection in humans and developed non-human primate pathogenesis models for several viruses.

a. CW Tan, K Wittwer, XF Lim, A Uehara, S Mani, L-F Wang and **DE Anderson**. Serological evidence and experimental infection of cynomolgus macaques with pteropine orthoreovirus reveal monkeys as potential hosts for transmission to humans. **Emerging Microbes and Infections**. 8(1):787-795. doi: 10.1080/22221751.2019.1621668, 2019.
b. S Mani, CW Tan, L-F Wang and **DE Anderson**. Sero ogical Cross Reactivity Between Zika and Dengue Viruses in Experimentally Infected Monkeys. Virologica Sinica. 33(4), 378-381, 2018.
c. **DE Anderson**, A Castan, M Bisaillon, and V von Messling Elements in the Canine Distemper Virus M 3' UTR Contribute to Control of Replication Efficiency and Virulence. PLoS ONE, 7(2): e31561. doi:10.1371/journal.pone.0031561, 2012.
d. **DE Anderson**, and V von Messling Region between the Canine Distemper virus M and F genes modulates virulence by controlling fusion protein expression. **Journal of Virology**, 82(21), 10510-10518, 2008.

3. **Pathogen discovery and outbreak investigation.** I am currently involved in developing novel diagnostic platforms for the identification of not only new paramyxoviruses, but also other clinically relevant emerging pathogens, such as MERS. Using these platforms, I was part of the team that discovered SADS coronavirus, and most recently, Mengla filovirus.
   a. US Kamaraj, JH Tan, OX Mei, L Pan, T Chawla, A Uehara, L-F Wang, EE Ooi, DJ Gubler, H Tissera, LC Ng, A Wilder-Smith, P Florez de Sessions, T Barkham, **DE Anderson** and OM Sessions. Application of a targeted-enrichment methodology for full-genome sequencing of Dengue 1-4, Chikungunya and Zika viruses directly from patient samples. PLoS **Neglected Tropical Diseases**. 13(4): e0007184. doi.org/10.1371/journal.pntd.0007184, 2019.
   b. S Ommeh, W Zhang, A Zohaib, J Chen, H Zhang, B Hu, X-Y Ge, X-L Yang, M Masika, V Obanda, Y Luo, S Li, C Waruhiu, B Li, Y Zhu, D Ouma, V Odendo, L-F Wang, **DE Anderson**, J Lichoti, E Mungube, F Gakuya, P Zhou, K-J Ngeiywa, B Yan, B Agwanda and Z-L Shi. Genetic evidence of Middle East Respiratory Syndrome Coronavirus (MERS-CoV) and widespread seroprevalence among camels in Kenya. **Virologica Sinica**, 33(6):484-492, 2018.
   c. A Uehara, CW Tan, S Mani, K Chua, YS Leo, **DE Anderson** and L-F Wang Serological evidence of human infection by bat orthoreov rus in Singapore. **Journal of Medical Virology**. 1-4, 2018.
   d. ZJM Ho, HC Hapuarachchi, T Barkham, A Chow, LC Ng, JMV Lee, YS Leo, K Prem, YHG Lim, PF de Sessions, MA Rabaa, CS Chong, CH Tan, J Rajarethinam, JH Tan, **DE Anderson**, XM Ong, AR Cook, CY Chong, LY Hsu, G Yap, YL Lai, T Chawla, L Pan, S Sim, I-CM Chen, KC Thoon, CF Yung, JH Li, HLD Ng, K Nandar, PL Ooi, RTP Lin, P Aw, A Uehara, PP De, W Soon, ML Hibberd, HH Ng, S Maurer-Stroh and OM Sessions. Outbreak of Zika in Singapore – An Epidemiological, Entomological, Virological and Clinical Account. **The Lancet Infectious Diseases**. 17(8), 813-21, 2017.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

NRF2018NRF-NSFC003SB-002 in-Fa Wang (PI) 1/19 – 12/21
Synthetic biology-driven smart virus sensors for prevention and control of emerging zoonotic viral diseases.
Role: Collaborator

Y80506AYZ4 Anderson (PI) 9/18 – 9/19
Wuhan National Biosafety Laboratory, Chinese Academy of Sciences Advanced Customer Cultivation Project.
Functional genomic strategies to discover antiviral mechanisms for Nipah and MERS in bats
Role: PI

[redacted] (b) (4)/2018/0016 Anderson (PI) 9/18 – 9/19
Investigation of Flavivirus Immunity on the Vertical Transmission of Zika Virus

Role:PI

NRF2016NRF-NSFC002-013 Lin-Fa Wang (PI) 11/16 – 11/19
Combating the next SARS- or MERS-like emerging infectious disease outbreak by improving active surveillance.
Role: Collaborator

Completed Research Support

NMRC/BNIG/2030/2015 Anderson (PI) 9/15 – 9/17
New Investigators Grant. Investigation of the role of the cellular ATPase ABCE1 in paramyxovirus replication and identification of small molecule drugs that interfere with ABCE1-paramyxovirus interactions.
Role: PI

MINDEF-NUS-DIRP/2015/05 Lin-Fa Wang (PI)
Fighting the "unknowns": novel platforms for rapid detection and identification of viral agents of defence, biosecurity and public health significance.
Role: Collaborator

[redacted] (b)(4).(Pilot)/2016/0018 Lin-Fa Wang (PI)
Field-based Diagnostics for Rapid Detection of Middle Eastern Respiratory Syndrome (MERS) Coronavirus Infection.
Role: Co-I

NMRC/ZRRF/0002/2016 1/17 -1/18
Zika Response Research Fund. Development of multiple serological platforms for differentiation of Zika and dengue virus infections.
Role: Co-I

OMB No. 0925-0001 and 0925-0002 (Rev. 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Wacharapluesadee, Supaporn

eRA COMMONS USER NAME (credential, e.g., agency login): (b) (6)

POSITION TITLE: Laboratory Chief

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Chiang Mai University, Thailand	B.S.	02/1991	Medical Technology
Mahidol University, Thailand	M.S.	01/1994	Biochemistry
Chulalongkorn University, Thailand	Ph.D.	03/2006	Biomedical Sciences

A. Personal Statement

I have 20+ years in research and 15+ years of experience in emerging viral zoonoses. I have managed many internationally funded research projects, that involves working with and managing international and local interdisciplinary teams. Majority of my research projects are field surveillance in wild mammals, human behavioral risk surveys, and clinical sampling. I conduct workshops on development of novel diagnostic approaches, appropriate sample collection and handling for different pathogens, and viral characterization *in vitro* and *in vivo*. I am the Deputy Chief of Thai Red Cross Emerging Infectious Diseases Health Science Centre which conducts research on emerging zoonoses. My research background is focused on understanding the process of zoonotic disease emergence, particularly viral zoonoses. This includes identifying the bat origin of Nipah virus and MERS-CoV, and pathogenesis and diagnoses of Rabies. My study on the emergence of novel betacoronaviruses found in Thai bats, as well as Nipah virus have been published. Our centre was the first laboratory to correctly diagnose the first human MERS case in Thailand, which led to swift execution of containment measures preventing a MERS outbreak in Thailand. We are now the government's reference laboratory for emerging infectious diseases. I have been the PI on 5 multidisciplinary research projects that use epidemiology, laboratory, field science and bioinformatics to diagnose and monitor the emergence of wildlife-origin viral zoonoses, including SARS-CoV Nipah and Hendra virus, Avian influenza and novel viruses from bats. I am also the Thailand country manager for large contracts from USAID involving successful management of teams of virologists, field biologists, veterinarians, epidemiologists, hospitals and laboratorians.

1. Phumee A, Buathong R, Boonserm R, Intayot P, Aungsananta N, Jittmittraphap A, Joyjinda Y, **Wacharapluesadee S**, Siriyasatien P (2019). Molecular Epidemiology and Genetic Diversity of Zika Virus from Field-Caught Mosquitoes in Various Regions of Thailand. **Pathogens** 8(1)pii:E30.
2. Joyjinda Y, Rodpan A, Chartpituck P, Suthum K, Yaemsakul S, Cheun-Arom T, Bunprakob S, Olival KJ, Stokes MM, Hemachudha T, **Wacharapluesadee S** (2019). First Complete Genome Sequence of Human Coronavirus HKU1 from a Nonill Bat Guano Miner in Thailand. **Microbiol Resour Announc** 8(6)pii:e01457-18.

3. **Wacharapluesadee S**, Duengkae P, Chaiyes A, Kaewpom T, Rodpan A, Yingsakmongkon S, Petcharat S, Phengsakul P, Maneeorn P, Hemachudha T (2019). Longitudinal study of age-specific pattern of coronavirus infection in Lyle's flying fox (Pteropus lylei) in Thailand. **Virol J** 20;15(1):38.
4. **Wacharapluesadee S**, Sintunawa C, Kaewpom T, Khongnomnan K, Olival KJ, Epstein JH, Rodpan A, Sangsri P, Intarut N, Chindampom A, Suksawa K, Hemachudha T (2013). Group C betacoronavirus in bat guano fertilizer, Thailand. **Emerg Infect Dis** 19(8).

B. Positions and Honors

Positions and Employment

1994 -97 Biochemical Technician, Department of Entomology, AFRIMS, Thailand
1997 Researcher, Department of Immunology, Chulabhorn Research Institute, Thailand
1997 -00 Medical Technologist, The HIV/AIDS Collaboration Thai-US, Thailand
2000 -16 Laboratory Chief, Neuroscience Centre for Research and Development & WHO Collaborating Centre for Research and Training on Viral Zoonoses, Faculty of Medicine, Chulalongkorn University Hospital, Thai Red Cross Society, Thailand
2016 - Deputy Chief of Thai Red Cross Emerging Infectious Diseases Health Science Centre, Faculty of Medicine, Chulalongkorn University Hospital

Other Experience and Professional Membership

2010 -14 PREDICT Thailand Country Coordinator
2014 - Thai Ministry of Public Health (MOPH) Ebola Diagnostic Committee
2015 - PREDICT 2 Thailand Country Coordinator
2016 - Steering committee, Bat One Health Research Network, BTRP DTRA

C. Contribution to Science

1. **Research on coronavirus prevalence in Thailand.** Numerous high impact emerging viruses appear to have bat reservoirs. Our surveillance projects study the diversity of coronavirus (CoV) in bats in Thailand. We have isolated and characterized CoVs from many bat species, and detected and sequenced CoV in bat guano miner. Our surveillance studies continue to analyze the drivers of their emergence, and risk factors for spillover.

   a. Joyjinda Y, Rodpan A, Chartpituck P, Suthum K, Yaemsakul S, Cheun-Arom T, Bunprakob S, Olival KJ, Stokes MM, Hemachudha T, **Wacharapluesadee S** (2019). First Complete Genome Sequence of Human Coronavirus HKU1 from a Nonill Bat Guano Miner in Thailand. **Microbiol Resour Announc** 8(6).pii:e01457-18.

   b. **Wacharapluesadee S**, Duengkae P, Chaiyes A, Kaewpom T, Rodpan A, Yingsakmongkon S, Petcharat S, Phengsakul P, Maneeorn P, Hemachudha T (2019). Longitudinal study of age-specific pattern of coronavirus infection in Lyle's flying fox (Pteropus lylei) in Thailand. **Virol J** 20;15(1):38.

   c. Plipat T, Buathong R, **Wacharapluesadee S**, Siriarayapon P, Pittayawonganon C, Sangsajja C, Kaewpom T, Petcharat S, Ponpinit T, Jumpasri J, Joyjinda Y, Rodpan A, Ghai S, Jittmittraphap A, Khongwichit S, Smith DR, Corman VM, Drosten C, Hemachudha T (2017). Imported case of Middle East respiratory syndrome coronavirus (MERS-CoV) infection from Oman to Thailand, June 2015. **Euro Surveill** 22(33):pii: 30598.

   d. **Wacharapluesadee S**, Duengkae P, Rodpam A, Kaewpom T, Maneeom P, Kanchanasaka B, Yingsakmongkon S, Sittidetboripat N, Chareesaen C, Khlangsap N, Pidthong A, Leadprathom K, Ghai S, Epstein JH, Daszak P, Olival KJ, Blair PJ, Callahan MV and Hemachudha T (2015). Diversity of Coronavirus in Bats from Eastern Thailand. **Virol J** 12(1):57.

2. **Research on Nipah virus prevalence in Thai bats.** Nipah virus outbreaks, previously in Thailand's neighbouring country, Malaysia, and ongoing in Bangladesh have high mortality rate. Our surveillance projects study the characterization of Nipah Virus (NiV) in bats in Thailand. Our surveillance studies continue to analyze the drivers of their emergence, understanding their seasonal preference, and risk factors for spillover.
   a. **Wacharapluesadee S**, Samseeneam P, Phermpool M, Kaewpom T, Rodpan A, Maneeorn P, Srongmongkol P, Kanchanasaka B, Hemachudha T (2016). Molecular characterization of Nipah virus from Pteropus hypomelanus in Southern Thailand. **Virol J** 13(1):53
   b. **Wacharapluesadee S**, Jittmittraphap A, Yingsakmongkon S, and Hemachudha T (2016). Molecular Detection of Animal Viral Pathogens. Nipah Virus. CRC Press.
   c. **Wacharapluesadee S**, Ngamprasertwong T, Kaewpom T, Kattong P, Rodpana A, Wanghongsa S, Hemachudha T (2013). Genetic characterization of Nipah virus from Thai fruit bats (*Pteropus lylei*). **Asian Biomedicine** 7(6);813-819.
   d. Breed AC, Meers J, Sendow I, Bossart KN, Barr JA, Smith I, **Wacharapluesadee S**, Wang L, Field HE (2013). The Distribution of Henipaviruses in Southeast Asia and Australasia: Is Wallace's Line a Barrier to Nipah Virus? **PLoS One** 8(4):e61316.

3. **Rabies Neuropathogenesis, diagnosis and management.** The centre worked many years on molecular analyses of rabies, including mutational effects, and designing primers to detect Thai street rabies virus. I regularly organize workshops to teach laboratories in the region on how to correctly collect specimen and test for rabies.
   a. Hemachudha T, Ugolini G, Sungkarat W, Laothamatas J, Shuangshoti S, **Wacharapluesadee S** (2013). Human Rabies: neuropathogenesis, diagnosis and management. **Lancet Neurology** 498-513.
   b. Shuangshoti S, Thepa N, Phukpattaranont P, Jittmittraphap A, Intarut N, Tepsumethanon V, **Wacharapluesadee S**, Thorner PS, Hemachudha T (2013). Reduced viral burden in paralytic compared to furious canine rabies is associated with prominent inflammation at the brainstem level. **BMC Vet Res** 14;9(1):31.
   c. Virojanapirom P, Khawplod P, Sawangvaree A, **Wacharapluesadee S**, Hemachudha T, Yamada K, Morimoto K, Nishizono A (2012). Molecular analysis of the mutational effects of Thai street rabies virus with increased virulence in mice after passages in the BHK cell line. **Arch Virol** 157(11):2201-5.
   d. Wilde H, Hemachudha T, **Wacharapluesadee S**, Lumlertdacha B, Tepsumethanon V (2013). Rabies in Asia: The Classical Zoonosis. **Curr Top Microbiol Immunol** 365:185-203.

4. **Investigating causes of encephalitis**. More than 50% of patients presenting with fever remain undiagnosed. Our centre has focused a lot of research into diagnosing fever of unknown origins (FUO). We study epidemiology, pathology and conduct surveillance studies into viral pathogens, and autoimmune diseases.
   a. Hemachudha P, **Wacharapluesadee S**, Buathong R, Petcharat S, Bunprakob S, Ruchiseesarod C, Roeksomtawin P, Hemachudha T (2019). Lack of Transmission of Zika Virus Infection to Breastfed Infant. **Clin Med Insights Case Rep** 12:1179547619835179.
   b. Phumee A, Buathong R, Boonserm R, Intayot P, Aungsananta N, Jittmittraphap A, Joyjinda Y, **Wacharapluesadee S,** Siriyasatien P (2019). Molecular Epidemiology and Genetic Diversity of Zika Virus from Field-Caught Mosquitoes in Various Regions of Thailand. **Pathogens** 8(1).pii: E30.
   c. Phumee A, Chompoosri J, Intayot P, Boonserm R, Boonyasuppayakorn S, Buathong R, Thavara U, Tawatsin A, Joyjinda Y, **Wacharapluesadee S**, Siriyasatien P (2019). Vertical transmission of Zika virus in Culex quinquefasciatus Say and Aedes aegypti (L.) mosquitoes. **Scientific reports** 9(1):5257.

d. Thanprasertsuk S, Pleumkanitkul S, **Wacharapluesadee S**, Ponpinit T, Hemachudha T, Suankratay C (2017). HTLV-1-Associated Myelopathy/Tropical Spastic Paraparesis: the First Case Report in Southeast Asia. **AIDS Res Hum Retroviruses.**

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

USAID Emerging Pandemic Threats Mazet (PI) 10/01/14 – 09/30/19
PREDICT-2
The goal is to conduct surveillance for novel pathogens in wildlife, livestock and people; characterize human risk behavior; analyze EID risk; and design interventions in >20 countries
Role: Thailand country coordinator

[redacted] (b) (4) Wacharapluesadee (PI) 07/01/18 – 08/31/19
The goal is to support the Defense Threat Reduction Agency's (DTRA) [redacted] (b) (4) evaluation program. Responsibilities include using the specified point-of-care diagnostic(s) through the procurement of supplies, enrollment of subjects according to inclusion and exclusion criteria, testing the samples, and reporting the data to the Naval Health Research Center (NHRC).

Pathogen Surveillance for Viral Zoonoses Wacharapluesadee (PI) 12/15/16 – 06/30/20
Disease surveillance analysis of wildlife-domestic animal-human interfaces, in coordination with PREDICT USAID project.

Surveillance for Emerging Infectious Disease Pathogens at the Animal-Human Interfaces in Thailand, in Coordination with PREDICT USAID Project and the Bat Serology Study
Wacharapluesadee (PI) 06/01/18 – 04/30/20
The goal of the study is to understand and mitigate zoonotic disease using multiplex serology developed by Utah State University (USU). This is also a disease surveillance analysis of wildlife-domestic animal-human interfaces, in coordination with PREDICT USAID project.

Completed Research Support (last 3 years only) out of 14 prior awards

[redacted] (b) (4) Wacharapluesadee (PI) 04/01/16 – 03/31/19
The goal of this study was to establish a viral laboratory network in Thailand for Emerging Infectious Disease preparedness among the university laboratories and government public health laboratory.

OMB No. 0925-0001 and 0925-0002 (Rev. 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Hughes, Tom

eRA COMMONS USER NAME (credential, e.g., agency login): (b) (6)

POSITION TITLE: Director, Conservation Medicine Ltd. Project Coordinator Malaysia, EcoHealth Alliance.

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University of East Anglia, Norwich	B.S. (hons)	2002	Development Studies & Natural Resources
Capel Manor College, UK	City & Guilds (Distinction)	2003	Amenity Horticulture Phase 2 in Arboriculture
London School of Hygiene & Tropical Medicine, University of London	Post-Grad Dipl.	2009	Public Health
Mahidol-Oxford Tropical Medicine Research Unit, Open University, Bangkok	Ph.D.	Ongoing	Zoonotic Disease

A. Personal Statement

The current project brings the disciplines of virology, immunology and disease ecology together to understand and predict viral spillover. My background is a good fit for this work: I am trained in ecology, international development and public health. For the past 10 years I have acted as the Malaysian Project Coordinator for EcoHealth Alliance. I have designed, initiated and managed collaborative projects on surveillance, viral discovery and ecology of wildlife reservoirs of zoonoses. As the Malaysia country coordinator for the USAID-funded EPT/PREDICT project, which tests hundreds of wildlife, livestock and human samples annually, I will be able to support the PCR-serology data needs of the project. My current Ph.D research is focused on concurrent sampling and testing of human, wildlife and livestock in forest-inhabitant communities in Peninsular Malaysia. I am also co-PI on the DTRA funded Serological Biosurveillance study cited in this proposal. In support of EcoHealth Alliance in-country projects, I manage a staff of 13; oversee the Sabah Wildlife Health Unit (5 staff) and the Wildlife Health Genetic and Forensic laboratory which I designed, oversaw the building of, and help manage. In 2014, I incorporated and became director of Conservation Medicine Ltd. in Malaysia, to manage these and other projects.

1. Tamblyn A, O'Malley R, Turner C, **Hughes T** (2009). The Bat Fauna (Mammilla Chiroptera) of Palau Perhentian, Peninsular Malaysia. **Malayan Nature Journal** 61(1), 10-22.
2. de Jong C, Field H, Tagtag A, **Hughes T**, Dechmann D, Jayme S, Epstein J, Smith C, Santos I, Catbagan D, Lim M, Benigno C, Daszak P, Newman S (2013). Foraging Behaviour and Landscape Utilisation by the Endangered Golden-Crowned Flying Fox (Acerodon jubatus), The Philippines. **PLoS ONE** 8(11): e79665. doi:10.1371/journal.pone.0079665.
3. Salgado Lynn M, William T, Tanganuchitcharnchai A, Jintaworn S, Thaipadungpanit J, Lee M.H, Jalius C, Daszak P, Goossens B, **Hughes T**, Blacksell SD (2018). Spotted Fever Rickettsiosis in a Wildlife Researcher in Sabah, Malaysia: A Case Study. **Trop. Med. Infect. Dis** 3, 29.

4. Satjanadumrong J, Robinson, MT, **Hughes T**, Blacksell SD (2019). Distribution and Ecological Drivers of Spotted Fever Group Rickettsia in Asia. **EcoHealth** https://doi.org/10.1007/s10393-019-01409-3.

B. Positions and Honors

Positions and Employment

2004 Expedition Leader, Tropical Forest Project Malaysia, Coral Cay Conservation
2005 -07 Field Officer, Malaysia, EcoHealth Alliance
2007 - Project Coordinator Malaysia, EcoHealth Alliance
2010 - PREDICT Country Coordinator Malaysia
2014 - Director, Conservation Medicine Ltd

Other Experience and Professional Memberships

2004 Lead, Community Education Program, Conservation Issues, The Perhentian Islands, Malaysia
2005 Member, The Henipavirus Ecology Research Group
2006 Lead, Community Education Program, Bat Ecology, Tioman Island, Malaysia
2008 Recipient, Scholarship to attend the International Ecology & Health Forum, Merida, Mexico
2008 - Reviewer, *EcoHealth* Journal
2010 Member, Philippine government/Food and Agriculture Organization of the United Nations mission to investigate Philippine bats as a possible reservoir of Reston Ebolavirus
2014 Invited Presenter, Disease Ecology, UN Special Rapporteur

C. Contributions to Science

1. Surveillance for emerging viruses in Southeast Asia

As project coordinator in Malaysia for EcoHealth Alliance, and now Director of Conservation Medicine Ltd, I have designed and led field programs that underpin advances in our understanding of wildlife-origin zoonoses (e.g. Macaques and Herpes B), risk factors for emergence (e.g. Nipah virus in fruit bats), the distribution of viruses (e.g. Ebola virus in the Philippines). Through the PREDICT project I currently lead a team that has found 71 novel viruses and 26 known viruses in wildlife reservoirs, livestock and humans. I have helped develop laboratory and personnel capacity for disease surveillance at the Department of Wildlife and National Parks (DWNP), Department of Veterinary Services and Ministry of Health in Malaysia. I have trained over 350 individuals from government partners, local universities and NGOs in surveillance and diagnostics techniques including sharing SOPs and protocols. In collaboration with Sabah Wildlife Department I established the Wildlife Health, Genetic and Forensic Laboratory that has all the equipment necessary to store samples, run extractions, PCR and analysis on biological samples for disease surveillance. The lab is used to screen samples for the PREDICT and to generate PCR and serological data for EcoHealth Alliance. I also establish the new molecular zoonosis laboratories at the DWNP's National Wildlife Forensic Laboratory. The lab is used to screen samples for the PREDICT & DTRA projects and to generate PCR and serological data for EcoHealth Alliance.

a. Epstein JH, Olival KJ, Pulliam JRC, Smith C, Westrum J, **Hughes T**, Dobson AP, Zubaid A, Rahman SA, Basir MM, Field HE & Daszak P (2009). *Pteropus vampyrus*, a hunted migratory species with a multinational home-range and a need for regional management. **Journal of Applied Ecology** 46: 991-1002.
b. Halpin K, Hyatt AD, Fogarty R, Middleton D, Bingham J, Epstein JH, Sohayati AR, **Hughes T**, Smith C, Field HE, Daszak P & HERG (2011). Pteropid bats are confirmed as the reservoir hosts of henipaviruses: A comprehensive experimental study of virus transmission. **Am J Trop Med Hyg** 85: 946-95.
c. Rahman SA, Hassan L, Epstein JH, Mamat ZC, Yatim AM, Hassan SS, Field HE, **Hughes T**, Westrum J, Naim MS, Suri AS, Jamaluddin AA, Daszak P, Henipavirus Ecology Research Group (2013). Risk factors for Nipah virus infection among pteropid bats, Peninsular Malaysia. **EID** 19: 51-60.

d. Lee M-H, Rostal MK, **Hughes T**, Sitam F, Lee C-Y, Japning J, Harden ME, Griffiths A, Basir M, Wolfe N, Epstein JH, Daszak P (2015). Macacine herpesvirus 1 in long-tailed macaques, Malaysia, 2009–2011. **EID** 21(7):1107-1113.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

DTRA Epstein (PI) 05/01/17 – 4/30/22
Serological Biosurveillance for Spillover of Henipaviruses and Filoviruses at Agricultural and Hunting Human-Animal Interfaces in Peninsular Malaysia.
Role: Co-PI

USAID Emerging Pandemic Threats Mazet (PI) 10/01/14 – 09/30/19
PREDICT-2
The goal of this work is to conduct surveillance for novel pathogens in wildlife, livestock and people; characterize human risk behavior; analyze EID risk; and design interventions in >20 countries
Role: Country Coordinator Malaysia

Completed Research Support

USAID 1414374 (RDMA, Thailand) Daszak (CoP) 10/01/13 - 02/28/19
Infectious Disease Emergence and Economics of Altered Landscapes (IDEEAL)
The goal of this cooperative agreement is to analyze how land use change affects disease risk in SE Asia, and how economic costs of disease can be used to develop novel intervention policies.
Role: Deputy Chief of Party

OMB No. 0925-0001 and 0925-0002 (Rev. 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Broder, Christopher C.

eRA COMMONS USER NAME: (b) (6)

POSITION TITLE: Professor of Microbiology, Immunology and Emerging Infectious Diseases

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	COMPLETION DATE	FIELD OF STUDY
Florida Institute of Technology, Florida	B.S.	06/1983	Biological Science
Florida Institute of Technology, Florida	M.S.	12/1985	Molecular Biology
University of Florida, Florida	Ph.D.	05/1989	Immunology and Med-Micro

A. Personal Statement

My laboratory has been collaborating with EcoHealth Alliance and other groups for over 8 years with a major focus on serological assays for the detection of henipaviruses and filoviruses in wildlife, livestock, and human populations. I have been an active researcher in enveloped virus-host cell interactions for the past 30 years. Together with my collaborators, I have made significant contributions to the field. I developed the first oligomeric HIV-1 gp140 glycoprotein subunit vaccine, the vaccinia virus-based reporter gene assay for measuring viral glycoprotein-mediated membrane fusion, defined the fusion tropism of HIV-1 followed by the discovery of the HIV-1 coreceptors (CXCR4 and CCR5). In 1999, I established a collaborative international group of experts in Hendra and Nipah virus research, in areas from structural biochemistry, animal models and *in vivo* pathogenesis, to the development and testing of vaccines and therapeutics. My work includes the discovery of the Hendra and Nipah virus entry receptors (ephrin-B2/B3), and the development of the feline, ferret and African green monkey models of Hendra and Nipah virus pathogenesis with my collaborators. My lab's henipavirus glycoprotein work, with collaborators, have made the structural solutions and characterization of the F and the G-ephrin receptor glycoprotein interactions, and the discovery and development of antiviral human monoclonal antibodies to ABLV and Hendra and Nipah viruses; one (m102.4) having a Phase I clinical trial completed in 2016, and has been used by emergency protocol in 13 people in Australia and one in the US because of significant risk of infection. I developed the Hendra/Nipah subunit vaccine based on soluble Hendra G glycoprotein (HeV-sG); called Equivac® HeV (Zoetis, Inc.) the first commercialized vaccine to a BSL-4 agent, and being developed as a human use Nipha/Hendra vaccine supported by CEPI. Relevant to the present proposal, we have developed the first reverse genetics system for the henipavirus, Cedar virus, which will serve as a platform to assay henipavirus neutralization; and we have developed a panel 17+ different soluble envelope glycoproteins from all the known filoviruses and henipaviruses for serological surveillance studies, and have the tools to conduct the studies, and carry out capacity building and training programs.

1. Bonaparte MI, Dimitrov AS, Bossart KN, Crameri G, Mungall BA, Bishop KA, Choudhry V, Dimitrov DS, Wang L-F, Eaton BT, **Broder CC*** (2005). Ephrin-B2 Ligand is a Functional Receptor for Hendra Virus and Nipah Virus. **Proc Natl Acad Sci USA** 102(30):10652-7. (*from the cover*)
2. Middleton D, Pallister J, Klein R, Feng YR, Haining J, Arkinstall R, Frazer L, Huang JA, Edwards N, Wareing M, Elhay M, Hashmi Z, Bingham J, Yamada M, Johnson D, White J, Foord A, Heine HG, Marsh GA, **Broder CC**, Wang LF (2014). Hendra virus vaccine, a one health approach to protecting horse, human, and environmental health **Emerg Infect Dis**. 20(3). PMCID: PMC3944873

3. Xu K, Chan YP, Bradel-Tretheway B, Akyol-Ataman Z, Zhu Y, Dutta S, Yan L, Feng Y, Wang LF, Skiniotis G, Lee B, Zhou ZH, **Broder CC**, Aguilar HC, Nikolov DB (2015). Crystal Structure of the Pre-fusion Nipah Virus Fusion Glycoprotein Reveals a Novel Hexamer-of-Trimers Assembly. **PLoS Pathog**. 8;11(12):e1005322. doi: 10.1371/journal.ppat.1005322. PMID: 26646856.
4. Mire CE, Satterfield BA, Geisbert JB, Agans KN, Borisevich V, Yan L, Chan YP, Cross RW, Fenton KA, **Broder CC**, Geisbert TW (2016). Pathogenic Differences between Nipah Virus Bangladesh and Malaysia Strains in Primates: Implications for Antibody Therapy. **Sci Rep**. 3;6:30916. doi: 10.1038/srep30916.

B. Positions and Honors

Positions and Employment

1990 -92 National Research Council, Research Associate, Laboratory of Viral Diseases, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, Maryland.

1993 -96 IRTA Fellow, LVD, NIAID, NIH, Bethesda, Maryland.
Assistant Professor, Department of Microbiology and Immunology, Joint appointment, Molecular and Cell Biology Graduate Program, Uniformed Services University, Bethesda, Maryland.

2000 -05 Associate Professor, Department of Microbiology and Immunology, Joint appointment, Emerging Infectious Diseases Graduate Program, USUHS, Bethesda, Maryland.

2005 - Professor, Department of Microbiology and Immunology, Joint appointment, Emerging Infectious Diseases Graduate Program, USUHS, Bethesda, Maryland.

2006 -18 Director, Emerging Infectious Diseases Graduate Program, USU, Bethesda, Maryland.

2018 - Chair, Department of Microbiology and Immunology, USU, Bethesda, Maryland.

Other Experience and Professional Affiliations

2009 Member, National Veterinary Stockpile Nipah virus Countermeasures Workshop; USDA. Australia

2011 Member, Discontools Nipah Virus Infection Panel Expert Group. Gap analysis. International Federation for Animal Health Europe, Brussels, Belgium

2011 Invited expert, National Academies, Washington, DC. Evaluation of site-specific risk assessment for the National Bio- and Agro-Defense Facility (NBAF) in Manhattan, Kansas

Editorial board of *J. of Virology* (2007), *Virology* (2010), *Viruses* and *Pathogens* (2011) *Virologica Sinica* (2012)

Honor and Awards

1996 The Fellows Award for Research Excellence, Office of Science Education, NIH

1996 American Association for the Advancement of Science: Breakthrough of the Year, Science Magazine; Newcomb Cleveland Prize

1996 Outstanding Instructor in Virology, USUHS, School of Medicine

2008 The Henry Wu Award for Excellence in Basic Science Research

2013 The 3rd Sidney Pestka Lecture; 22nd Annual Philadelphia Infection & Immunity Forum

2013 The 2013 Federal Laboratory Consortium (FLC) Award for Excellence in Technology Transfer

2013 Second Finalist for the Australian Infectious Diseases Research Centre Eureka Prize

2013 The CSIRO Chairman's Medal, The Commonwealth Scientific and Industrial Research Organisation (CSIRO); Australia's national science agency

2014 The Cinda Helke Award for Excellence in Graduate Student Advocacy

2016 The James J. Leonard Award for Excellence in Translational/Clinical Research

2019 The 2019 Federal Laboratory Consortium (FLC) Award for Excellence in Technology Transfer

2019 USU Outstanding Biomedical Graduate Educator Award

C. Contributions to Science

1. **My Ph.D. thesis studies centered on the discovery and characterization of a specific receptor for human plasmin on Group A Streptococci during a rotation project as a 1st year student.** My studies revealed that certain group A streptococci elaborated surface receptors that could bind selectively a key fibrinolytic enzyme, plasmin, while having no binding ability towards the zymogen precursor plasminogen or

other serine proteases. The bacterium-bound plasmin remained enzymatically active including its ability to hydrolyze a fibrin clot. Bound plasmin could not be inhibited by its physiological regulator, alpha 2-plasmin inhibitor. Since these organisms produced streptokinase, a protein that complexes with plasminogen producing an active enzyme that can convert plasminogen to plasmin, they could accelerate the destruction of the extracellular matrix environment: findings that formed a molecular-pathogenic model for the "flesh-eating streptococci".

a. Lottenberg R, **Broder CC**, Boyle MDP (1987). Identification of a Specific Receptor for Plasmin on a Group A Streptococcus. Infection and Immunity. 55(8):1914-1918.
b. **Broder CC**, Lottenberg R, Boyle MDP (1989). Mapping of the Domain of Human Plasmin Recognized by its Unique Group A Streptococcal Receptor. Infection and Immunity. 57(9): 2597-2605.
c. **Broder CC**, Lottenberg R, von Mering GO, Johnston K, Boyle MDP (1991). Isolation of a prokaryotic plasmin receptor: relationship to a plasminogen activator produced by the same microorganism. **J. Biol. Chem.** 266:4922-28.
d. Lottenberg R, **Broder CC**, Boyle MDP, Kain SJ, Schroeder BL, Curtiss R III (1992). Cloning, Sequence Analysis, and Expression in *Escherichia coli* of a Streptococcal Plasmin Receptor. **J. Bacteriology** 174:5204-5210.

2. **My independent postdoctoral fellowship focused on the early stages of HIV-1 envelope glycoprotein mediated membrane fusion as a surrogate model of HIV-1 entry.** I established a vaccinia virus-based reporter gene assay for measuring viral (HIV-1) glycoprotein-mediated membrane fusion and generated the first panel of T-cell tropic and Macrophage-tropic HIV-1 envelope glycoprotein (Env) encoding recombinant vaccinia virus vectors and I used these tools to be the first to hypothesize that the cellular tropism of HIV-1 could be explained by specific membrane fusion factors required for the different classes of HIV-1 Envs. I also developed the first soluble and secreted full-length oligomeric HIV-1 gp140 glycoprotein and explored the importance of its native oligomeric structure in terms of its presentation of conformational and virus-neutralizing epitopes through the development and characterization of more than 100 murine monoclonal antibodies.
   a. **Broder CC,** Dimitrov DS, Blumenthal R, Berger EA (1993). The block to HIV-1 envelope glycoprotein-mediated membrane fusion in animal cells expressing human CD4 can be overcome by a human cell component(s). **Virology** 193:483-491.
   b. Nussbaum O, **Broder CC,** Berger EA (1994). HIV-1 Envelope Glycoprotein/CD4 Mediated Cell Fusion: A Novel Recombinant Vaccinia Virus-Based Assay Measuring Activation of a Reporter Gene by Bacterio-phage T7 RNA Polymerase Selectively In Fused Cells. **J.Virol.** 68:5411-5422.
   c. **Broder CC,** Earl PL, Long D, Moss B, Doms RW (1994). Antigenic implications of HIV-1 envelope glycoprotein quaternary structure: oligomer-specific and -sensitive mAbs. **PNAS** 91:11699-11703.
   d. **Broder CC**, Berger EA (1995). Fusogenic Selectivity of the Envelope Glycoprotein is a Major Determinant of HIV-1 Tropism for CD4+ T-Cell Lines vs. Macrophages. **PNAS** USA. 92:9004-08.

3. **My early studies on the cellular and viral membrane fusion tropism of HIV-1 and the development of a sensitive and specific reporter gene assay of cell-cell membrane fusion facilitated the discovery of the first membrane fusion accessory factor** (fusin, now known as CXCR4) that we earlier hypothesized existed, and this rapidly led to the discovery by us and others of the second factor for macrophage-tropic Envs (CCR5); the HIV-1 coreceptors. These findings were a significant breakthrough in HIV research leading to numerous new directions in understanding HIV-1 pathogenesis as well as new therapeutic strategies.
   a. Feng Y, **Broder CC**, Kennedy PE, Berger EA (1996). HIV-1 Entry Cofactor: Functional cDNA Cloning of a Seven-Transmembrane, G Protein-Coupled Receptor. **Science** 272:872-877.
   b. Alkhatib* G*, Combadiere C*, **Broder CC***, Feng Y*, Kennedy PE*, Murphy PM, Berger EA (1996). CC CKR5: a RANTES, MIP-1α , MIP-1β Receptor as a Fusion Cofactor for Macrophage-Tropic HIV-1. **Science** 272:1955-1958. (*equal contribution).

c. Rucker J, Samson M, Doranz BJ, Libert F, Berson JF, Yi Y, Collman RG, **Broder CC**, Vassart G, Doms RW, Parmentier M (1996). Regions in β-chemokine Receptors CCR-5 and CCR-2b that Determine HIV-1 Cofactor Specificity. **Cell** 87:1-10.
d. Edinger AL, Amedee A, Miller K, Doranz BJ, Endres M, Sharron M, Samson M, Lu Z-h, Clements JE, Murphey-Corb M, Peiper SC, Parmentier M, **Broder CC**, Doms RW (1997). Differential utilization of CCR5 by macrophage and T cell tropic simian immunodeficiency virus strains. **PNAS** USA. 94:4005-4010.

4. **My initial work on HIV-1 entry led to further independent studies which focused on follow-up investigations characterizing the roles of the HIV-1 coreceptors in the virus entry process.** These studies revealed the interplay between the HIV-1 entry receptors, mapped important domains of the coreceptors involved in HIV-1 Env interaction, and also revealed possible avenues of how an HIV-1 Env might engage and differently utilize the CXCR4 and CCR5 coreceptors for infection. In addition, I also engaged in collaborative follow-up studies exploring the utility of soluble oligomeric HIV-1 envelope glycoproteins as subunit vaccine immunogens (gp140) which I initiated at NIH while a postdoctoral fellow, with the unusual R2 HIV-1 Env isolate and led to the first NIAID program project grant funded at USU.
   a. Chabot DJ, Zhang PF, Quinnan GV, **Broder CC** (1999). Mutagenesis of CXCR4 Identifies Important Domains for HIV-1 X4 Isolate Envelope-Mediated Membrane Fusion and Virus Entry and Reveals Cryptic Coreceptor Activity for R5 Isolates. **J. Virol**. 73:6598-6609.
   b. Xiao X, Wu L, Stantchev TS, Feng Y-R, Ugolini S, Chen H, Shen Z, **Broder CC**, Sattentau QJ, Dimitrov DS (1999). Constitutive cell surface association between CD4 and CCR5. **PNAS** 96:7496-7501.
   c. Chabot DJ, Chen H, Dimitrov DS, **Broder CC** (2000). N-linked Glycosylation in CXCR4 Masks Coreceptor Function for CCR5-Dependent HIV-1 Isolates. **J. Virol.** 74:4404-4413.
   d. Zhang PF, Cham F, Dong M, Choudhary A, Bouma P, Zhang Z, Shao Y, Feng YR, Wang L, Mathy N, Voss G, **Broder CC**, Quinnan GV Jr (2007). Extensively cross-reactive anti-HIV-1 neutralizing antibodies induced by gp140 immunization. **PNAS** USA. 104(24):10193-8.

5. **My most recent research has been on emerging viruses that impact human and domestic livestock populations; including Australian bat lyssavirus (rabies-like virus), filoviruses (Ebola and Marburg) and the henipaviruses (Hendra and Nipah).** My lab was the first to publish on Hendra virus outside of Australia. I obtained the first NIAID funded project providing monetary support on select agent research to an overseas laboratory (2003). Henipavirus research has been the major focus of my lab for the past 20 years, covering areas from structural biochemistry, *in vivo* pathogenesis and animal model development to the development and testing of vaccines and therapeutics. My lab developed the first peptide henipavirus fusion inhibitors, subunit vaccine and neutralizing human monoclonal antibodies (mAb), and supported the development of the feline and ferret models of Hendra and Nipah infection and pathogenesis in Australia and the development of the first nonhuman primate model (USAMRIID). We and our collaborators tested the *in vivo* efficacy of the Hendra/Nipah vaccine (HeV-sG) and an anti-HeV/NiV G-specific neutralizing human mAb. One human mAb (m102.4) has been used by compassionate emergency protocol in 13 people in Australia and one individual in the United States; a Phase I clinical trial was completed in May, 2016. The henipavirus subunit vaccine, HeV-sG, was launched; called Equivac® HeV (Zoetis, Inc.) and is the first commercialized and deployed vaccine to a BSL-4 agent. Additional findings include the discovery of the henipavirus entry receptors (ephrin-B2/B3) and produced soluble versions of the G and F proteins facilitating their structural solutions.
   a. Bossart KN, Zhu Z, Middleton D, Klippel J, Crameri G, Bingham J, McEachern JA, Green D, Hancock TJ, Chan YP, Hickey AC, Dimitrov DS, Wang L-F, **Broder CC*** (2009). A neutralizing human monoclonal antibody protects against lethal disease in a new ferret model of acute Nipah virus infection. **Plos Pathogens** 5(10). PMCID: PMC2765826.
   b. Bossart KN, Geisbert TW, Feldmann H, Zhu Z, Feldmann F, Geisbert JB, Yan L, Feng Y-R, Brining D, Scott D, Wang Y, Dimitrov AS, Callison J, Chan Y-P, Hickey AC, Dimitrov DS, **Broder CC***,

Rockx B (2011). A neutralizing human monoclonal antibody protects African Green monkeys from Hendra virus challenge. **Sci. Transl. Med.** 3, 105ra103. *corresponding author (***from the cover***). PMCID: PMC3313625.

c. Bossart KN, Rockx B, Feldmann F, Brining D, Scott D, Lacasse R, Geisbert JB, Feng YR, Chan YP, Hickey AC, **Broder CC***, Feldmann H, Ge sbert TW (2012). A Hendra virus G glycoprotein subunit vaccine protects African green monkeys from Nipah virus challenge. **Sci Transl Med**. 4(146):146ra107. *corresponding (***from the cover***) PMCID: PMC3516289.

d. Geisbert TW*, Mire CE, Geisbert JB, Chan YP, Agans KN, Feldmann F, Fenton KA, Zhu Z, Dimitrov DS, Scott DP, Bossart KN, Feldmann H, **Broder CC*** (2014). Therapeutic treatment of Nipah virus infection in nonhuman primates with a neutralizing human monoclonal antibody. **Sci Transl Med.** *corresponding author 6(242):242ra82. PMCID: PMC4467163.

(166 publications; total citations: >19,800). more complete list of published work in MyBibliography:
http://www.ncbi.nlm.nih.gov/sites/myncbi/christopher.broder.1/bibliography/41141103/public/?sort=date&direction=ascending

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

HDTRA1-17-10037 Epstein (PI) 05/01/17 - 04/30/20
Serological Biosurveillance for Spillover of Henipaviruses and Filoviruses at Agricultural and Hunting Human-Animal Interfaces in Peninsular Malaysia.
To characterize the distribution and detect the spillover of henipaviruses and filoviruses among indigenous farming and hunting communities in Peninsular Malaysia.
Role: Co-PI)

R21 AI137813-01 Broder (PI) 04/01/18 - 03/31/20
A Recombinant Cedar Virus-based Henipavirus Replication Platform for High-throughput Inhibitor Screening.
Develop, characterize and adapt a rCedPV reporter virus for use in HTS; Optimize the HTS parameters; and pilot an HTS assay using a small molecule library.

CRADA Broder (PI) 07/01/12 - 09/30/40
Collaborative development and evaluation of an equine vaccine against Hendra virus

(b) (4) Eldridge (PI) 05/24/18 - 05/23/23
A Subunit Vaccine (HeV-sG) to Protect Against Nipah and Hendra Diseases

CRADA from (b) (4) Broder (PI)
Development of a Cedar virus-based Henipavirus neutralization assay
Develop, characterize and test chimeric, luciferase/GFP encoding henipaviruses using CedPV.

NIAID/NIH (CETR) U19AI142764 Broder (PI) 03/01/19 - 02/28/24
Advancement of Vaccines and Therapies for Henipaviruses
The Center focus on developing strategies effective against all pathogenic henipaviruses. The primary objective of the Center is to perform pivotal studies that will facilitate the development of products used for the prevention and treatment of Nipah and Hendra infections. RPs, and Center Cores: Administrative; human monoclonal antibody; and BSL-4, work together to provide broadly effective countermeasures.

Administrative Core (A) Broder (PI) 03/01/19 - 02/28/24
Description: Core A: organize, schedule, coordinate meetings between the RPs, Cores B and C, and the Scientific Advisory Committee; oversee and manage the submission of progress reports; serve as a liaison and facilitate communication between the RPs, Core staff, Scientific Advisory Committee, and the NIAID/NIH.

Recombinant CedPV-based vaccine development Broder (PI) 03/01/19 - 02/28/24
Objective of RP3 will be to use recombinant Cedar virus (rCedPV) as an authentic, non-pathogenic, live attenuated henipavirus system. RP3 will examine its potential as a live-attenuated universal henipavirus vaccine platform that can induce a long-lasting and balanced protective immune response.

OMB No. 0925-0001 and 0925-0002 (Rev. 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Laing, Eric D.

eRA COMMONS USER NAME (credential, e.g., agency login): (b) (6)

POSITION TITLE: Research Assistant Professor

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University of Maryland, College Park, MD	B.S. (hons)	05/2008	Biology
Uniformed Services University, Bethesda, MD	Ph.D.	10/2016	Emerging Infectious Diseases

A. Personal Statement

Bats are increasingly identified as animal reservoirs of medically-relevant emerging RNA viruses (e g Nipah virus, Ebola virus and SARS-coronavirus). However, the environmental, behavioral and host dynamics that contribute to spill over into human populations remains largely unknown, this is especially true for ebolaviruses. In the past year, two novel filoviruses with unknown pathogenicity have been discovered: Bombali virus and Mengla virus. We anticipate that a diversity of related-filoviruses exists undetected in bat reservoir hosts, and identifying these unknown viruses and understanding known filovirus-host interactions will improve our knowledge of bat species that are hosts for ebolaviruses. Collectively, these results will be used to understand transmission dynamics in wildlife hosts and generate risk-models for Ebola virus disease outbreaks. I have had a collaborative research relationship with the EcoHealth Alliance (EHA) for 5+ years, and this Emerging Infectious Diseases Research Centers Coordination Center (EIDRC CC) for the Emerging Infectious Diseases Research Centers (EIDRC) proposal will allow for an important extension of our collaboration and mutual research interests on emerging viruses, infectious disease surveillance and building threat reduction networks. Additionally, I have expertise in virology, biosurveillance and capacity training in international settings to successfully contribute to the aims of this proposal. In collaboration with EHA, we have developed a multiplex serologically immunoassay that can detect antibodies specific to or cross-reactive with all presently described filoviruses. This immunoassay tool will be key for detecting the serological footprint of known and unknown filoviruses in bat hosts. This assay is presently being used for biosurveillance by collaborators in Southeast Asia and South Asia. Assay validation is being undertaken between our laboratory (USU) and collaborators at the Dr. Vincent Munster's group at the NIH Rocky Mountain Laboratory and United States Army Medica Institute of Infectious Diseases.

1. **Laing ED***, Mendenhall IH*, Chen Y, Yan L, Wen DLH, Lynn JLS, Sterling SL, Skiles M, Lee BPY-H, Linster M, Wang L-F, Broder CC, Smith GJD (2018). Serologic evidence of fruit bat exposure to filoviruses, Singapore, 2011–2016. **Emerg Infect Dis.** 24(1):122-126.

B. Positions and Honors

Positions and Employment

2003 -04 Howard Hughes Medical Institute student intern, Cellular and Developmental Neurobiology Section, National Institute of Neurological Disorders and Stroke, National Institutes of Health, Bethesda, MD.
2005 -06 Undergraduate research assistant, Department of Animal and Avian Sciences, University of Maryland, College Park, MD.
2007 -08 Undergraduate research assistant, Biology Departmental Honors research, Department of Biology, University of Maryland, College Park, MD.
2008 -09 Research assistant, Department of Pharmacology, Uniformed Services University, Bethesda, MD.
2010 Research assistant, Department of Microbiology, Uniformed Services University, Bethesda, MD.
2010 -16 Graduate research student, Department of Microbiology, Uniformed Services University, Bethesda, MD.
2016 -17 Postdoctoral fellow, Henry M. Jackson Foundation, Department of Microbiology, Uniformed Services University, Bethesda, MD.
2017 -18 Scientist, Henry M. Jackson Foundation, Department of Microbiology, Uniformed Services University, Bethesda, MD.
2019 - Research Assistant Professor, Uniformed Services University, Department of Microbiology and Immunology, Uniformed Services University, Bethesda, MD.

Other Experience and Professional Membership

2009 Mentor, At-Risk Student Mentoring, Bethesda Chevy Chase High School, Bethesda, MD.
2009- 10 Mentor, EnvironMentors, Washington, D.C.
2013 Mentor, high school, undergraduate, and graduate students, Uniformed Services University, Bethesda MD.
2014 Participant, American Society of Microbiology Kadner Institute
2014 -15 Volunteer, AAAS/Senior Scientists and Engineers STEM Volunteer Program
2014 -17 Member, American Society of Tropical Medicine and Hygiene
2014 -19 Member, American Society of Microbiology
2015 -16 Member, USU Global Health Interest Group

Honors

2004 -07 Maryland House of Delegates Scholarship
2005 -07 Semester Academic Honors
2006 College Park Life Sciences Scholars Program Citation
2008 High Honors, Biology Departmental Honors Program
2015 USU Research Days Graduate Student Poster Presentation Finalist (Won)
2015 NSF East Asia and Pacific Summer Institutes (EAPSI) Fellowship
2015 -16 Val G. Hemming Fellowship, Henry M. Jackson Foundation

C. Contributions to Science

1. **Virus-host interactions.** My Ph.D. thesis research was focused on virus-host interactions: understanding bats as hosts of zoonotic viruses and Australian bat lyssavirus (ABLV) cellular entry. This work entailed exploring the antiviral mechanisms that enable cellular persistence of viruses in bats, particularly, authophagy. Findings revealed that the autophagy pathway is induced upon infection with Australian bat lyssavirus (ABLV), a Rabies-virus related virus carried by Australian *Pteropus* bats. The combined pharmacological and genetic studies of the autophagy pathway in the context of this virus-host interaction indicated that autophagy functions as an antiviral defense. The study also demonstrated that bat-derived cell lines have elevated levels of basal autophagy, which might help to explain the cellular mechanism that contribute to the ability of bats to act as host to these viruses. An additional finding from these studies was that activation of autophagy may have therapeutic benefits during neurotropic virus infection.

a. Weir DL, **Laing ED**, Smith IL, Wang L-F, Broder CC (2013). Host cell entry mediated by Australian bat lyssavirus G envelope glycoprotein occurs through a clathrin-mediated endocytic pathway that requires actin and Rab5. **Virology Journal** 11:40.
b. **Laing ED**, Sterling SL, Weir DL, Beauregard CR, Smith IL, Larsen SE, Wang L-F, Snow AL, Schaefer BC, Broder CC (2019). Enhanced autophagy contributes to reduced viral infection in black flying fox cells. **Viruses** 11:260.

2. **Molecular virology technologies.** My research experience as a postdoctoral fellow furthered my training in molecular virology techniques. I constructed a recombinant Cedar virus cDNA plasmid and optimized a reverse genetics approach to rescue a recombinant Cedar virus reporter virus, a non-pathogenic *Henipavirus* species. This virus will be used as a model *Henipavirus* to explore host cell-pathogen interactions, cellular tropism, and test novel therapeutics against henipaviruses.
   a. **Laing ED***, Amaya M*, Navaratnarajah CK, Cattaneo R, Wang L-F, Broder CC (2019). Rescue and characterization of recombinant Cedar virus, a non-pathogenic *Henipavirus* species. **Virology Journal** 15(1):56.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

(b) (4) Hertz (PI) 10/01/18 – 09/30/19
Sero-survey of Nipah virus and other pathogenic bat borne paramyxoviruses in Cambodia
The goal of this study is to retrospectively investigate potential human exposure to Nipah virus and related paramyxoviruses in geographies with and without *Pteropus* colonies to inform risk assessments of Nipah virus spillover.
Role: Co-Investigator

(b) (4) Epstein (PI) 05/01/17 – 04/30/20
Serological Biosurveillance for Spillover of Henipaviruses and Filoviruses at Agricultural and Hunting Human-Animal Interfaces in Peninsular Malaysia
The overarching goal is to characterize the distribution and detect the spillover of henipaviruses and filoviruses among indigenous farming and hunting communities in Peninsular Malaysia. As part of this process, we will build capacity at key government labs in human and animal health sectors to enhance serological surveillance in animals and human populations for these high consequence pathogens.
Role: Scientist

Completed Research Support

(b) (4) Broder (PI) 12/01/18 – 04/30/19
Chulalongkorn Luminex Training and Research Preparedness
The goal of this study was to transfer a multiplex serological assay to collaborators at the Thai Red Cross Emerging Infectious Diseases (TRC-EID) Research Center and provide in-country assay training and collaborative support. This serological assay has been designed to detect antibodies reactive with antigens from all presently described filoviruses and henipaviruses, and complement Nipah virus biosurveillance work at the TRC-EID.
Role: Co-Principal Investigator

OMB No. 0925-0001 and 0925-0002 (Rev. 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Keusch, Gerald T.

eRA COMMONS USER NAME (credential, e.g., agency login): (b) (6)

POSITION TITLE: Professor of Medicine, Associate Director, NEIDL. BU School of Medicine

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Columbia College, New York, NY	AB	06/1958	Pre-Medicine
Harvard University, Boston MA	M.D.	06/1963	Medicine
State University of NY, Buffalo NY		06/1995	Intern and Resident in Medicine
National Institutes of Health, Bethesda MD		06/1997	Research Associate
Tufts University School of Medicine/New England Medical Center, Boston MA		06/1970	Fellow in Infectious Diseases

A. Personal Statement

I have considerable experience in collaborative international research and training programs. I have held major academic leadership positions over my career. I was the Founding Chief of the Division of Geographic Medicine and Infectious Diseases at Tufts Medical School and oversaw its participation in the Rockefeller Foundation's "Great Neglected Diseases Biomedical Research Network" from 1979-1988. For the next decade I was responsible for a Rockefeller Foundation funded research and training partnership with Christian Medical College, Vellore, India. From 1998 through 2003 I was Associate Director for International Research and Director of the Fogarty International Center at the NIH. I returned to Boston in 2004 as Associate Provost for Global Health at Boston University. Since 2009 I have been the Associate Director of the National Emerging Infectious Diseases Laboratory at BU, responsible for international collaborations. I am an internist with specialty training in infectious diseases and I practiced clinical medicine in academic medical centers from 1970-1998, first at Mt. Sinai in New York and then as Division Chief at Tufts in Boston. I have been a bench and field researcher in infectious diseases from the time I was a research associate at NIAID from 1965-1967, assigned to the SEATO Medical Research Laboratory in Bangkok, Thailand, until I closed my lab in 2000. My publication record is evidence of the productivity of my laboratory. I have personally led research projects in Asia, Africa, and Latin America with NIH and other sources of support, including a major NIAID International Collaboration for AIDS Research grant in the Democratic Republic of the Congo. I have been the PI of multiple NIH training grants and have mentored and overseen the training of dozens of fellows from the U.S. and other countries. I have also personally supervised capacity building programs in low and middle income countries, and as Director of the Fogarty International Center I conceptualized and implemented programs in global health, including both communicable and non-communicable diseases. I am committed to developing sustainable, fair, equitable, and quality partnerships and supporting mutually beneficial research between research institutions in developed countries with collaborating institutions in the developing world.

B. Positions and Honors

Positions and employment

1960 -61 Research Assistant, Department of Experimental Medicine, Hebrew University, Jerusalem, Israel
1965 -67 Research Associate, National Institute of Allergy and Infectious Diseases, NIH, Bethesda MD
1967 -70 Research Fellow in Infectious Diseases (NIAID T-32 training grant) and Chief Resident in Medicine (Infectious Diseases), Tufts-New England Medical Center, Boston MA
1970 -72 Assistant Professor of Medicine, Department of Medicine, Mount Sinai School of Medicine, NY NY
1972 -77 Associate Professor of Medicine, Department of Medicine, Mount Sinai School of Medicine, NY NY
1977 -78 Professor of Medicine, Department of Medicine, Mount Sinai School of Medicine, NY NY
1977 -78 Visiting Professor of Microbiology, Columbia University College of Physicians & Surgeons, NY NY
1979 -98 Professor of Medicine and Chief, Division of Geographic Medicine and Infectious Diseases, Tufts University School of Medicine and New England Medical Center, Boston MA
1998 -03 Director Fogarty International Center and Associate Director for International Research, Office of the Director, National Institutes of Health, Bethesda MD
2004 - Professor of Medicine and International Health, Boston University, Boston MA
2004 -09 Associate Provost for Global Health, Boston University Medical Center, Boston MA
2009 - Associate Director, National Emerging Infectious Diseases Laboratory at Boston University, and Director, Collaborative Core, Boston MA

Other Experience and Professional Memberships

National Research Council/National Academy of Sciences: Committee on International Relations, World Food and Nutrition Study, Member Study Team #9; Food and Nutrition Board; Committee on International Nutrition Programs, Member and Chair, Subcommittee on Interactions of Nutrition and Infection, Member Subcommittee on Nutrition and Diarrheal Diseases Control; Roundtable on Science and Technology for Sustainability, Member; Taskforce on Linking Knowledge to Action for Sustainable Development, Member; Institute of Medicine: Committee on Health, Biomedical Research and Development, Member; Committee on Issues and Priorities for New Vaccine Development, Member; Board on Global Health, Member and Co-Chair; Forum on Microbial Threats, Member;

National Academy of Medicine: Committee on Global Surveillance Systems for Emerging Infectious Diseases of Zoonotic Origin, Co-Chair; Committee on Integrating Clinical Research Into Epidemic Response: The Ebola Experience, Co-Chair; Committee on Enhancing Global Health Security Through International Biosecurity and Health Engagement Programs, Co-Chair

National Institutes of Health: NIDDK: US-Japan Cooperative Medical Sciences Program, Nutrition and Metabolism Panel, Member and Chairman; NIAID: Bacteriology and Mycology Study Section 1; Special Emphasis Panel, "Research for the Development of Vaccines, Adjuvants, Therapeutics, Immunotherapeutics, and Diagnostics for Biodefense and SARS; Indo-U.S. Vaccine Action Program, Chair US Delegation, NICHD, Global Network for Women's and Infant Research; Multilateral Initiative on Malaria, Chair Secretariat

World Health Organization: Advisory Committee on Tobacco and Health; Advisory Committee on Health Research; TDR, Expert Advisory Panel on Health Science and Technology; Advisory Committee on Tropical Medicine (TropIKA), Chair; Strategy Advisory Committee on Stewardship for Infectious Diseases of Poverty; Global Report for Research on Infectious Diseases of Poverty, Member, Disease Reference Group 6

United States Agency for International Development: Nutrition Collaborative Research Support Program, External Evaluation Panel; Consultative Group on Vaccine Development, Member and Chair

Accreditation Council for Graduate Medical Education: Pre-review Committee for Internal Medicine Subspecialty Residency Programs (Infectious Diseases)

Infectious Diseases Society of America: Fellow; Council member; Society Awards Committee, Member

Wellcome Trust: Tropical Medicine Interest Group, Member; Joint Global Health Clinical Trials Committee, Member
Gates Foundation: Founding Board, Global Alliance to Improve Nutrition; Grand Challenges in Global Health, Scientific Advisory Board; MAL-ED Advisory Committee, Member; EED Consultation Committee, Chair
One Health Commission: Council of Advisors
Consortium of Universities for Global Health: Founding Board Member
National Center for Genetic Engineering and Biotechnology, National Science and Technology Development Agency, Government of Thailand: International Scientific Advisory Committee, Member
Institute for Healthcare Improvement: Scientific Advisory Committee, Member
Council on Health Research for Development (COHRED): Board of Directors, Chair
Nevin Scrimshaw International Nutrition Foundation: Board of Directors, Member, Vice-Chair
American Federation for Clinical Research: Member
American Society for Microbiology: Member and Fellow,
American Association for the Advancement of Science: Member
American Society for Clinical Investigation: Member
Association of American Physicians: Member
New York Academy of Sciences: Member

Honors

1972 -	American Board of Internal Medicine, Diplomate, Internal Medicine and Infectious Disease
1973 -76	Career Scientist Award, Health Research Council of the City of New York
1974 -79	Research Career Development Award, NIAID
1981	Oswald Avery Award, Infectious Diseases Society of America
1991	Heath-Clark Visiting Professor, University of London, School of Hygiene and Tropical Medicine
1997	Maxwell Finland Lectureship, Infectious Diseases Society of America
2000	Edward K. Barsky Award, Physicians Forum/Physicians for Social Responsibility
2002	Alexander Fleming Award, Infectious Diseases Society of America
2002	National Academy of Medicine, Elected Member
2009	Rama-Robbins Award, Indo-U.S. Vaccine Action Program, NIAID
2013	Distinguished Leadership Award, Consortium of Universities for Global Health

C. Contributions to Science

1. **I rediscovered Shiga toxin during my fellowship, while participating in a training program at the Institute of Nutrition for Central America and Panama in 1969.** A significant part of my research career has focused on Shiga toxin and its role in pathogenesis. The major recognized virulence factor of *Shigella* was its ability to invade gut epithelial cells; the previously described Shiga 'neurotoxin' was long forgotten until I showed that a protein produced by *Shigella dysenteriae* type 1 (Sd) caused inflammatory mucosal damage of the bowel and bloody inflammatory exudates similar to dysentery in a rabbit model. I later proved the two toxin activities were due to the same protein. My work resulted in purification of Shiga toxin (Stx), sequenced the binding subunit, identified its mammalian cell receptor, described its translocation to the cell cytoplasm via receptor mediated endocytosis, and identified its effects on vascular endothelium. This work paved the way to understand the pathogenesis of *E. coli* O157 and other serotypes associated with hemorrhagic colitis and hemolytic-uremic syndrome (HUS). My lab developed monoclonal antibodies essential for a rapid commercial diagnostic test for all Stx producing bacteria. I was principal investigator in all of these studies.

   a. **Keusch GT**, Grady GF, Mata LJ, McIver JM (1972). The pathogenesis of Shigella diarrhea. 1. Enterotoxin production by Shigella dysenteriae I. **J. Clin. Invest.** 51:1212-1218.

b. Donohue-Rolfe A, **Keusch GT**, Edson C, Thorley Lawson D, Jacewicz M (1984). Pathogenesis of Shigella diarrhea. IX. Simplified high yield purification of Shigella toxin and characterization of subunit composition and function by the use of subunit specific monoclonal and polyclonal antibodies. **J. Exp. Med.** 160:1767-1781.
c. Jacewicz M, Clausen H, Nudelman E, Donohue-Rolfe A, **Keusch GT** (1986). Pathogenesis of shigella diarrhea. XI. Isolation of a shigella toxin binding glycolipid from rabbit jejunum and HeLa cells and its identification as globotriaosylceramide. **J. Exp. Med.** 163:1391-1404.
d. Kandel G, Donohue-Rolfe A, Donowitz M, Keusch GT (1989). Pathogenesis of Shigella diarrhea. XVI. Selective targetting of Shiga toxin to villus cells of rabbit jejunum explains the effect of the toxin on intestinal transport. **J. Clin. Invest.** 84:1509-1517.

2. **In the 1980's I began work on the molecular pathogenesis of giardiasis and cryptosporidiosis.** We first developed a method to grow Giardia trophozoites in bulk using roller bottle culture, and used these parasites to Identify a trypsin-activated mannose-6-P lectin mediating binding to mammalian cell surfaces. These properties were consistent with activation in upper small bowel precisely where Giardia colonizes. We also discovered a Cryptosporidium parvum lectin which mediated binding to mammalian cells, and showed it is a member of a family of mucin-like glycoproteins containing α-N-acetylgalactosamine. Together these pioneering studies documented the role and relevance of carbohydrate binding ligands in the pathogenesis of intestinal protozoal infections. I was primary or co-investigator in all of these studies.
   a. Lev B, Ward H, **Keusch GT**, Pereira MEA (1986). Lectin activation in Giardia lamblia by host protease: A novel host parasite interaction. **Science** 232:71-73
   b. Ward HD, Alroy J, Lev BI, **Keusch GT**, Pereira MEA (1988). Analysis of surface carbohydrates of Giardia lamblia: Detection of N acetyl D glucosamine as the only saccharide moiety and identification of two distinct subsets of trophozoites by lectin binding. **J. Exp. Med.** 167:73 88.
   c. Hamer DH, Ward H, Tzipori S, Pereira MEA, Alroy JP, **Keusch GT** (1994). Attachment of Cryptosporidium parvum sporozoites to MDCK cells in vitro. **Infect Immun** 62:2208 13.
   d. Ortega-Barria E, Ward HD, **Keusch GT**, Pereira MEA (1994). Growth inhibition of the intestinal parasite Giardia lamblia by a dietary lectin is associated with arrest of the cell cycle. **J. Clin. Invest.** 94:2283-2288.

3. **I have made multiple contributions to the understanding of nutrition-infection interactions in laboratory and field research.** I developed a rat model of protein energy malnutrition and demonstrated macrophage functional abnormalities, including chemotaxis, phagocytosis, and intracellular bactericidal activity. Together with colleagues in Guatemala we documented multiple host defense defects in malnourished children including impaired neutrophil function, decreased serum opsonic activity, complement deficiency, and T-cell deficits, and their reversal with nutritional interventions. Subsequent studies in Zaire (now DRC) in AIDS patients on the pathogenesis of wasting syndrome revealed markedly elevated pro-inflammatory cytokine levels that could drive metabolic shifts underlying cachexia. HIV-infected but clinically stable non-wasted subjects also had high pro-inflammatory cytokine levels, however this was countered by elevated levels of the antagonist cytokines IL-1RA and TNFα-soluble receptor p55 at a molar ratio known to block inflammatory effects of IL-1β and TNFα in vitro. This was the first biologically plausible mechanism to explain the preservation of weight and body composition in long term clinical non-progressors.
   a. **Keusch GT**, Douglas SD, Hammer G, Braden K (1978). Macrophage antibacterial functions in experimental protein calorie malnutrition. II. Cellular and humoral factors for chemotaxis, phagocytosis, and intracellular bactericidal activity. **J. Infect. Dis.** 138:134

b. Cruz JR, Chew F, Fernandez RA, Torun B, Goldstein AL, **Keusch GT** (1987). Effects of nutritional recuperation on E rosetting lymphocytes and in vitro response to thymosin in malnourished children. **J. Ped. Gastro. Nutr.** 6:350-358.
c. Thea DM, Porat R, Khondi N, Matela B, St. Louis ME, Kaplan G, Dinarello CA, **Keusch GT** (1996). Relationship of cytokine and cytokine antagonist plasma levels to disease progression in African women with HIV-1 infection. **Ann Int Med** 124:757-762.
d. Kotler DP, Thea DM, Heo M, Allison DB, Engelson ES, Wang J, Pierson RN Jr, St Louis M, **Keusch GT** (1999). Relative influence of sex, race, environment, and HIV infection on body composition in adults. **Am J Clin Nutr** 69:432-439.

4. **I have helped the development of global health as a field of inquiry.** At the NIH I shaped the agenda for a systematic exploration of the importance of micronutrients on susceptibility to and outcome of infectious diseases, and led changes in the management of intellectual property to improve outcomes for low and middle income countries. I have promoted the inclusion of low and middle income countries in the setting of priorities and governance for research, and called for a new investment and partnerships for a global health system. I initiated research and training in diverse topics such as ethics, stigma, macroeconomics and health, and environment and health and economic development. I played a lead role in the creation of the Consortium of Universities for Global Health.
   a. **Keusch GT** (2000). The National Institutes of Health agenda for international research in micronutrient nutrition and infection interactions. **J. Infect. Dis.** 182 (Suppl 1):S139-S142.
   b. **Keusch GT** (2004). Intellectual Property and Licensing Impacts on Global Public Goods for Health: Options for public sector and academic leadership. **IP Strategy Today** 10:1-22.
   c. **Keusch GT**, Medlin CA (2003). Tapping the power of small institutions. **Nature** 422: 561-562.
   d. **Keusch GT**, Kilama WL, Moon S, Szlezák NA, Michaud CM (2010). The Global Health System: Linking Knowledge with Action - Learning from malaria. **PLoS Medicine** 7:e1000179.

Complete List of Published Work in MyBibliography
https://www.ncbi.nlm.nih.gov/pubmed/?term=keusch+gt

D. Research Support

Ongoing Research Support

5UC7 AI09532-03 R. Corley (PI) 06/01/16 – 05/31/20
National Emerging Infectious Diseases Laboratories Operations
The award provides core support for this NBL and its mission to study pathogenesis of emerging and re-emerging infectious diseases and develop diagnostics, drugs, vaccines, and treatments against them, and to support NIAID's strategic plan for biodefense research.
Role: Associate Director and Director, Collaborative Research Core

Completed Research Support (last 3 years only)

1UC7 AI0953215 R. Corley (PI) 06/01/14 – 05/31/16
National Emerging Infectious Diseases Laboratories Operations
This award provided core support for this NBL and its mission to study pathogenesis of emerging and re-emerging infectious diseases and develop diagnostics, drugs, vaccines, and treatments against them, and to support NIAID's strategic plan for biodefense research.
Role: Associate Director and Director, Collaborative Research Group Core

OMB No. 0925-0001 and 0925-0002 (Rev. 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Corley, Ronald B.

eRA COMMONS USER NAME (credential, e.g., agency login): (b) (6)

POSITION TITLE: Director, National Emerging Infectious Diseases Laboratories at Boston University
Professor and Chair, Department of Microbiology, Boston University School of Medicine

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Duke University, Durham, NC	B.S.	05/1970	Zoology
Duke University, Durham, NC	Ph D	05/1975	Microbiology & Immunology

A. Personal Statement

My role in the current application is as Contact Co-Principal Investigator. My responsibilities will include the overall administration of the Center, including monitoring of scientific progress and ensuring effective communication between EIDRC components, ensuring that budgeted funds are appropriately used, and to manage any changes that occur as the result of interactions with the EIDRC CC and with NIAID staff. I have over 4 decades of research and management experience to bring to the administration of complex applications, including the EIDRC. I have extensive experience in research in immunology and in the interactions between immune cells and viruses in experimental systems. I came to Boston University in 1994 as Chair of Microbiology, and built a research-intensive department focusing on RNA viral biology and pathogenesis. Building in these areas have continued as Director of the NEIDL. My experience in recruiting and team building will help foster a sense of shared commitment throughout the organization. I have experience in building multidisciplinary teams of faculty for innovative projects, and also foster a sense of shared commitment in team building. Because of my experience in working with faculty in diverse research fields, I was appointed Associate Provost for Research for the Boston University Medical Campus, a position in which I gained experience in working in complex organizations and dealing with diverse constituencies to achieve common goals. Since becoming director of the NEIDL, I have continued to work toward building the NEIDL from an institute that not only carries out emerging infectious diseases research at all biosafety levels, but also engages internationally for the global public health.

B. Positions and Honors

Positions and Employment

1975 -77 Member, Basel Institute for Immunology, Basel, Switzerland
1977 -79 Assistant Medical Research Professor, Department of Microbiology and Immunology, Duke University Medical Center, Durham, NC 27710
1977, Visiting Scientist, Basel Institute for Immunology, Basel, Switzerland
1979 Visiting Scientist, Basel Institute for Immunology, Basel, Switzerland
1980 Visiting Scientist, Basel Institute for Immunology, Basel, Switzerland
1978 -94 Member, Comprehensive Cancer Center, Duke University, Durham, NC
1980 -82 Assistant Professor of Immunology, Duke University School of Medicine

1982 -94 Associate Professor of Immunology, Duke University School of Medicine
1994 - Professor and Chair, Department of Microbiology, Boston University School of Medicine
2007 -14 Associate Director, National Emerging Infectious Diseases Laboratories Institute, Boston University
2009 -14 Associate Provost for Research, Boston University Medical Campus
2014 - Director, National Emerging Infectious Diseases Laboratories Institute, Boston University

Other Experience and Professional Membership

1988 -92 Immunobiology Study Section, NIH
1996 -00 Immunobiology Study Section, NIH
2004 Immunobiology Study Section, NIH
1978 - American Association of Immunologists; AAI program committee, 1991-1994
1991 - American Society for Microbiology
1992 -93 Special Reviewer, NIH SBIR Study Section
1997 -98 Chair, Cell Biology and Immunology Predoctoral Committee, HHMI/NRC
2000 Chair, Cell Biology and Immunology Predoctoral Committee, HHMI/NRC
2001 -03 Member, Research Training Fellowships for Medical Students Committee, HHMI
2005 Member, Research Training Fellowships for Medical Students Committee, HHMI
2002 Advisory Panel, Alliance for Lupus Research, NY
2005 -06 Chair, "Med into Grad Initiative" Review Committee, HHMI
2007 Member, NIH Review Panels on "B Cell Immunology and Protective HIV-1 Vaccines"
2009, 10 Member, NIH Review Panels on "Basic HIV Discovery Research"
2011 -13 Member, *ad hoc* Review Panel, "Immune Mechanisms of Virus Control" Program, NIH/NIAID
2011 -14 SmithGroup JJR Science & Technology Advisory Board
2016, 17 Reviewer, National Research Foundation, Competitive Research Program, Singapore
Ongoing: Security Risk Assessment (SRA) cleared by the FBI/CJIS through CDC for access to Biological Select Agents and Toxins (BSAT)
Ongoing: BSL-4 suit-trained and certified, Boston University

Honors

1979 -84 Leukemia Society of America Scholar
2015 Fellow of the American Association for the Advancement of Science

C. Contributions to Science

1. **Innate role of B lymphocytes in antigen capture and transport.** A body of work had shown that secreted IgM antibodies had unique functions in concentrating pathogens and antigen into secondary lymphoid organs, and prevented dissemination into vital organs. We sought to understand how IgM was responsible for these activities, and to understand the consequences for the immune system. We demonstrated that IgM immune complexes became concentrated onto marginal zone B cells, which then transported these complexes to follicular dendritic cells for deposition. This suggested an unappreciated innate role for this subset of B lymphocytes in the early steps of initiation of primary immune responses. A role for orchestrated transport of antigen and immune complexes in secondary lymphoid organs is now widely accepted as early events in immune responses.

   a. Ferguson AR, **Corley RB** (2005). Accumulation of marginal zone B cells and accelerated loss of follicular dendritic cells in NF-κB p50-deficient mice. **BMC Immunology** 6:8.
   b. Ferguson AR, Youd ME, **Corley RB** (2004). Marginal zone B cells transport and deposit IgM-containing immune complexes onto follicular dendritic cells. **Int. Immunol.** 16: 1411-1422 ("featured article of the month").
   c. Youd ME, Ferguson AR, **Corley RB** (2002). Synergistic roles of IgM and complement in antigen trapping and follicular localization. **Eur. J. Immunol.** 32: 2328-2337.

2. **The function of alternative forms of IgM antibodies in immune responses.** Data from our laboratory and others had indicated that IgM antibodies were not always secreted as pentameric molecules with J chain, but little evidence existed to indicate if these antibodies shared functions with pentameric IgM, or if they had unique functions. We demonstrated that two alternative forms of IgM, IgM hexamers and IgM monomers, had discrete activities. Hexamers active complement far more efficiently than pentamers and could be deleterious in certain autoimmune diseases, while monomers did not fix complement, lacked the ability to function in antigen trapping, and could also accelerate disease manifestations in autoimmune prone mice. These data supported the important role for strict quality control standards in the assembly and secretion of IgM antibodies for maintenance of proper homeostasis in the immune system.
   a. Youd ME, Luus L, **Corley RB** (2004). IgM monomers accelerate disease manifestations in autoimmune-prone *fas*-deficient mice. **J. Autoimmunity** 23:333-343.
   b. Hughey CT, Brewer JW, Colosia AD, Rosse WF, **Corley RB** (1998). Production of IgM hexamers by normal and autoimmune B cells: Implications for the physiologic role of hexameric IgM. **J. Immunol.** 161: 4091-4097.
   c. Brewer JW, **Corley RB** (1997). Late events in assembly regulate the polymeric structure and biological activity of secretory IgM. **Mol. Immunol.** 34: 323-331.
   d. Brewer JW, Randall TD, Parkhouse RME, **Corley RB** (1994). IgM hexamers? **Immunol. Today** 15: 165-168.

3. **Quality control in modulating the assembly and secretion of IgM.** Prior to these studies there was controversy in the field as to how J chain was added to assembling IgM, and whether the addition of J chain was responsible for catalyzing assembly of IgM into polymers. Where assembly occurred was also controversial. We demonstrated, however, that IgM assembly is regulated in the endoplasmic reticulum by a process involving thiol regulation. Further, J chain plays no role in mediated IgM assembly, and its addition is a terminally late step in the production of polymeric IgM. To complete these studies, we made use of various biochemical assays including pulse chase experiments. We also cloned and expressed J chain to demonstrate its role in modulating polymer assembly, and this work remains the definitive description of IgM assembly.
   a. Reddy PS, **Corley RB** (1999). The contribution of ER quality control to the biologic functions of secretory IgM. **Immunol. Today** 20: 582-588.
   b. Brewer JW, **Corley RB** (1996). Quality control in protein biogenesis: thiol-mediated retention monitors the redox state of proteins in the endoplasmic reticulum. **J. Cell Sci.** 109:2383-2392.
   c. Brewer JW, Randall TD, Parkhouse RME, **Corley RB** (1994). Mechanism and subcellular localization of secretory IgM polymer assembly. **J. Biol. Chem.** 269: 17338-17348.
   d. Randall TD, Brewer JW, **Corley RB** (1992). Direct evidence that J chain regulates the polymeric structure of IgM in antibody secreting B cells. **J. Biol. Chem.** 267: 18002-18007.

4. **Defining mouse mammary tumor virus as an endogenous superantigen, and demonstrating the role of B lymphocytes in the MMTV life cycle.** Prior to these studies there was evidence for the existence of that endogenous superantigens which played important roles in shaping the T cell repertoire in mice, but the identity and nature of these superantigens were unknown. During a differential subtraction cloning process, we identified a mouse mammary tumor virus, Mtv-9, as a differentially expressed gene during activation of B cells, and later linked this to superantigens and suggested a role for B cells in the MMTV life cycle.
   a. Sharma S, King LB, **Corley RB** (1988). Molecular events during B lymphocyte differentiation. Induction of endogenous mouse mammary tumor proviral *env* transcripts following B cell stimulation. **J. Immunol.** 141: 2510-2518.

b. King LB, Lund FE, White DA, Sharma S, **Corley RB** (1990). Molecular events in B lymphocyte differentiation. Inducible expression of the endogenous mouse mammary tumor proviral gene, *Mtv-9*. **J. Immunol.** 144: 3218-3227.
c. King LB, **Corley RB** (1990). Lipopolysaccharide and dexamethasone induce mouse mammary tumor proviral gene expression and differentiation in B lymphocytes through distinct regulatory pathways. **Mol. Cell. Biol.** 10: 4211-4220.
d. **Corley RB**, Lund FE (1991). Endogenous superantigens and retroviruses: "who's zooming who?". **Current Biol.** 1: 278-280.

5. **Studies on emerging viruses.** Emerging viruses present a number of interesting and important problems in understanding how they are transmitted, how they disseminate through the body, and in determining interruption strategies that could be used to combat these pathogens. Collaborative work in the NEIDL represents some aspects addressed at these concerns.
   a. Olejnik J, Ryabchikova E, **Corley RB**, Mühlberger E (2011). Intracellular events and cell fate in filovirus infection. **Viruses** 3: 1501-1531.
   b. Schultz MJ, Isern S, Michael SF, **Corley RB**, Connor JH, Frydmann HM (2017). Variable inhibition of Zika virus replication by different *Wolbachia* strains in mosquito cell cultures. **J. Virol.** 91(14). pii: e00339-17. doi: 10.1128/JVI.00339-17.

Published Work in My Bibliography:

http://www.ncbi.nlm.nih.gov/pubmed/?term=Corley+RB

D. Research Support

Ongoing Research Support

5UC7 AI095321-06 R.B. Corley (PI) 06/01/14 – 05/31/2021
National Emerging Infectious Diseases Laboratories Operations
The award provides core support for this NBL, the mission of which is to study and develop diagnostics, drugs, vaccines, and treatments against emerging and re-emerging infectious diseases and to support NIAID's strategic plan for biodefense research.
Role: NEIDL Director and Director, Immunology Core

OMB No. 0925-0001 and 0925-0002 (Rev. 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Sims, Amy Catherine

eRA COMMONS USER NAME (credential, e.g., agency login): (b) (6)

POSITION TITLE: Research Associate Professor

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University of Alabama at Birmingham, AL	B.S.	05/1995	Molecular Biology
Vanderbilt University, TN	Ph.D.	05/2001	Microbiology & Immuno.
Duke University, NC	Postdoctoral	08/2002	RNA/Protein Interaction
University of North Carolina at Chapel Hill, NC	Postdoctoral	10/2005	Virology

A. Personal Statement

The identification of highly pathogenic human coronaviruses (SARS-CoV and MERS-CoV) underscored the importance of understanding how viruses emerge from zoonotic reservoirs and how these emergent viruses replicate and cause pathogenesis in the new host. My research has focused on several key aspects of these questions by working to understand the cellular tropism of SARS-CoV and MERS-CoV in primary human lung cells, how host genetic pathways and gene networks affect virus replication and pathogenesis and how manipulating the coronavirus genome changes the host innate immune response to virus infection. I have more than 15 years' experience working with highly pathogenic human coronaviruses primarily as part of large multi-institutional projects that require constant lines of communication and data sharing to be successful. I have worked closely with Dr. Baric to lead and manage at least 4 large multi-institutional projects/awards and am familiar with all of the day to day and long term requirements for a successful collaboration. This project will extend an existing collaboration with Dr. Daszak and team at EcoHealth and world-wide and the required lines of communication have already been established to make this application a success.

Relevant publications: My most relevant work to date focuses on using primary human lung cells as culture models for human coronavirus strains which can be used to characterize the virus strains we propose to study in the current proposal.

1. **Sims A***, Sheahan TP*, Graham RL, Menachery VD, Gralinski LE, Case JB, Leist SR, Pyrc K, Feng JY, Trantcheva I, Bannister R, Park Y, Babusis D, Clarke MO, Mackman RL, Siegel D, Ray AS, Cihlar T, Jordan R, Denison MR, Baric RS (2017). Broad-spectrum antiviral GS-5734 inhibits both epidemic and zoonotic coronaviruses. **Sci Transl Med** 28;9(396). * co-first authors

2. Becker MM, Graham RL, Donaldson EF, Rockx B, **Sims A**, Sheahan T, Pickles R, Corti D, Johnston RE, Baric RS, Denison MR (2008). Platforms for the Synthetic Reconstitution of Noncultivable Zoonotic Viruses. **PNAS** 105(50): 19944-49.

3. Scobey T, Yount BL, **Sims A**, Donaldson EF, Agnihothram SS, Menachery VD, Graham RL, Swanstrom J, Bove PF, Kim JD, Grego S, Randell SH, Baric RS (2013). Reverse genetics with a full-

length infectious cDNA of the Middle East respiratory syndrome coronavirus. **PNAS** 1;110(40):16157-62.

4. Menachery VD, Yount BL, **Sims A**, Agnihothram S, Gralinski LE, Plante JA, Graham RL, Scobey T, Royal S, Pickles RJ, Randell SH, Lanzavecchia A, Marasco WA, Shi Z-L, Baric RS. (2016). SARS-like WIV1-CoV poised for human emergence. **PNAS** 15:113(11):3048-53.

B. Positions and Honors

Positions and Employment

1993 American Society of Microbiology Undergraduate Research Award
1994 Albert Einstein College of Medicine Summer Student Award
1996 -01 Graduate Student, Laboratory of Mark Denison, Vanderbilt University, Nashville, TN
1999 Dissertation Enhancement Award, Vanderbilt University
2001 -02 Postdoctoral Fellow, Duke University, Durham, NC
2002 -04 Infectious Disease Pathogenesis Training Grant Fellow (NIH/NIAID 5T32AI07151-27)
2002 -05 Postdoctoral Fellow, University of North Carolina at Chapel Hill
2005 -17 Research Assistant Professor, Department of Epidemiology, University of North Carolina
2017- Research Associate Professor, Department of Epidemiology, University of North Carolina Hons.

C. Contributions to Science

1. **In vitro models for emerging human respiratory viruses.** Finding suitable in vitro models for studying newly identified or emerged human respiratory viruses can be a challenge. Primary cells isolated from the human conducting airway can be cultured at an air liquid interface and following maturation recapitulate the morphology of the airway epithelium. These cultures provide a unique in vitro model and for one human coronavirus, HKU1, provide the only in vitro model for studying this virus.

   a. **Sims A**, Pyrc K, Dijkman R, Jebbink M, Long C, Deming D, Donaldson E, Vabret A, Baric R, van der Hoek L, Pickles R (2010). Culturing the unculturable: human coronavirus HKU1 infects, replicates, and produces progeny virions in human ciliated airway epithelial cell cultures. **J.Virol**. 84(21):11255-63.

   b. **Sims A**, Baric RS, Yount B, Burkett SE, Jeffers L, Pickles RJ (2005). SARS-CoV infection of human ciliated airway epithelium: the role of the ciliated cell in viral spread in the conducting airways of the lung. **J Virol**. 79(24):15511-15524.

   c. Huang X, Dong W, Milewska A, Golda A, Qi Y, Zhu Q, Marasco W, Baric R, **Sims A***, Pyrc K*, Li W, Sui J* (2015). HCoV-HKU1 Spike protein uses O-acetylated sialic acid as an attachment receptor determinant and employs HE protein as a receptor-destroying enzyme. **J Virol**. 89(14):7202-13. *indicates co-senior authorship

2. **Development of coronavirus infectious clones**. The isolation of coronavirus infectious clones has drastically increased the understanding of how specific genes or open reading frames affect replication and pathogenesis as well as identifying sets of mutations that can make coronavirus genomes recombination proof live vaccine vector candidates.

   a. Thornbrough JM, Jha BK, Yount B, Goldstein SA, Li Y, Elliott R, **Sims A**, Baric RS, Silverman RH, Weiss SR (2016). Middle East Respiratory Syndrome Coronavirus NS4b Protein Inhibits Host RNase L Activation. **MBio** 29;7(2).

   b. Menachery VD, Gralinski LE, Mitchell HD, Dinnon KH 3rd, Leist SR, Yount BL, Graham RL, McAnarney ET, Stratton KG, Cockrell AS, Debbink K, **Sims A**, Waters KM, Baric RS (2017). Middle East Respiratory Syndrome Coronavirus Nonstructural Protein 16 is Necessary for Interferon Resistance and Viral Pathogenesis. **mSphere** 2(6). e00346-17.

3. **Research to determine the genes that regulate the host virus interaction in primary human lung cells following highly pathogenic human coronavirus infection**. In collaboration with researchers at the University of Wisconsin Madison and Pacific Northwest National Laboratories, I have been working to identify specific host gene networks and pathways that regulate lethal human respiratory virus replication and pathogenesis. Specifically, I was interested in determining genes that regulate SARS-CoV and MERS-CoV replication in human cell lines, models of the human conducting airway and mouse models.

   a. **Sims A***, Tilton SC, Menachery VD, Gralinski LE, Schäfer A, Matzke MM, Webb-Robertson BM, Chang J, Luna ML, Long CE, Shukla AK, Bankhead III AR, Burkett SE, Zornetzer G, Tseng CK, Metz TO, Pickles R, McWeeney S, Smith RD, Katze MG, Waters KM, Baric RS (2013). Release of SARS-CoV Nuclear Import Block Enhances Host Transcription in Human Lung Cells. **J Virol**. 87(7):3885-902.

   b. Menachery VD*, Eisfeld AJ, Josset L, **Sims A**, Schaefer A, Proll S, Fan S, Li C, Neumann G, Tilton SC, Chang J, Gralinski LE, Long C, Green R, Matzke MM, Webb-Robertson BJ, Shukula AK, Burkett S, Metz TO, Pickles R, Smith RD, Waters KM, Katze M, Kawaoka Y, Baric RS (2014). Pathogenic influenza and coronaviruses utilize similar and contrasting approaches to control global ISG responses. **MBio** 5(3): e01174-14.

   c. Aevermann BD*, Pickett BE, Kumar S, **Sims A**, Sova P, Tam VC, Tchitchek N, Thomas PG, Tilton SC, Totura A, Wang J, Webb-Robertson BJ, Wen J, Weiss J, Yang F, Yount B, Zhang Q, McWeeney S, Smith RD, Waters KM, Kawaoka Y, Baric R, Katze AA, Scheuermann R (2014). A Comprehensive Collection of Systems Biology Data Characterizing the Host Response to Viral Infection. **Nature's Scientific Data** 1:140033.

   d. Menachery VD*, Schäfer A*, Burnum-Johnson KE, Mitchell HD, Eisfeld AJ, Walters KB, Nicora CD, Purvine SO, Casey CP, Monroe ME, Weitz KK, Stratton KG, M. Webb-Robertson BJ, Gralinski LE, Metz TO, Smith RD, Waters KM, Kawaoka Y^, Baric RS^, **Sims A**^ (2018). MERS-CoV and H5N1 influenza virus antagonize antigen presentation by altering the epigenetic landscape.**PNAS** 115(5):E1012-E1021. * co-first authors and ^ co-senior authors

Complete List of Published Work in NCBI MyBibliography:
http://www.ncbi.nlm.nih.gov/myncbi/collections/bibliography/49189460/

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

U19 AI142759 CETR — Whitley (PI) — 03/07/19 - 02/29/24
Antiviral Drug Discovery and Development Center
The specific aims of the proposal will identify small molecule inhibitors of CoV fidelity and RNA capping, define their mechanism of action, and determine their efficacy against SARS-CoV and across CoV families using in vivo mouse models of acute and persistent CoV disease.
Role: Investigator

U19 AI109761 CETR — Lipkin (PI) — 03/01/14 - 02/28/20
Diagnostic and Prognostic Biomarkers for Viral Severe Lung Disease
The overall goal of this program is to develop new platform technologies that use functional genomics as diagnostic and prognostic indicators of severe end stage lung disease following virus infection of the lung.
Role: Investigator

R01 AI110700 — Baric (PI) — 04/01/15 - 03/31/20
Mechanisms of MERS-CoV Entry, Cross-species Transmission and Pathogenesis

The overall goal is to build a comprehensive understanding of the molecular mechanisms guiding group 2c CoV receptor recognition, entry and pathogenesis.
Role: Investigator

1R01 AI132178-01 Sheahan/Baric (MPI) 08/06/17 - 07/31/22
Broad-spectrum antiviral GS-5734 to treat MERS-CoV and related emerging CoV
In partnership with Gilead Sciences, we aim to accelerate the preclinical development of GS-5734 and promote IND Licensure. We define the pharmacokinetics, pharmacodynamics, resistance profile, efficacy breadth and mechanism of action of GS-5734 against MERS-CoV and related emerging CoV.
Role: Investigator

Completed Research Support (last 3 years only)

[redacted] (b) (4) Kawaoka (PI) 06/01/14 - 05/31/16
Epigenetic Regulation of Interferon-Stimulated Genes Following MERS-CoV Infection
The overriding hypothesis of this supplemental application is that MERS-CoV and H5N1 manipulate host epigenetic programs to specifically down-regulate certain classes of ISGs, which likely antagonize virus replication efficiency in vitro The goal is to develop systems biology datasets and unbiased modeling algorithms to deconvolute the complex pathogen-host interactions that regulate severe disease outcomes following infection and identify common host pathways/genes that can be exploited for therapeutic control.
Role: Project PI

U19-AI100625 Baric (PI) 08/05/12 - 07/31/17
Systems Immunogenetics of Biodefense Pathogens in the Collaborative Cross
Specific Aims: In this proposal, we are utilizing the Collaborative Cross (CC), a novel panel of reproducible, recombinant inbred (RI) mouse lines to identify genes and gene interactions, which regulate the induction, kinetics, and magnitude of the innate, inflammatory and adaptive arms of the immune response following virus infection. Specifically, we will develop novel modeling algorithms to predict and validate the causal relationships between natural genetic variation and host signaling networks, immune cell recruitment, and immune function.
Role: Investigator and Co-Education Director

[redacted] (b) (4) Kawaoka (PI) 06/01/16 - 05/31/17
Systems Virology for MERS-CoV in vivo
The goal is to develop systems biology datasets and unbiased modeling algorithms to deconvolute the complex pathogen-host interactions that regulate severe disease outcomes following infection and identify common host pathways/genes that can be exploited for therapeutic control. These studies will build on our current data set by collecting data sets for MERS-CoV in vivo.
Role: Project PI

[redacted] (b) (4) Sims (PI) 06/07/17 - 06/06/18
[redacted] (b) (4)
The overall goal of this project is to test [redacted] (b) (4) protease inhibitor/interferon cocktails in comparison to and with nucleoside analog compounds to determine the best course of treatment for patients infected with highly pathogenic human coronaviruses.

U19-AI106772-01 Kawaoka (PI) 06/01/13 - 05/31/19
MERS-CoV Supplement for [redacted] (b) (4)
The proposed studies will provide a more detailed look at the intracellular environment by taking "snapshots" of the lipids, metabolytes, and proteins present during viral infection time courses. These assays will allow us to

determine the innate immune response occurring immediately following virus infection and to determine how the virus and cell interact over a 72-hour window.
Role: Project PI

OMB No 0925-0001 and 0925-0002 (Rev 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Latinne, Alice

eRA COMMONS USER NAME (credential, e.g., agency login):

POSITION TITLE: Research Scientist

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University of Namur, Belgium	B.S.	2004	Biology
University of Liege, Belgium	M.S.	2006	Animal Biology
University of Liege, Belgium	DEA	2008	Biology of Organisms
University of Liege, Belgium	Ph.D.	2012	Biology

A. Personal Statement

My research focuses on understanding the dynamics of pathogens within and among wildlife populations, livestock, and humans. I have conducted fieldwork in Asia for the past 10 years, focused on the evolutionary dynamics and co-evolution of host-pathogen (rodent-virus; bat-virus) interactions using phylogenetic and phylogeographic tools. My main interest is to analyze the risk of zoonotic pathogen emergence at high-risk human-wildlife interfaces. My published work analyzes patterns and likelihood of pathogen sharing among species, and to determine how the host phylogenetic and phylogeographic structure affects pathogen distribution and cross-species transmission. Prior to my current position at EcoHealth Alliance, I was a Marie Curie COFUND fellow conducting postdoctoral research at the Institut des Sciences de l'Evolution in Montpellier (ISEM, France) and at the Kasetsart University in Thailand.

1. **Latinne A**, Bezé F, Delhaes L, Pottier M, Gantois N, Nguyen J, Blasdell K, Dei-Cas E, Morand S, Chabé M (2018). Genetic diversity and evolution of *Pneumocystis* fungi infecting wild Southeast Asian murid rodents. **Parasitology** 145(7): 885-900.
2. Olival KJ, **Latinne A**, Islam A, Engstrand R, Hersch R, Amato G, Epstein JH, Daszak P (2016). Using bat population genetics to understand Nipah virus dynamics and cross-species transmission in south and southeast Asia. **International Bat Research Conference**, Durban.
3. Morand S, Bordes F, Chen H, Claude J, Cosson J, Galan M, Czirjak GA, Greenwood A D, **Latinne A**, Michaux J, Ribas A (2015). Global parasite and *Rattus* rodent invasions: the consequences for rodent-borne diseases. **Integrative Zoology** 10(5), 409-423.
4. **Latinne A**, Meynard CN, Herbreteau V, Waengsothorn S, Morand S, Michaux J (2015). Influence of past and future climate changes on the distribution of three Southeast Asian murine rodents. **Journal of Biogeography** 42(9), 1714-1726.

B. Positions and Honors

Employment and Positions

2012 -13 Research Associate, University of Liege, Belgium
2013 -14 Postdoctoral Researcher, Kasetsart University, Thailand

2013 -14 Postdoctoral Researcher, University Montpellier 2, France
2014 - Research Associate, University of Liege, Belgium
2015 - Research Scientist, EcoHealth Alliance

Honors

2007 Belgian Government graduate scholarship, Belgian Fund for Research in Industry and Agriculture, Belgium
2008 Belgian Government graduate scholarship, Belgian Fund for Scientific Research, Belgium
2013 Award "VOCATIO" (Vocation grant) from the Belgian Foundation of Vocation (VOCATIO)
2013 Marie Curie COFUND fellowship from European Union

C. Contributions to Science

1. **Understanding the origin and cross-species transmission of bat coronaviruses.** Bats harbor a large diversity of coronaviruses (CoVs) and have been identified as the natural reservoirs and evolutionary sources of several emerging human coronaviruses, including Severe Acute Respiratory Syndrome (SARS-CoV) that emerged in China in 2002. However, CoV evolution and diversification in their bat hosts remain poorly understood. In this study, I used a Bayesian statistical framework to study the macroevolution of bat CoVs and their cross-species transmission dynamics and dispersal in China. This work reveals that alpha-CoVs were able to switch hosts more frequently and between more distantly related taxa than beta-CoVs during their evolution and suggest that phylogenetic distance among hosts represents higher constraint on host switches for beta- than alpha-CoVs. We identify the host taxa and geographic regions that together define hotspots of CoV phylo-diversity in China, allowing for more targeted surveillance of bat-borne CoVs and early detection to mitigate disease emergence and outbreaks in the future.

   a. **Latinne A**, Hu B, Zhu G, Zhang L, Zambrana-Torrelio C, Olival KJ, Li B, Zhang W, Shi Z, Daszak P **(November 2018).** Diversity and origin of bat coronaviruses in China. Presentation at **The 3rd Symposium of Biodiversity and Health in Southeast Asia**, Chiayi, Taiwan.

   b. **Latinne A,** Hu B, Zhu G, Zhang L, Zambrana-Torrelio C, Olival KJ, Li B, Zhang W, Shi Z, Daszak P **(October 2018).** Origin and cross-species transmission of bat coronaviruses in China. Presentation at **The 8th International Symposium on Emerging Viral Diseases**, Wuhan, China.

2. **Phylogeography of Nipah virus and its bat host in Bangladesh.** The structure and connectivity of wildlife host populations may strongly influence zoonotic disease dynamics, evolution, and therefore spillover risk to people. In Bangladesh, *Pteropus medius* is the putative reservoir for Nipah virus. In this study, I use mitochondrial DNA and nuclear microsatellite markers to measure the population structure, demographic history, and phylogeography of *P. medius* in Bangladesh to better inform the dynamics, distribution, and evolutionary history of Nipah virus. We combine this with a phylogeographic analysis of all known Nipah virus sequences and strains currently available.

   a. Olival KJ, **Latinne A**, Islam A, Engstrand R, Hersch R, Amato G, Epstein JH, Daszak P (2016). Using bat population genetics to understand Nipah virus dynamics and cross-species transmission in south and southeast Asia. **International Bat Research Conference**, Durban.

3. **Research on rodent pathogens diversity and co-evolution.** Rodents are recognized as hosts of at least 60 zoonotic diseases that represent a serious threat to human health. Rodents have also been involved in the emergence and spread of infectious diseases of human health importance such as plague, murine typhus, scrub typhus, leptospirosis and hantavirus hemorrhagic fever. My postdoctoral work aimed at better understanding the co-evolution of rodent pathogens and their hosts in Southeast Asia.

a. **Latinne A**, Bezé F, Delhaes L, Pottier M, Gantois N, Nguyen J, Blasdell K, Dei-Cas E, Morand S, Chabé M (2017). Genetic diversity and evolution of *Pneumocystis* fungi infecting wild Southeast Asian murid rodents. **Parasitology** 145(7): 885-900.
b. Morand S, Bordes F, Chen H, Claude J, Cosson J, Galan M, Czirjak GA, Greenwood A D, **Latinne A**, Michaux J, Ribas A (2015) Global parasite and *Rattus* rodent invasions: the consequences for rodent-borne diseases. **Integrative Zoology** 10(5), 409-423.

4. **Research on rodent evolution and phylogeography in Southeast Asia.** Southeast Asia is a diversification center of murine rodents but this important rodent diversity remains poorly known. My PhD work aimed at better understanding the evolution and ecology of rodents in Southeast Asia.

   a. **Latinne A**, Meynard CN, Herbreteau V, Waengsothorn S, Morand S, Michaux J (2015). Influence of past and future climate changes on the distribution of three Southeast Asian murine rodents. **Journal of Biogeography** 42(9), 1714-1726.

   b. **Latinne A**, Galan M, Waengsothorn S, Rojanadilok P, Eiamampai K, Sribuarod K, Michaux J (2014). Diet analysis of *Leopoldamys neilli*, a cave-dwelling rodent in Southeast Asia, using Next-Generation Sequencing from feces. **Journal of Cave and Karst Studies**, 76(2): 139-145.

   c. **Latinne A**, Waengsothorn S, Rojanadilok P, Eiamampai K, Sribuarod K, Michaux J (2013). Diversity and endemism of Murinae rodents in Thai limestone karsts. **Systematics and Biodiversity** 11(3): 323-344.

   d. **Latinne A**, Waengsothorn S, Rojanadilok P, Eiamampai K, Sribuarod K, Michaux J (2012). Combined Mitochondrial and Nuclear Markers Revealed a Deep Vicariant History for *Leopoldamys neilli*, a Cave-Dwelling Rodent of Thailand. **PLOS One** 7(10), e47670.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

USAID Emerging Pandemic Threats Mazet (PI) 10/01/14 - 09/30/19
PREDICT-2
The goal is to conduct surveillance for novel pathogens in wildlife, livestock and people; characterize human risk behavior; analyze EID risk; and design interventions in >20 countries
Role: Research Scientist

OMB No 0925-0001 and 0925-0002 (Rev 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Phelps, Kendra

eRA COMMONS USER NAME (credential, e.g., agency login):

POSITION TITLE: Field Scientist

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Auburn University, USA	B.S.	05/2003	Zoology
Oklahoma State University	M.Sc.	12/2006	Zoology
Texas Tech University	Ph.D.	08/2016	Zoology
Texas Tech University	Post Doc	12/2017	Zoology – Bat Ecology

A. Personal Statement

Human-environment-wildlife interactions are the driving interest behind my research pursuits. Specifically, my research aims to identify the consequences of land-use change and increased human-wildlife interactions on the persistence of wildlife populations as well as the implications for zoonotic disease spillover to exposed human populations. My research takes a multidisciplinary approach, incorporating applied ecology, wildlife epidemiology, and disease surveillance, to understand the role of human disturbance in shaping wildlife communities, ranging from assemblage composition and population demographics to individual health and infection dynamics. I have 17 years of experience conducting field-based research on the ecology and health of wildlife, with a focus on bats and rodents, and 3 years of international experience in bat disease surveillance in often resource-limited and remote sites. Moreover, I integrate principles of ecophysiology and disease ecology to identify specific environmental and ecological drivers that enhance pathogen persistence and transmission between bat hosts and to proactively prevent spillover events and safeguard human and animal health. My research has led to a better understanding of the consequences of environmental manipulation on bat health and disease dynamics at the human-wildlife interface, and development of a cave prioritization index to promote bat conservation.

1. **Phelps KL**, Jose R, Labonite M, Kingston T (2016). Correlates of cave-roosting bat diversity as an effective tool to identify priority caves. **Biological Conservation** 201: 201-209.
2. **Phelps KL**, Kingston T (2018). Environmental and biological context modulates the physiological stress response of bats to human disturbance. **Oecologia** 188: 41-52.
3. Willoughby AR, **Phelps K**, PREDICT Consortium, Olival KJ (2017). A comparative analysis of viral richness and viral sharing in cave-roosting bats. **Diversity** 9: 35.
4. Olival KJ, **Phelps K**, Alhmoud N, Sidamonidze K, Urushadze L, Ali S, Bilgin R, Hamel L, Karesh W (2018). Bats and viruses in Western Asia: a model for One Health surveillance using research networks A poster presented at the 48th North American Symposium on Bat Research

B. Positions and Honors

Positions and Employment

2001 -03 Laboratory technician, College of Veterinary Medicine – Auburn University (USA)
2003 -06 Graduate teaching assistant, Department of Zoology – Oklahoma State University (USA)
2003 -06 Field technician, Oklahoma Cooperative Fish & Wildlife Research Unit (USA)
2006 -08 Research associate, Sternberg Museum of Natural History (USA)
2008 -14 Graduate teaching assistant, Department of Biological Sciences – Texas Tech University (USA)
2014 -15 Research technician, Department of Biological Sciences – Texas Tech University (USA)
2016 -17 Postdoctoral research associate, Department of Biological Sciences – Texas Tech University (USA)
2017 - Biostatistics consultant, Texas Integrated Diving and Ecological Studies Laboratory (USA)
2018 - Field scientist, EcoHealth Alliance (USA)

Other Experience and Professional Memberships

2009 - Member, North American Society for Bat Research
2011 - Member, Society of Conservation Biology
2011 - Steering committee member, Southeast Asian Bat Conservation Research Unit (SEABCRU)
2011 - Member, Cave Bat Working Group – SEABCRU
2015 - Member, Bat-Human Interactions Working Group – SEABRU
2016 - Red List Authority (Bats), International Union for the Conservation of Nature (IUCN)
2018 - Implementing member, Western Asia Bat Research Network
Reviewer: *Frontiers in Ecology & Evolution*, *Integrative and Comparative Biology*, *PeerJ*, *Journal of Applied Ecology*, *Acta Chiropterologica*, *Diversity*, *EcoHealth*, *Environmental Monitoring and Assessment*, *Ecological Research*, *American Midland Naturalist*, *Environmental Science and Pollution Research*, *Western North American Naturalist*, *The Prairie Naturalist*, *The Southwestern Naturalist*

Honors

2008 -13 AT&T Foundation Chancellor Fellow, Texas Tech University
2009 Luis F. Bacardi Fruit Bat Conservation and Research Scholar
2010 Bat Conservation International Student Scholar
2011 Fulbright Fellow - Malaysia, U.S. Department of State
2011 Student Explorer, The Explorers Club Exploration Fund
2011 Lewis and Clark Fund for Exploration and Field Research Scholar
2012 Fulbright Fellow - Philippines, U.S. Department of State
2012 Ralph Stone Fellow, National Speleological Society
2012 Bat Conservation International Student Scholar
2012 James D. and Marry Hazlewood Graduate Fellow, Texas Tech University
2012 Graduate Research Scholar, Cave Research Foundation
2013 Student of Integrated Scholarship, Texas Tech University
2014 -16 Helen DeVitt Jones Graduate Scholar, Texas Tech University
2015 -16 Doctoral Dissertation Fellow, Texas Tech University

C. Contributions to Science

1. **Wildlife ecology & conservation.** Human-bat interfaces, such as bat-occupied caves visited for tourism or guano harvesting or bushmeat markets, must be considered when monitoring public health while promoting wildlife conservation, and demands a multidisciplinary approach. Bats and rodents are the two largest

mammalian orders, yet many populations are declining globally. Working with collaborators in the Philippines, I identified anthropogenic and environmental drivers of assemblage composition, population abundance, and individual health in cave-roosting bats of the Philippines. This research led to the identification of environmental and human disturbance factors that are most influential in structuring bat assemblages, thus allowing for prioritization of caves to conserve cave bats. Moreover, my findings highlight that human disturbance at roosting and foraging sites contributes to reduced diversity and simplified composition in cave bat assemblages. Minimizing disease risks to public health requires integrating tools from applied ecology and analytical modelling to identify ecological drivers that promote virus persistence and spread in bat assemblages. We found that transmission rates of viruses between bat species is strongly associated with roosting ecology, with species that roost in caves having the highest rate of virus sharing with co-roosting species. Caves often house a diversity of bat species, some of which form large aggregations, so assemblage composition and population structure likely contributes to infection dynamics in cave-roosting bats.

a. **Phelps KL**, Jose R, Labonite M, Kingston T (2018). Assemblage and species threshold responses to environmental and disturbance gradients shape bat diversity in disturbed cave landscapes. **Diversity** 10: 55.

b. **Phelps KL**, Jose R, Labonite M, Kingston T (2016). Correlates of cave-roosting bat diversity as an effective tool to identify priority caves. **Biological Conservation** 201: 201-209.

c. Willoughby AR, **Phelps K**, PREDICT Consortium, Olival KJ (2017). A comparative analysis of viral richness and viral sharing in cave-roosting bats. **Diversity** 9: 35.

d. **Phelps KL** McBee K. (2009). Ecological characteristics of small mammal communities at a Superfund Site. **American Midland Naturalist** 161: 57-68.

2. **Bat health & disease surveillance.** Bats are reservoir hosts for numerous zoonotic diseases, including fatal diseases such as rabies, Hendra, and Marburg. Despite the potentially devastating consequences of zoonotic disease spillover on public health, few studies have examined the ecological mechanisms that promote zoonotic disease persistence in diverse bat assemblages. To understand the underlying individual-level mechanisms that drive compositional turnover and species loss in bat communities, I assessed physiological health of 725 individual bats (i.e., neutrophil-to-lymphocyte ratios, leukocyte counts, body condition, and ectoparasite counts) exposed to gradients of cave disturbance. I also included measures of cave quality (i.e., size and complexity), social context (i.e., species richness, conspecific and heterospecific abundance), and intrinsic traits (i.e., sex, reproductive state) to understand how context-specific factors may modulate individual health when exposed to disturbance. My findings reveal the importance of assemblage and population dynamics and ecological traits (e.g., sex, reproductive state) on the health of cave-roosting bats, which may influence an individual's susceptibility to infection. Working with regional collaborators from Turkey, Armenia, Georgia, Pakistan, and Jordan, I am characterizing the diversity and composition of bat species and associated coronaviruses across Western Asia in conjunction profiling bat-human interfaces at sampled sites to assess the risk of zoonotic disease emergence in the region.

   a. **Phelps KL**, Kingston T (2018). Environmental and biological context modulates the physiological stress response of bats to human disturbance. **Oecologia** 188: 41-52.

   b. Olival KJ, **Phelps K**, Alhmoud N, Sidamonidze K, Urushadze L, Ali S, Bilgin R, Hamel L, Karesh W (2018). Bats and viruses in Western Asia: a model for One Health surveillance using research networks. A poster presented at the 48th North American Symposium on Bat Research.

   c. Willoughby AR, **Phelps K**, PREDICT Consortium, Olival KJ (2017). A comparative analysis of viral richness and viral sharing in cave-roosting bats. **Diversity** 9: 35.

d. **Phelps** KL, Olival KL, Kingston T (2010). Influence of anthropogenic disturbance on cave-roosting bats and the potential emergence of associated zoonotic diseases. A poster presented at the 15th International Bat Research Conference.

3. **Network coordination & capacity building.** Zoonotic threats to public health are typically shared across a region due to shared host species distributions, consequently our ability to take proactive actions against such threats requires coordinated initiatives to build the capacity of multidisciplinary partners to study host ecology and disease surveillance across the region. I serve on the steering committee of the NSF-funded Southeast Asian Bat Research Unit (2011 – present), and work collaboratively with a large multidisciplinary network of 30+ international bat researchers to promote capacity building and research activities of local bat biologists in Southeast Asian countries. Specifically, I conduct workshops on how to design and implement research studies in bat ecology, including publishing results in peer-reviewed journals. I provide hands-on training on proper techniques for capturing, handling, and identifying bat species; collecting morphological measurements and ecological and acoustic data; taking diagnostic samples to assess measures of stress physiology; surveying and mapping cave systems, and site characterization to assess human disturbance levels and types of bat-human interactions) in Vietnam, Malaysia, Indonesia, Philippines, and Thailand. Furthermore, I serve as the Field Scientist for the DTRA-funded Western Asia Bat Research Network (WAB-Net, 2018 – present) with the primary responsibility to establish and build capacity in zoonotic disease field surveillance with local multidisciplinary partners across Western Asia. Working with 10+ WAB-Net partners, I developed standardized field protocols for collecting non-lethal samples from bats and characterization of study sites to identify potential routes of interactions between bats and humans and/or domestic animals as well as developed standardized laboratory protocols for detecting and characterizing coronavirus diversity. I coordinate (e.g., procure research permits, necessary supplies and equipment, export and import permits, etc.) and oversee all sampling events across the region to ensure standardization of data collection and sample testing as well as biosafety (PPE) guidelines.

   a. Al-Mateen, XA, Alias N, Furey NR, Ingle N, **Phelps K**, Sedlock JL, Waldien D (2011). Participants weigh in on the status of cave bats in Southeast Asia. Report to the 2nd International Southeast Asian Bat Conference. http://www.seabcru.org/index.php/cave-bats/72-conference- participants-weigh-in-on-the-status-of-cave-bats-in- southeast-asia

   b. **Phelps KL**, Hamel L, Alhmoud N, Ali S, Bilgin R, Sidamondize K, Urushadze L, Karesh W, and Olival KJ (2019). Bat research networks and viral surveillance: gaps and opportunities in Western Asia. **Viruses** 11: 240.

   c. Standard Operating Protocols – Sampling for Bat-Associated Viruses & Site Characterization of Bat-Human Interactions, Western Asia Bat Research Network. (2018). **Phelps KL** developed and integrated feedback from network partners at Boğaziçi University (Turkey), R. Lugar Center (Georgia), and the Royal Scientific Society (Jordan), University of Veterinary and Animal Sciences (Pakistan), the WAB-Net Scientific Advisory Board.

   d. Laboratory Protocols for the Detection & Characterization of Bat-Associated Coronaviruses, Western Asia Bat Research Network. (2018). **Phelps KL** developed and integrated feedback from laboratory partners at the R. Lugar Center (Georgia) and the Royal Scientific Society (Jordan) and the WAB-Net Scientific Advisory Board.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

HDTRA11710064 Olival (PI) 10/02/17-10/01/22

"Understanding the Risk of Bat-Borne Zoonotic Disease Emergence in Western Asia"

The goal of this project is to characterize pathogen diversity, strengthen zoonotic disease surveillance capacity, and test key hypotheses about the risk of bat-borne zoonotic disease emergence in Western Asia.
Role: Field Scientist

Combating Wildlife Trafficking Program, U.S. Fish & Wildlife Service van Weerd (PI) 08/01/17 – 07/31/19
"Identifying and addressing factors contributing to flying fox trafficking in Southeast Asia"
The goal of this project is to identify the actors and drivers in the illegal hunting, selling, buying, and consumption of flying foxes in the Philippines, Malaysia, and Indonesia, and to use results to develop national and multinational programs to reduce flying fox hunting.
Role: Co-PI

OMB No 0925-0001 and 0925-0002 (Rev 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Mendelsohn, Emma

eRA COMMONS USER NAME (credential, e.g., agency login):

POSITION TITLE: Research Scientist

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Wesleyan University, Middletown, CT	B.A.	05/2010	Earth and environmental sciences
Duke University, Durham, NC	M.E.M.	05/2015	Ecotoxicology and environmental health

A. Personal Statement

I am an environmental researcher and data scientist specializing in dynamic systems modeling, machine learning and biostatistics, web application development, and data engineering. With a background in environmental health and risk assessment, I provide data science and subject-matter expertise to projects related to global emerging infectious diseases, non-communicable diseases, environmental exposures, antimicrobial resistance, and behavioral health. My leadership and research experience includes oversight of a longitudinal study to characterize human exposure to potential toxicants in consumer products. I have been project lead on multiple human and ecological risk assessments for state, federal, and international agencies. Currently, I co-lead data management, analysis, and workflow design and automation for the USAID-funded PREDICT project. I have consulted in both the community and private sectors, using data to understand risk, support decision making, and inform actionable goals and policies.

1. **Mendelsohn E**, Hagopian A, Hoffman K, Butt CM, Lorenzo A, Congleton J, Webster TF Stapleton HM (2016). Nail polish as a source of exposure to triphenyl phosphate. **Environ. Int.** 86:45–51.
2. Hoffman K, Butt CM, Webster TF, Preston EV, Hammel SC, Makey C, Lorenzo A, Cooper EM, Carignan C, Meeker JD, Hauser R, Soubry A, Murphy SK, Price TM, Hoyo C, **Mendelsohn E**, Congleton J, Daniels JL, Stapleton HM (2017). Temporal trends in exposure to organophosphate flame retardants in the United States. **Environ. Sci. Technol. Lett.** 4(3):112-118.
3. Kopelovich, L, Perez AL, Jacobs N, **Mendelsohn E**, Keenan JJ (2015). Screening level human health risk assessment of toluene and dibutyl phthalate in nail lacquers. **Food Chem. Toxicol.** 81:46–53.

B. Positions and Honors

Positions and Employment

2014 Environmental Health Science Intern, Cardo ChemRisk, California
2014 Applied Data Analysis Teaching Assistant, Duke University, North Carolina
2015 -18 Project Scientist, Integral Consulting, New York
2018 - Research Scientist, EcoHealth Alliance New York

Other Experience and Professional Memberships

2015 -18 Member Society of Environmental Toxicology and Chemistry
2019 - Member RLadies
2019 - Member ROpenSci

Honors

2013 Merit Award Scholarship, Duke University Nicholas School of the Environment
2015 American Water Resources Association Richard A. Herbert Memorial Scholarship

C. Contributions to Science

1. **Research on associations between human-animal interactions and zoonotic disease risk.** I am a lead author on a study that analyzes paired human survey and serological data to characterize associations between human-animal interaction and zoonotic spillover risk in Southern China (recently submitted for publication). The study provides the first serological evidence of bat-born SARS-related coronavirus and HKU10 coronavirus spillover and shows that domestic animals, in addition to wildlife, are an important link in understanding transmission from bat to human populations. As the lead data analyst on the study, I oversaw the statistical design, execution, and reporting. In addition to this study, I am a lead on analysis and reporting of human survey data collected in over 20 countries under the PREDICT project. In this role, I have developed an automatic report generator that provides data summaries, maps and graphics, and results of statistical analyses to global partners. This tool allows researchers and policy makers to understand and interpret links between animal contact and self-reported illness drawn from a complex data set.

2. **Toxicological and exposure modeling in environmental risk assessment.** I have formal training in human health and ecological risk assessment and three years of experience consulting in risk assessment under state environmental departments, the United States Environmental Protection Agency (USEPA) and the European Food Safety Authority (EFSA). In this time, I worked to advance risk assessment techniques to make better use of available toxicological and exposure data through statistical modeling. I frequently presented on the topic and contributed to novel risk assessments that incorporated mechanic, probabilistic and Bayesian modeling techniques to improve risk characterization and communication.
   a. **Mendelsohn E**, Goodrum P, Summers H (2017). More than just point estimates: Probabilistic methods for toxicology. Invited webinar. Sediment Management Work Group. December 15.
   b. **Mendelsohn E**, Summers H, Goodrum PE (2016). Rethinking the use of uncertainty factors for the derivation of toxicity reference values. Platform presentation. **Society of Environmental Toxicology and Chemistry North America 37th Annual Meeting**, Orlando, FL. November 7–10.
   c. Iwai, H, Hoberman AM, Goodrum PE, **Mendelsohn E**, Anderson JK (2019). Addendum to Iwai and Hoberman (2014)—Reassessment of Developmental Toxicity of PFHxA in Mice. **Int. J. Toxicol.**
   d. **Mendelsohn E**, Summers H, Goodrum PE, Durda J (2017). Development of tissue-based PCB toxicity reference values and exposure-response curves for fish. Platform presentation. Sediment Management Workgroup Fall Sponsor Symposium, Charleston, SC. September 27–28.

3. **Software development and information technology operations (DevOps) to support scientific research.** I develop tools that support researchers. For USAID-funded PREDICT, I develop and maintenance R packages and pipelines for data querying, cleaning, quality assurance, visualization, and synthesis. I have developed dashboards and web-based apps on multiple projects to facilitate analysis and interaction with data. I also train and support researchers across fields in programming, analysis, and quality control methods.
   a. EIDITH R package https://ecohealthalliance.github.io/eidith/

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

USAID Emerging Pandemic Threats Mazet (PI) 10/01/14 – 09/30/19
PREDICT-2
The goal is to conduct surveillance for novel pathogens in wildlife, livestock and people; characterize human risk behavior; analyze EID risk; and design interventions in >20 countries
Role: Research Scientist

OMB No. 0925-0001 and 0925-0002 (Rev 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors
Follow this format for each person. **DO NOT EXCEED FIVE PAGES**

NAME: Dawson, Patrick

eRA COMMONS USER NAME (credential, e.g., agency login):

POSITION TITLE: Research Scientist

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Northwestern University, Evanston, IL	B.A.	06/2010	Biological Sciences
Columbia University, New York, NY	M.P.H.	05/2012	Epidemiology
Columbia University, New York, NY	Ph.D.	05/2019	Epidemiology

A. Personal Statement

I am well prepared to use my research, leadership, project management, and communication skills to assist the PIs as a co-investigator in successfully carrying out the proposed research project. My academic and practical training in epidemiology have equipped me with advanced knowledge of and experience with epidemiologic analysis, study design, biostatistical modeling, public health surveillance, and causal inference. My research on Middle East Respiratory Syndrome Coronavirus (MERS-CoV) in Egypt and Jordan for the USAID PREDICT-2 project and for the CDC Global Disease Detection Program have provided me with more than six years of experience in Egypt and Jordan working with communities along the camel value chain to identify MERS-CoV spillover from dromedary camels and behavioral risks for human MERS infection. Additionally, I have worked with an infectious disease surveillance system operating in 8 countries in the Middle East and North Africa region for influenza and other respiratory viruses to characterize seasonal transmission patterns and to monitor activity against alert thresholds in real time. I have also investigated tuberculosis transmission among New York City public housing residents using molecular, geospatial, and sociodemographic techniques. As the PREDICT-2 country liaison for Egypt and Jordan, I have cultivated critical management abilities that will prove beneficial in the proposed research project, including time management, budgeting, research planning, liaising with community leaders, cross-cultural communication, stakeholder engagement, and results communication.

1. Abdallat M, **Dawson P**, Haddadin AJ, El-Shoubary W, Dueger E, Sanouri T, Said MM, Talaat M (2016). Influenza Hospitalization Epidemiology from a Severe Acute Respiratory Infection Surveillance System in Jordan, January 2008–February 2014. **Influenza and Other Respiratory Viruses** 10(2): 91-7.
2. **Dawson P**, Perri BR, Ahuja SD (2016). High Tuberculosis Strain Diversity among New York City Public Housing Residents. **American Journal of Public Health** 106(3): 563-8.

B. Positions and Honors

Positions and Employment

2010 -12 Research Assistant, Columbia University Mailman School of Public Health, New York, NY
2011 -12 Epi Scholar, New York City Department of Health and Mental Hygiene, New York, NY
2012 -14 Regional Epidemiologist, U.S. Centers for Disease Control and Prevention, Cairo, Egypt

2014 -18 Teaching Assistant, Columbia University Mailman School of Public Health, New York, NY
2016 - Research Scientist, EcoHealth Alliance, New York, NY

Other Experience and Professional Memberships

2007 Intern, Bayshore Hospital, Holmdel, NJ
2009 Intern, EdgeAlliance AIDScare Progressive Services, Chicago, IL
2014 Consultant, NYCRx, Inc, New York, NY
2015 Consultant, EcoHealth Alliance, New York, NY

Honors

2006 New Jersey Bloustein Distinguished Scholar
2006 CollegeBoard AP Scholar Award
2010 DERU Honors Society (top 1% of class for scholarship, leadership, and character), Northwestern University
2011 Best Epidemiology Practicum Abstract (1st Prize), Columbia University Mailman School of Public Health
2012 William Farr Award in Epidemiology, Columbia University Mailman School of Public Health
2014 -16 PhD Merit Award Scholarship, Columbia University Mailman School of Public Health
2016 Wellcome Trust / DBT India Alliance Poster Award Finalist, 17th International Congress on Infectious Diseases
2019 Sydney Kark Global Health Award in Epidemiology, Columbia University Mailman School of Public Health

C. Contributions to Science

1. **Using molecular and geospatial data to conduct epidemiological investigations.** My early research as an epidemiologist focused on the transmission of tuberculosis (TB) among New York City (NYC) public housing residents. TB incidence in NYC had reached a peak in the 1990s and has significantly declined due to advances in case detection and treatment protocols. By the early 2010s, a majority of TB cases in NYC were among foreign-born individuals who became infected in TB-endemic countries before arriving to the United States. However, in early 2011, a number of TB cases among U.S.-born NYC public housing residents raised concern that TB may be spreading within public housing facilities or directly between public housing residents. If true, this TB transmission occurring within NYC posed an opportunity for public health intervention aimed at interrupting further TB transmission. Working with the NYC Department of Health and Mental Hygiene Bureau of Tuberculosis Control, I reviewed all confirmed TB cases in NYC between 2001 and 2009, and geocoded all patient addresses to obtain their residence's building identification numbers (BINs) and ran them against the New York City Housing Authority (NYCHA) registered BINs to classify cases as public housing residents (NYCHA) or non-public housing residents. Overall, I found U.S.-born NYCHA residents had twice the TB incidence of all other U.S.-born NYC residents. However, comparing the molecular TB strain data among NYCHA residents, I found they had high strain diversity. Further, there was no molecular evidence of TB strain clustering within NYCHA buildings, NYCHA complexes, or between NYCHA residents. Therefore, I concluded the increased burden of TB among NYCHA residents is due to public housing's role as a social safety net (which concentrates a population having many independent TB risk factors: history of homelessness, poverty, etc.) rather than due to spread within buildings or between residents. Due to these findings, the Bureau partnered with NYCHA to raise awareness of TB among residents and to provide information on getting free testing and treatment.
    a. **Dawson P**, Perri BR, Ahuja SD (2016). High Tuberculosis Strain Diversity among New York City Public Housing Residents. **American Journal of Public Health** 106(3): 563-8.

2. **Turning epidemiological surveillance data into evidence-based policy positions.** While working for the CDC Global Disease Detection Regional Center in Cairo, Egypt, I served as team lead for the Eastern Mediterranean Acute Respiratory Infection Surveillance (EMARIS) Network which operated in Egypt, Iraq, Iraq-Kurdistan, Jordan, Oman, Pakistan, Qatar, and Yemen. The prevailing thought on influenza seasonality was that many countries or regions with arid/desert-like or tropical climates do not experience pronounced seasonal activity as do other countries with temperate climates (which experience Northern Hemisphere or Southern Hemisphere seasonal patterns). Understanding seasonal influenza patterns is an important public health priority because it may impact seasonal influenza vaccination policy and timing the allocation of hospital and clinic resources. I analyzed influenza patterns across seven years of patient data from the EMARIS Network in Egypt and Jordan, and found that both countries clearly exhibit Northern Hemisphere influenza seasonal patterns, with increased activity between November and May typically reaching peak activity between January and March. We communicated this information to our hospital partners in the EMARIS Network and with the Ministries of Health in order to support redistribution of relevant hospital and clinic resources during times of peak influenza activity as well as to add on to the evidence base supporting the adoption of Northern Hemisphere seasonal influenza vaccination in both countries.

    a. Abdallat M, **Dawson P**, Haddadin AJ, El-Shoubary W, Dueger E, Sanouri T, Said MM, Talaat M (2016). Influenza Hospitalization Epidemiology from a Severe Acute Respiratory Infection Surveillance System in Jordan, January 2008–February 2014. **Influenza and Other Respiratory Viruses** 10(2): 91-7.

    b. Kandeel A, **Dawson P**, Labib M, Said M, Refaey S, Naguib A, Talaat M (2016). Morbidity, Mortality, and Seasonality of Influenza Hospitalizations in Egypt, November 2007-November 2014. **PLOS ONE** 11(9): e0161301.

3. **Examining causal pathways of zoonotic disease transmission for intervention development.** In addition to the contributions described above, I have been working with the PREDICT-2 team to describe viral spillover, including MERS, in Egypt and Jordan and to characterize behavioral risks for MERS. We conduct triangulated viral surveillance among people, wildlife, and livestock along animal-human interfaces in both countries to detect known and novel viruses from the viral families of Coronaviruses, Influenza viruses, Filoviruses, and Paramyxoviruses as well as to detect antibodies to MERS-CoV. All enrolled participants are asked to have nasopharyngeal and oropharyngeal swabs and sera collected and to complete a standardized questionnaire assessing social and demographic characteristics and behavioral practices. In Jordan, I developed additional questionnaire modules specifically addressing exposures and behavioral practices pertaining to dromedary camels which are being used to characterize specific risk behaviors for MERS spillover from camels to humans. Analyses are currently underway and will be completed in the first half of 2019.

    a. Kandeil A, Gomaa MR, Shehata MM, El Taweel AN, Mahmoud SH, Bagato O, Moatasim Y, Kutkat O, Kayed AS, **Dawson P**, Qui X, Bahl J, Webby RJ, Karesh WB, Kayali G, Ali MA (2018). Isolation and characterization of a distinct influenza A virus from Egyptian bats. **Journal of Virology** JVI.01059-18.

    b. **Dawson P**, Abu-Basha E, Amarneh B, Fahmawi A, Alshammari A, Alzaqa E, Hijazeen Z, Talafha H, Omari B, Al-Zghoul B, Ababneh M, Ismail ZB, Karesh WB (2018). Knowledge, Attitudes, Beliefs, and Practices Pertaining to Camel-to-Human Disease Risks in Jordan. **International Meeting on Emerging Diseases and Surveillance** (IMED), November 2018, Vienna, Austria (poster).

    c. **Dawson P**, Karesh WB, Kandeil A, Sayed A, Ali MA, Kayali G (2018). Identifying Behavioral Risk Intervention Points to Prevent Zoonotic Spillover at Animal Markets, Farms, and Abattoirs in Egypt. **18th International Congress on Infectious Diseases**, March 2018, Buenos Aires, Argentina (oral presentation, Zoonoses & One Health).

Complete List of Published Work in MyBibliography:
https://www.ncbi.nlm.nih.gov/sites/myncbi/1f1_DuePhbbQmO/bibliography/57398700/public/?sort=date&direction=ascending

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

USAID Emerging Pandemic Threats Mazet (PI) 10/01/14 – 09/30/19
PREDICT-2
The goal is to conduct surveillance for novel pathogens in wildlife, livestock and people; characterize human risk behavior; analyze EID risk; and design interventions in >20 countries
Role: Research Scientist

OMB No 0925-0001 and 0925-0002 (Rev 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Martinez, Stephanie

eRA COMMONS USER NAME (credential, e.g., agency login):

POSITION TITLE: Behavioral Risk Surveillance Program Coordinator

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University of California, Los Angeles, USA	B.A.	06/2011	International Development
University of California, Los Angeles, USA	B.A.	06/2011	Spanish
Columbia University Mailman School of Public Health, USA	M.P.H.	05/2017	Population and Family Health
Columbia University School of International and Public Affairs USA	M.I.A.	05/2017	Economic and Political Development

A. Personal Statement

I have five years of research training and experience in transforming extensive sets of in-depth interviews and focus group discussions into insightful analyses for critical global health issues. My research with these ethnographic datasets has included working with transcripts from Indonesia, Bangladesh, the Democratic Republic of the Congo, the Republic of the Congo, Cote d'Ivoire, and Zambia, investigating sensitive health-seeking and risky behaviors that are often at odds with local norms and regulations. I am the Program Coordinator for Behavioral Risk Surveillance at EcoHealth Alliance, a US-based 501(c)3 institution that conducts research on emerging zoonoses. Under USAID's PREDICT-2, I am leading several qualitative analyses of behaviors at critical environmental and occupational interfaces known to put vulnerable human populations in close contact with taxa that are often linked to significant emerging infectious disease risk. Under a framework of analyzing knowledge, attitudes, skills, and behaviors, I am leading international teams in generating country-specific insights that will play a critical role in creating evidence-based intervention recommendations designed to protect local populations from the next pandemic. I leverage my public health research training and experience to guide analyses that are sensitive to local gender and socioeconomic norms. I also build capacity by training multidisciplinary scientific partners in coding and analyzing qualitative datasets.

1. Casey SE, Steven VJ, Deitch J, Dumas EF, Gallagher MC, **Martinez S**, Morris CN, Rafanoharana RV, and Wheeler E (2019). "You must first save her life": community perceptions towards induced abortion and post-abortion care in North and South Kivu, Democratic Republic of the Congo. **Sexual and Reproductive Health Matters** 27(1): 1571309.
2. Schlegelmilch J, Petkova EP, **Martinez S**, and Redlener I. Acts of terrorism and mass violence targeting schools: analysis and implications for preparedness in the USA (2017). **Journal of Business Continuity & Emergency Planning** 10(3): 280-289.

3. Petkova, EP, **Martinez S**, Schlegelmilch J, and Redlener I (2017). Schools and Terrorism: Global Trends, Impacts, and Lessons for Resilience. **Studies in Conflict & Terrorism** 40(8): 701-711.

B. Positions and Honors

Positions and Employment

2011-13 United States Peace Corps, Community Health Educator, Cameroon
2014-16 Office Assistant and Graduate Research Assistant, National Center for Disaster Preparedness
2017 RAISE Initiative Research Assistant, Columbia University
2017 - Research Consultant, Population Council, New York
2017 Behavioral Risk Surveillance Program Assistant, EcoHealth Alliance, New York
2018 Behavioral Risk Surveillance Program Assistant and Researcher, EcoHealth Alliance, New York
2018 - Behavioral Risk Surveillance Program Coordinator, EcoHealth Alliance, New York

Other Experience and Professional Memberships

2016- American Public Health Association (International Health Section, Environment Section)
2016- Association for Women's Rights in Development
2016- WE ACT for Environmental Justice

Honors

2015 Mailman School of Public Health Heilbrunn Scholarship
2014 International House Women's International Leadership Scholarship
2014 Columbia School of International and Public Affairs Scholarship
2014 International House New York City's Paul A. Volcker Scholarship
2011 UCLA Chancellor's Service Award
2011 UCLA Carroll B. Johnson Distinguished Senior Award
2007 UCLA Alumni Scholarship

C. Contributions to Science

1. **Qualitative analyses of global datasets attuned to socially-sensitive topics.** Nuanced attitudes and beliefs are difficult to surface through quantitative human research tools alone, and qualitative explorations are a boon for researchers investigating populations living in environments with rigid social traditions. Through my qualitative work with Columbia University's RAISE Initiative, I collaboratively leveraged the focus group dataset to understand the complex ways in which focus groups initially expressed locally conforming beliefs about highly sensitive reproductive health issues, before offering more nuanced beliefs and attitudes related to gender, age, and circumstance. My other work, including those currently in progress at EcoHealth Alliance, has benefitted from this approach in framing the observations not only against the social environment, but against the progression of ideas within a given transcript.
   a. Casey SE, Steven VJ, Deitch J, Dumas EF, Gallagher MC, **Martinez S**, Morris CN, Rafanoharana RV, and Wheeler E (2019). "You must first save her life": community perceptions towards induced abortion and post-abortion care in North and South Kivu, Democratic Republic of the Congo. **Sexual and Reproductive Health Matters** 27(1): 1571309.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

USAID Emerging Pandemic Threats Mazet (PI) 10/01/14 - 09/30/19
PREDICT-2

The goal is to conduct surveillance for novel pathogens in wildlife, livestock and people; characterize human risk behavior; analyze EID risk; and design interventions in >20 countries
Role: Staff

Completed Research Support
Not Applicable

OMB No. 0925-0001 and 0925-0002 (Rev. 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

NAME: Chmura, Aleksei

eRA COMMONS USER NAME: (b) (6)

POSITION TITLE: Research Scientist

EDUCATION/TRAINING:

INSTITUTION AND LOCATION	DEGREE	COMPLETION DATE	FIELD OF STUDY
Columbia University, New York	B.S.	06/2004	Biology
Kingston University, UK	Ph.D.	08/2018	Biology

A. Personal Statement

Aleksei Chmura comes from an interdisciplinary background of ecology, conservation medicine, and tropical field ecology, as well as extensive on-the-ground experience working with field sampling and laboratory work in China, Brazil, and Malaysia. His expertise adds to this project for a better understanding of the animal-human interactions and the consequential health effects at both individual and community levels. Coordinating with both the laboratory and field teams in internationally, Dr. Chmura has been working on SARS-Coronavirus, Paramyxovirus, Astrovirus, and other emerging infectious diseases of bats and rodents in southern China under the USAID EPT-2, NSF, and NIH projects research since 2005. He works closely with EcoHealth Alliance's field teams and lead field coordinators. As part of his doctoral work, he spent over a year in the Wuhan Institute of Virology laboratory in China.

B. Positions and Honors

Positions and Employment

2001 -04 Volunteer Curator, Dept. of Mammalogy, American Museum of Natural History, USA
2001 -05 Program Assistant Center for Env'tl Research and Conservation, Columbia University, USA
2002 -05 Instructor, Columbia University Tropical Field Ecology Programs, USA/Dominican Republic/Brazil
2005- Research Scientist, EcoHealth Alliance, USA
2006 - Managing Editor, *EcoHealth*, New York. USA

Other Experience and Professional Membership

2000 -05 The Explorers Club
2002 - American Museum of Natural History
2005 - International Association for Ecology and Health
2009 - Society for Applied Microbiology

C. Contribution to Science

1. **Research on the origins of emerging viruses.** Numerous high impact emerging viruses appear to have bat reservoirs (e g. SARS-CoV, EBOV, NiV, HeV, MERS-CoV, SADS-CoV). As research assistant and program coordinator on four prior R01s my work has helped demonstrate their bat origin (SARS-CoV, SADS-CoV), analyze the drivers of their emergence and risk factors for spillover. Collaborating with virologists in China, I have identified SARS-like CoVs and other viruses in bats and other mammals. This work provides critical reagents and resources that have helped advance understanding of virus-host binding and may contribute to vaccine development.

a. Wu ZQ; Lu L, Du J, Yang L, Ren XW, Liu B, Jiang JY, Yang J, Dong J, Sun LL, Zhu YF, Li YH, Zheng DD, Zhang C, Su HX, Zheng YT, Zhou HN, Zhu GJ, Li HY, **Chmura** AA, Yang F, Daszak P, Wang JW, Liu QY, Jin Q (2018). Comparative analysis of rodent and small mammal viromes to better understand the wildlife origin of emerging infectious diseases. **Microbiome** 6(178). 10.1186/s40168-018-0554-9.

b. Zeng LP, Ge XY, Peng C, Yang XL, Tan B, Gao YT, Chen J, **Chmura AA,** Daszak P, Shi ZL (2016) Bat Severe Acute Respiratory Syndrome-Like Coronavirus WIV1 Encodes an Extra Accessory Protein, ORFX, Involved in Modulation of the Host Immune Response. **Journal of Virology** 90(14): 6573-6582.

c. Hu B, **Chmura AA**, Li JL, Zhu GJ, Desmond JS, Zhang YZ, Zhang W, Epstein JH, Daszak P, Shi ZL (2014). Detection of diverse novel astroviruses from small mammals in China. **Journal of General Virology** 95(11): 2442-2449.

d. Ge X-Y, Li J-L, Yang X-L, **Chmura AA**, Zhu G, Epstein JH, Mazet JK, Hu B, Zhang W, Peng C, Zhang Y-J, Luo C-M, Tan B, Wang N, Zhu Y, Cramer G, Zhang S-Y, Wang L-F, Daszak P, Shi Z-L (2013). Isolation and characterization of a bat SARS-like Coronavirus that uses the ACE2 receptor. **Nature** 503: 535-538.

2. **Analyzing the Process of Disease Emergence.** Emerging infectious diseases are a significant threat to global health and their emergence is sporadic, complex, and seemingly unpredictable. I collaborated on efforts to employ analytical approaches to identify predictable patterns in the process of disease emergence.

   a. Bogich TL, Funk S, Malcolm TR, Chhun N, Epstein JH, **Chmura AA,** Kilpatrick AM, Brownstein JS, Hutchison OC, Doyle-Capitman C, Deaville R, Morse SS, Cunningham AA, Daszak P (2013). Using network theory to identify the causes of disease outbreaks of unknown origin. **Journal of the Royal Society, Interface** 10(81), 10.1098/rsif.2012.0904.

   b. Kilpatrick AM, **Chmura AA**, Gibbons DW, Fleischer RC, Marra PP, Daszak P (2006). Predicting the global spread of H5N1 avian influenza. **PNAS**, 103: 19368-19373.

3. **Studies of wildlife disease ecology to understand emerging zoonoses.** The majority of EIDs are zoonotic, with the majority of these originating in wildlife. Over the past 15-years, I have collaborated on international and national research programs on how the ecology of specific wildlife-origin zoonoses can help explain patterns of risk to people.

   a. Wu ZQ, Lu L, Du J, Yang L, Ren XW, Liu B, Jiang JY, Yang J, Dong J, Sun LL, Zhu YF, Li YH, Zheng DD, Zhang C, Su HX, Zheng YT, Zhou HN, Zhu GJ, Li HY, **Chmura AA**, Yang F, Daszak P, Wang JW, Liu QY, Jin Q (2018). Comparative analysis of rodent and small mammal viromes to better understand the wildlife origin of emerging infectious diseases. **Microbiome**, 6(178) 10.1186/s40168-018-0554-9.

   b. Monagin C, Ning L, Schneider B, **Chmura AA**, Epstein JH, Wu D, Paccha B, Ke CW, Daszak P, Rabinowitz P (2018) Serologic and Behavioral Risk Survey of Workers with Wildlife Contact in China. **PLOS ONE**, 13(4) 10.1371/journal.pone.0194647.

   c. Nava A, Shimabukuro JS, **Chmura AA,** Luz LBS (2017) The Impact of Global Environmental Changes on Infectious Disease Emergence with a Focus on Risks for Brazil. **Institute for Laboratory Animal Research** 58(3): 393-400.

   d. Newman S, **Chmura AA,** Converse K, Kilpatrick AM, Patel N, Lammers E, Daszak P (2007) Disease Associated Aquatic Bird Mortality as an Indicator of Changing Aquatic Ecosystem Health: Analysis of a 30-year USA Mortality Database. **Marine Ecosystem Progress Series** 352: 299-309.

D. Additional Information: Research Support and/or Scholastic Achievements

Ongoing Research Support

Emerging Pandemic Threat Program, USAID Mazet (PI) 10/01/14-09/30/19

PREDICT 2
The goal of this project is to create and implement a global virus surveillance system in animals and humans and analyze spillover risk.
Role: Program Coordinator

Completed Research Support
(not showing 4 previous awards, none completed within last 3 years)

OMB No. 0925-0001 and 0925-0002 (Rev. 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: LI, Hongying

eRA COMMONS USER NAME (credential, e.g., agency login): [redacted] (b) (6)

POSITION TITLE: China Programs Coordinator & Research Scientist

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Sun Yat-Sen University, China	B.S.	06/2012	Biosciences
Emory University, US	MPH	05/2015	Health Policy
Kingston University, UK	Ph.D. (candidate)	2018 -	Infectious Diseases

A. Personal Statement

I have an interdisciplinary background in ecology, public health, and human behavior, coupled with extensive on-the-ground experience working with communities, governmental and academic partners in China. For the past 3 years I have worked as China Programs Coordinator at EcoHealth Alliance, acting as the key point-of-contact among EcoHealth staff and our partners in China. I have coordinated fieldwork to conduct bat sampling, and human behavioral risk assessments across 5 provinces in southern China. I have also liaised directly with all key partners on this proposal. Additionally, I coordinate EcoHealth Alliance's wildlife trade research in China and SE Asia focusing on analyzing incentives to trade and consume wildlife. I work closely with Chinese Health and Forestry governmental departments, research institutes, and local organizations to foster collaboration and communication as part of my PhD research on *"Policy and Human Behavioral Strategies to Mitigate Zoonotic Disease Emergence in Southern China"*.

B. Positions and Honors

Positions and Employment

2011 -12 Research Assistant, HIV Prevention Program, Yunnan Mat. and Children's Hospital, China
2013 -14 Program Assistant, School HIV/AIDS & School Edu., UNESCO Beijing, China
2015 - China Programs Coordinator & Research Scientist, EcoHealth Alliance, New York
2017 - Coordinator, National Virome Project Initiative, China

Other Experience and Professional Memberships

2018 - Member, IUCN SSC Pangolin Specialist Group
2018 - Member, Society for Applied Microbiology
2017 - Member, China Health Policy and Management Society
2016 - Member, International Association for Ecology & Health
2016 - Columnist, *China Environment*
2016 - Asian Representative, Conservation Leadership Programme

Honors

2010 National Scholarship, Ministry of Education, the Pooplo's Ropublic of China.

2012 Outstanding Graduate Award, Sun Yat-sen University, China
2016 Invited speaker, China Conservation Network workshop. "Impacts of wildlife trade on public health"
2017 Invited Speaker, International Association for Ecology & Health. "Understanding the wildlife trade in China"

C. Contributions to Science

1. Understanding the risk factors of zoonotic disease mergence among the high-risk communities. With its rapid urbanization and development as well as the high diversity of animal species, southern China is facing major social and ecological changes that result in human and animal interactions favoring the emergence of zoonotic diseases. In order to identify the zoonotic risks and develop a risk-mitigation strategy, the study used a biological-behavioral surveillance method to demonstrate the serological evidence of viral spill-over into human population, and identify demographic factors and human-animal interactions associated with viral exposure and self-reported severe acute respiratory and influenza-like illness symptoms. Combining existing protective factors and intervention opportunities, individual, social, community, and policy-level mitigation strategies are recommended to prevent zoonotic risk in Southern China.

a. Wu Z, Lu L, Du J, Yang L, Ren X, Liu B, **Li H**, Zhu Y (2018). Comparative analysis of rodent and small mammal viromes to better understand the wildlife origin of emerging infectious diseases. **Microbiome** 6(1), 178.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

USAID Emerging Pandemic Threats Mazet (PI) 10/01/14 - 09/30/19
PREDICT 2
The goal of this project is to create and implement a global virus surveillance system in animals and humans and analyze spillover risk.
Role: Country Coordinator for China

Completed Research Support

R01 AI110964 Daszak (PI) 06/01/14 - 05/31/19
Understanding Risk of Bat Coronaviruses
The goal of this study is to analyze the risk of coronavirus spillover from bats to humans in Southern China
Role: Project Coordinator & Human Research Lead

China Environmental Protection Foundation
Conservation of Chinese pangolin in National Nature Reserve Zhang (PI) 01/01/16 - 12/31/17
The goal of this study is to understand the current population and distribution of the critically endangered Chinese pangolin *(Manis pentadactyle)* in mainland China
Role: Community Research Lead

OMB No. 0925-0001 and 0925-0002 (Rev. 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Hemachudha, Thiravat

eRA COMMONS USER NAME (credential, e.g., agency login): (b) (6)

POSITION TITLE. Director

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Chulalongkorn University Hospital, Thailand	M.D.	06/1981	Internal Medicine
Chulalongkorn University Hospital, Thailand	Board	12/1983	Neurology Res dency
John Hopkins University School of Medicine	Fellowship	12/1986	Fogarty (NIH) Fellowship in Neurology & Neuroimmunology

A. Personal Statement

I have 20+ years of internationally funded research in various fields, from immunological studies, to rabies pathology, to CNS infection pathology. I am a member of the WHO Expert Advisory Panel on Rabies since 1990 I have served as president in Academic Affairs of Thai Neurological Association and was elected a fellow of American College of Physicians in 2010. I am a WHO member of the International Health Regulations Roster of Experts, as an expert in the human-animal interface (zoonoses). I am also on the national board on emerging infectious diseases, and I am a member of the subcommittee on strategic planning on emerging infectious diseases. I have been the PI on several multidisciplinary projects over the years.

1. Plipat T, Buathong R, Wacharapluesadee S, Siriarayapon P, Pittayawonganon C, Sangsajja C, Kaewpom T, Petcharat S, Ponpinit T, Jumpasri J, Joyjinda Y, Rodpan A, Ghai S, Jittmitraphap A, Khongwichit S, Smith D, Corman V, Drosten C, **Hemachudha T** (2017). Imported case of Middle East respiratory syndrome coronavirus (MERS-COV) infection from Oman to Thailand, June 2015. **Euro Surveill** 22(33).pii:30598.
2. Fooks AR, Cliquet F, Finke S, Freuling C, **Hemachudha T**, Mani RS, Müller T, Nadin-Davis S, Picard-Meyer E, Wilde H, Banyard AC (2017). Review Subsection on Pathogenesis, Management of Bitten Persons and Diseased Patient. **Nat Rev Dis Primers** 3:17091
3. **Hemachudha T**, Ugolini G, Sungkarat W, Shuangshoti S, Wacharapluesadee S Laothamatas J (2013). Human Rabies: neuropathogenesis d agnosis and management. **Lancet Neurol** 12(5):498-513
4. Shantavasinkul P, Tantawichien T, Wacharapluesadee S, Jeamanukoolkit A, Udomchaisakul P, Chattranukulchai P, Wongsaroj P, Khawplod P, Wilde H, **Hemachudha T** (2010). Failure of rabies postexposure prophylaxis in patients presenting with unusual manifestations. **Clin Infect Dis.** 1;50(1):77-9.

B. Positions and Honors

Positions and Employment

1982 - Neurology staff, Chulalongkorn University Hospital, Thailand
1984 -88 Consultant Neurologist, Queen Saovabha Memorial Institute, Thai Red Cross Society
1989 -90 Secretary to Associate Dean in Research Affairs, Chulalongkorn University Hospital. Thailand
1990 -93 Assistant Director, Queen Saovabha Memorial Institute, Thai Red Cross Society

1990 -93	Director, WHO Collaborating Centre for Research on Rabies Pathogenesis and Prevention
1997 -98	President, Academic Affairs, Thai Neurological Association
2000 -	Director of Neuroscience Centre for Research and Development, Chulalongkorn University Hospital, Thailand
2008 -	Director, WHO Collaborating Centre for Research and Training on Viral Zoonoses
2017 -	Director, Thai Red Cross Emerging Infectious Diseases – Health Science Centre

Other Experience and Professional Membership

1989 -98	Member of the Board Committee of the Thai Neurological Association
1990 -	Member of the WHO Expert Advisory Panel on Rabies
1998 -01	Member of the Board Committee of the Thai Royal College of Physicians
1999 -03	Member of the Board Committee of the National Research Council, Thailand
1999 -	Member of the New York Academy of Sciences
2006 -	Member of the Scientific Committee of the International Conference: Towards the Elimination of Rabies in Eurasia (2007)
2006 -	Member of the Technical Advisory Group of Alliance for Rabies Control (UK)
2006 -	Member of Rabies Control in Asia
2007 -08	Board member of Office of Knowledge Management and Development
2007 -08	Board member of Thai Government Pharmaceutical Organization
2013 -	WHO member of the International Health Regulations Roster of Experts as an expert in Human-animal interface (Zoonoses)
2017 -	Member of National Health Reform committee

Honors

1992	National Research Council award for distinguished research projects
1993	Mahidol University – B. Brown Prize for distinguished researcher
1994	National Research Council award for distinguished researcher
2000	(Elected) Corporate Member of American Neurological Association
2001	Invited expert in "Treatment options in Human Rabies" organized by CDC (USA), Toronto
2001	Invited expert in "Rabies international meeting in the Americas" organized by CDC (USA), Ontario
2004	Outstanding Scientist Award from Foundation for the Promotion of Science and Technology under the Patronage of His Majesty the King
2009	Rabies Oration lecture in honor of Eddie and Piloo Bharucha and received honorary plaque at the World Congress of Neurology, Bangkok
2010	(Elected) Fellow of American College of Physicians
2014	Member of the National Board on Emerging Infectious Diseases, Thailand
2014	Member of Subcommittee on strategic planning on Emerging Infectious Diseases, Thailand
2015	Co-chair Scientific Committee and Plenary lecture – International Congress of Pathogens at Humana and Animal Interface (ICOPHAI)
2017	Honorary lecturer: NTD (Neglected Tropical Disease) Asia

C. Contributions to Science

1. **Research on the neuroimmunology of neurological diseases.** I have spent years researching neuroimmunology in neurological diseases such as autoimmune encephalitis, myasthenia gravis, Guillain-Barré syndrome, and stroke. I have developed clinical and lab-based diagnostics, and have conducted research to differentiate between immune- and infectious encephalitis in order to facilitate treatments.

a. Mungaomklang A, Chomcheoy J, Wacharapluesadee S, Joyjinda Y, Jittmittraphap A, Rodpan A, Ghai S, Saraya A and **Hemachudha T** (2016). Influenza virus associated acute fatal necrotizing encephalopathy: role of non-permissive viral infection? **Clin Med Insights.**
b. Thanprasertsuk S, Pleumkanitkul S, Wacharapluesadee S, Ponpinit T, **Hemachudha T**, Suankratay C (2017). HTLV-1-Associated Myelopathy/Tropical Spastic Paraparesis: the First Case Report in Southeast Asia. **AIDS Res Hum Retroviruses.**
c. **Hemachudha T**, Phanthumchinda K (1994). Encephalitis in Southeast Asia. **Trav Med Int** 12:207-13.
d. **Hemachudha T**, Phanthumchinda K, Indrakoses A, Wilde H (1984). Intractable hiccups (singultus) as a presenting manifestation of Japanese encephalitis. **J Med. Assoc. Thailand** 67:620-3.

2. **Extensive research on rabies.** I have researched and published extensively on rabies, working specifically on topics such as: streamlining of vaccination regimens, neuropathogenesis of rabies virus, and finding alternative treatment plans. I have analyzed rabies from the clinical, proteomics, and molecular level, hoping to be able to paint the full picture of rabies virus infection. I have also analyzed the socio-political level of rabies management and continue to do so at the national level. The papers below are selected from nearly 200 other studies I've published on this topic.
   a. **Hemachudha T**, Ugolini G, Sungkarat W, Shuangshoti S, Wacharapluesadee S Laothamatas J (2013). Human Rabies: neuropathogenesis, diagnosis and management. **Lancet Neurol** 12(5):498-513.
   b. Virojanapirom P, Yamada K, Khawplod P, Nishizono A, **Hemachudha T** (2016). Increased pathogenicity of rabies virus due to modification of a non-coding region. **Arch Virol** 161(11):3255-61.
   c. Ghai S, **Hemachudha T** (2018) .Evaluating human rabies control in Asia: using 'One Health' principles to assess control programmes for rabies. **Rev Sci Tech** 37(2):617-627.
   d. Denis M, Knezevic I, Wilde H, **Hemachudha T**, Briggs D, Knopf L (2018). An overview of the immunogenicity and effectiveness of current human rabies vaccines administered by intradermal route. **Vaccine** pii: S0264-410X(18)31635-9.

3. **Wildlife virus surveillance at the human interface in Thailand.** My lab has been at the forefront of zoonotic disease surveillance in Thailand for over 20 years, including active surveillance for Nipah virus, Ebola viruses, and coronaviruses in wildlife. This work also includes international collaborations to better understand the global distribution of key groups of viruses, e.g. novel hepaciviruses.
   a. Drexler JF, Corman VM, Müller MA, Lukashev AN, Gmyl A, Coutard B, Adam A, Ritz D, Leijten LM, van Riel D, Kallies R, Klose SM, Gloza-Rausch F, Binger T, Annan A, Adu-Sarkodie Y, Oppong S, Bourgarel M, Rupp D, Hoffmann B, Schlegel M, Kümmerer BM, Krüger DH, Schmidt-Chanasit J, Setién AA, Cottontail VM, **Hemachudha T**, Wacharapluesadee S, Osterrieder K, Bartenschlager R, Matthee S, Beer M, Kuiken T, Reusken C, Leroy EM, Ulrich RG, Drosten C (2013). Evidence for novel hepaciviruses in rodents. **PLoS Pathog** 9(6):e1003438.
   b. Wacharapluesadee S, Ngamprasertwong T, Kaewpom T, Kattong P, Rodpan A, Wanghongsa S, **Hemachudha T** (2013). "Genetic Characterization of Nipah Virus from Thai Fruit Bats (Pteropuslylei)." Asian Biomed 7(6):813-19.
   c. Wacharapluesadee S, Olival KJ, Kanchanaska B, Duengkae P, Kaewchot S, Srongmongkol P, Ieamsaard G, Maneeorn P, Sittidetvoripat N, Kaewpom T, Petcharat S, Yingsakmongkon S, Rollin PE, Towner JS, **Hemachudha T**. Surveillance for Ebola Virus in Wildlife, Thailand. **Emerg Infect Dis.** 21(12):2271-3.
   d. Wacharapluesadee S, Duengkae P, Chaiyes A, Kaewpom T, Rodpan A, Yingsakmongkon S, Petcharat S, Phengsakul P, Maneeorn P, **Hemachudha T** (2018). Longitudinal study of age-specific pattern of coronavirus infection in Lyle's flying fox)Pteropus lylei (in Thailand .**Virol J** 15)1:(38.

4. **Identifying viral etiological agents in symptomatic patients.** Our research has shown that a large proportion of clinical cases, including encephalitides, remain undiagnosed in Thailand across Southeast

Asia. I have led several projects to identify etiological agents from clinical cases, and also to help facilitate the rapid detection and characterization of key groups of emerging pathogens in Thailand, like MERS-CoV and Ebola.

a. Plipat T, Buathong R, Wacharapluesadee S, Siriarayapon P, Pittayawonganon C, Sangsajja C, Kaewpom T, Petcharat S, Ponpinit T, Jumpasri J, Joyjinda Y, Rodpan A, Ghai S, Jittmitraphap A, Khongwichit S, Smith D, Corman V, Drosten C and **Hemachudha T** (2017). Imported case of Middle East respiratory syndrome coronavirus (MERS-COV) infection from Oman to Thailand, June 2015. **Euro Surveill** 22(33).pii:30598
b. Saraya A, Mahavihakanont A, Shuangshoti S, Sittidetboripat N, Deesudchit T, Callahan M, Wacharapluesadee S, Wilde H, **Hemachudha T** (2013). Autoimmune Causes of Encephalitis Syndrome in Thailand: Prospective Study of 103 Patients. **BMC Neurology** 2013.
c. Hemachudha P, Wacharapluesadee S, Buathong R, Petcharat S, Bunprakob S, Ruchiseesarod C, Roeksomtawin P, **Hemachudha T** (2019). Lack of Transmission of Zika Virus Infection to Breastfed Infant. **Clin Med Insights Case Rep.** 12:1179547619835179.
d. Joyjinda Y, Rodpan A, Chartpituck P, Suthum K, Yaemsakul S, Cheun-Arom T, Bunprakob S, Olival KJ, Stokes MM, **Hemachudha T**, Wacharapluesadee S (2019). First Complete Genome Sequence of Human Coronavirus HKU1 from a Nonill Bat Guano Miner in Thailand. **Microbiol Resour Announc** 8(6)pii:e01457-18.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

WHO Zika Project Hemachudha (PI) 04/01/18 - 09/30/19
The goal is to study Zika epidemiology, reservoir host, vector dynamics and genetics in a presumptive endemic setting in the Mekong sub-region in Thailand.

Completed Research Support (last 3 years only)

NSTDA Chair Research Grant Hemachudha (PI) 04/01/16 - 03/31/19
The goal was to study Zoonotic diseases, and the role of reservoirs and vectors, diagnosis, mechanism and potential therapeutics.

OMB No 0925-0001 and 0925-0002 (Rev. 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors
Follow this format for each person **DO NOT EXCEED FIVE PAGES.**

NAME: William, Timothy

eRA COMMONS USER NAME (credential, e.g., agency login):

POSITION TITLE: President

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University of Malaysia	MBBS	1995	Medicine
The Royal College of Physicians, UK	MRCP	2002	Medicine
The Royal College of Physicians, UK	FRCP	2013	Infectious Diseases

A. Personal Statement

I am a Senior Clinical Researcher at the Malaysian Ministry of Health's Clinical Research Centre, Kota Kinabalu Sabah (2008 – present) and also Head of Infectious Diseases at Gleneagles Hospital, Kota Kinabalu (2018-present). Prior to these appointments, from 2008 – 2015 I was the State Infectious Diseases Physician for Sabah. I am President of the Infectious Diseases Society, Kota Kinabalu Sabah, which has an excellent track record of administering research grants with Menzies and other international partners. My basic Physician Training at the Queen Elizabeth Hospital in Sabah was followed by Infectious Diseases Subspecialty Training from 2004 to 2008, including three years at the Kuala Lumpur General Hospital and one year with at Royal Darwin Hospital, Australia. I am a Fellow of the Royal College of Physicians of Edinburgh and an Honorary Research Consultant with the Menzies School of Health Research Darwin. I am a key member of the Malaysian National Clinical Practice Guideline Committee for Malaria, Infection Control, HIV/AIDS and Adult Vaccinations. My research on *P. knowlesi* with the Menzies-CRC collaboration has been incorporated into not only National but also WHO Guidelines for the Treatment for Severe Malaria (2014, 2015 and now 2017).

1. **William T**, Menon J, Rajahram G, Chan L, Ma G, Donaldson S, Khoo S, Fredrick C, Jilip J, Anstey NM, Yeo TW (2011). Severe *Plasmodium knowlesi* Malaria in a Tertiary Hospital, Sabah, Malaysia. **Emerg Infect Dis** 7: 17: 1248-55.

2. **William T**, Rahman HA, Jelip J, Ibrahim MY, Menon J, Grigg M, Yeo TW, Anstey NM, Barber BE (2013). Increasing incidence of *Plasmodium knowlesi* malaria following control of *P. falciparum* and *P. vivax* malaria in Sabah, Malaysia. **PLoS Negl Trop Dis** 7 (1): e2026.

3. Barber BE, **William T**, Grigg M, Menon J, Auburn S, Marfurt J, Anstey NM, Yeo TW (2013). A prospective comparative study of knowlesi, falciparum and vivax malaria in Sabah, Malaysia: high proportion with severe disease from *Plasmodium knowlesi* and *P. vivax* but no mortality with early referral and artesunate therapy. **Clin Infect Dis** 56: 383-97.

4 **William T**, Jelip J, Menon J, Anderios F, Mohammad, Mohammad TA, Matthew J Grigg MJ, Yeo TW, Anstey NM, Barber BE (2014). Changing epidemiology of malaria in Sabah, Malaysia: increasing incidence of *Plasmodium knowlesi*. **Malaria J** 13 (1): 390.

B. Positions and Honors

Positions and Employment

1995 -96	House Officer
1996 -99	Medical Officer and Hospital Director, Tambunan Hospital, Sabah, Malaysia.
1999 -02	Medical Officer, Dept. of Medicine, Queen Elizabeth Hospital, Kota Kinabalu, Sabah, Malaysia
2002 -05	General Physician for Internal Medicine and Clinical Specialist of Infectious Diseases, Kuala Lumpur Hospital, Malaysia
2006	General Physician for Internal Medicine and Clinical Specialist of Infectious Diseases, Queen Elizabeth Hospital, Kota Kinabalu, Sabah, Malaysia
2007	Registrar, Dept. of Medicine, Royal Darwin Hospital, NT, Australia
2008 -15	Consultant, Infectious Disease Unit, Queen Elizabeth Hospital, Kota Kinabalu, Sabah
2008 -	Clinical Researcher, Queen Elizabeth Hospital Clinical Research Centre, Kota Kinabalu
2012 -	Honorary Associate, Menzies School of Health Research, Darwin Australia
2012 -	President, Infectious Disease Society of Kota Kinabalu, Sabah, Malaysia
2017 -	Infectious Disease Consultant and Head Infectious Disease Unit, GLENEAGLES Hospital, Kota Kinabalu, Sabah Malaysia

Other Experience and Professional Membership

Member, Malaysian Medical Association
Member, Malaysian Medical Council
Executive Committee, Sabah Medical Association
President, Infectious Disease Society of Kota Kinabalu Sabah

Honors

2000	Professional Excellence Award, Ministry of Health, Sabah, Malaysia
2003	Professional Excellence Award, Ministry of Health, Sabah, Malaysia
2003	Royal Rotary Club Award (Kuala Lumpur), Service for the Treatment of patients with Severe Acute Respiratory Distress Syndrome
2009	Professional Excellence Award, Ministry of Health, Sabah, Malaysia
2010	Professional Excellence Award, Ministry of Health, Sabah, Malaysia
2013	American Society of Tropical Medicine and Hygiene Travel Award
2017	Merdeka Award for Health, Science and Technology

C. Contributions to Science

1. **Publications.** Since 2011, I have co-authored >80 publications with >2000 citations. These publications have made a major contribution to the knowledge of the epidemiology, clinical features and treatment of *P. knowlesi* malaria. My studies on artesunate in severe knowlesi and vivax malaria (William *et al, Emerg Infect Dis* 2011, Barber *et al, Clin Inf Dis* 2013) have changed global (WHO) and SE Asian policy and practice. With collaborators Anstey, Barber and Grigg, my RCTs of artemisinin combination therapy (ACT) for non-falciparum species have led to national policy change to universal ACT for uncomplicated vivax and knowlesi malaria. In Sabah, I lead a large ongoing program of research into the prevention, surveillance and management of malaria and other tropical infections with national and international collaborators. In 2017 I was a joint recipient of Malaysia's prestigious Merdeka Award in Health, Science and Technology, for outstanding contribution to the treatment of knowlesi malaria.

a Grigg MJ, **William T**, Menon J, Dhanaraj P, Barber BE, Wilkes CS, von Seidlein L, Rajahram GS, Pasay C, McCarthy JS, Price RN, Anstey NM†, Yeo TW† (†: equal contribution authors) (2016). A randomized open-label clinical trial of artesunate-mefloquine versus chloroquine for the treatment of uncomplicated *Plasmodium knowlesi* malaria in Sabah, Malaysia (ACT KNOW trial). **Lancet Infect Dis** 16(2):180-8.

b. Rajahram GS, Barber BE, **William T**, Grigg MJ, Menon J, Yeo TW, Anstey NM (2016). Falling *Plasmodium knowlesi* malaria death rate among adults despite rising incidence, Sabah, Malaysia, 2010-2014. **Emerg Infect Dis** 22(1).

c. Grigg MJ, Cox J, **William T**, Jelip J, Fornace KM, Brock PM, von Seidlein L, Barber BE, Anstey NM, Yeo TW Drakeley CJ (2017). Individual factors associated with the risk of acquiring human *Plasmodium knowlesi* malaria in Malaysia: a case-control study. **Lancet Planet Hlth** 1 (3), e97–e104.

d. Grigg MJ, **William T**, Barber BE, Rajahram GS, Menon J, Schimann E, Wilkes CS, Patel K, Chandna A, Price RN, Yeo TW, Anstey NM (2018). Artemether-lumefantrine versus chloroquine for the treatment of uncomplicated Plasmodium knowlesi malaria: an open-label randomized controlled trial (CAN KNOW). **Clin Infect Dis** 66 (2): 229-236.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

NIH 1R01 AI116472-01 William (PI) 2015-2020

Comparative incidence and clinical spectrum of *Plasmodium knowlesi* malaria, a longitudinal study in Sabah, Malaysia.

Aus. Gov. Dept. of Foreign Affairs and Trade William (PI) 2016-2019

Strengthening regional research collaboration in the prevention and containment of multidrug-resistant tuberculosis and malaria

Completed Research Support

MRC (UK) William (Malaysian PI) 2012-2017

Environmental and Social Ecology of Human Infectious Diseases (ESEI) Grant

Defining the biomedical, environmental and social risk factors for human infection with *Plasmodium knowlesi*

OMB No. 0925-0001 and 0925-0002 (Rev. 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Lasimbang, Helen Benedict

eRA COMMONS USER NAME (credential, e.g., agency login): (b) (6)

POSITION TITLE: Chief Executive Officer, Hospital Universiti Malaysia Sabah.

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable*	Completion Date MM/YYYY	FIELD OF STUDY
University Malaya, Kuala Lumpur	MMed (O&G)	1998	Obstetrics and Gynaecology
University Malaya, Kuala Lumpur	MBBS	1991	General medicine and surgery

A. Personal Statement

I have 12 years' experience working as a gynecologist with the Malaysian Ministry of Health. I have 20+ years of experience in doing research on various field of expertise ranging from maternal health to creating alcohol intervention tool-kit to empower indigenous communities. I am the Head of Development and Health Research Unit (DHRU), supported by the U.S Agency for International Development (USAID), DHRU is an EcoHealth Alliance (EHA) – Universiti Malaysia Sabah (UMS) platform for multi-disciplinary research, publications and other collaborative activities in the scope of land-use change disease-emergence and in related social and public health aspects. I was also the Professor in the Deputy Dean office for Postgraduate and Research, University Malaysia Sabah and currently the Chief Executive Officer Hospital Universiti Malaysia Sabah which will open November 2020 and will be part of the clinical studies planned for this project.

1. **Lasimbang HB**, Teo JBH, Tha NO, Amir LE (2018). Knowledge, Attitudes and Practice of Contraception by Doctors and Women in Kota Kinabalu, Sabah. **Borneo Journal of Medical Sciences** 12(1): 23-30

2. Awang H, Low WY, Tong WT, Tan LY, Cheah WL, **Lasimbang HB**, Hassan HM (2018). Differentials in sexual and reproductive health knowledge among east malaysian adolescents. **J. Biosoc. Sci**. 00, 1–10, Cambridge University Press, doi:10.1017/S0021932018000214.

3. Syva SH, Ampon K, **Lasimbang HB,** Fatimah SS (2017). Microenvironmental factors involved in human amnion mesenchymal stem cells fate decisions. **Journal of Tissue Engineering and Regenerative Medicine** 11(2): 311-320. https://doi.org/10.4269/ajtmh.17-0081.

4. Gumpil SL, Ampon K, **Lasimbang HB**, Fatimah SS, Kumar SV (2017). Comparison between fresh and cryopreserved Human Amnion Mesenchymal Stem Cells (HAMCs) in terms of series passaging, morphology and differentiation potential during long term culture. **Biomedical Research and Therapy** 4(5): 134-135.

B. Positions and Honors

Positions and Employment

1991 -92 Housemanship, Queen Elizabeth Hospital, Kota Kinabalu
1992 -94 Hospital Director, Papar Hospital, Papar

1994 -98 Post graduate trainee, Department of Obstetrics and Gynaecology, University Malaya, Kuala Lumpur. Department of Obstetrics and Gynaecology at Tengku Ampuan Rahimah Hospital, Klang, Selangor
1998 -99 Specialist, Obstetrics and Gynaecology at Maternity Hospital Kuala Lumpur.
1999 -02 Specialist/Consultant, Obstetrics and Gynaecology, Queen Elizabeth Hospital, Kota Kinabalu.
2003 -12 Resident Consultant, Obstetrics & Gynaecology, Sabah Medical Centre, Kota Kinabalu.
2012 -14 Head of RHD, Reproductive Health Department (RHD), University Malaysia Sabah.
2014 -15 Associate Professor, Deputy Dean Research and Postgraduate, University Malaysia Sabah.
2015 -17 Associate Professor, Deputy Dean Clinical Services, University Malaysia Sabah.
2016 - Head of Development and Health Research Unit (DHRU)
2017 -18 Associate Professor, Deputy Dean Postgraduate and Research, University Malaysia Sabah.
2018 - Chief Executive Officer Hospital Universiti Malaysia Sabah.

Other Experience and Professional Membership

1999 -03 Committee member of Sabah Cancer Society
1999 - Life member of Sabah Cancer Society
1999 Member of Sabah Child Welfare Association
1999 - Member of Partners of Community Organisation (PACOS Trust)
2000 - Life member of Sabah Society
2003 -17 Life member of MERCY Malaysia
2003 -17 Chairperson of MERCY Malaysia, Sabah Chapter
2009 - Committee member of Intervention Group of Alcohol Misuse (IGAM), MERCY Malaysia
2011 -14 Ex-Officio member of MERCY Malaysia
2012 - Vice President of Kinabalu Running Club
2016 - Board of Director, EduLife Berhad
2016 - President, Association for the Prevention of Alcohol Misuse
2017 - Member of International Society of Quality of Life Studies
2017 - President of Persatuan Larian Berhalangan Sabah
2018 Organizing Chairperson, 1st Borneo Quality of Life Conference

Honors

2012 Anugerah Kesatria Puteri Perubatan, IDEA Malaysia
2012 Talented Staff Award, School of Medicine, University Malaysia Sabah
2012 Sport Leadership Award, School of Medicine, University Malaysia Sabah
2012 Outstanding Dedication and Significance Contributions Award, MERCY Malaysia
2013 APC, University Malaysia Sabah
2013 Talented Staff Award, School of Medicine, University Malaysia Sabah
2013 Sport Leadership Award, School of Medicine, University Malaysia Sabah
2014 Augerah Sukan Untuk Semua (ASUS) 2014, Peringkat Negeri Sabah

C. Contribution to Science

1. **Over 12 years of practicing and 20 years of research on women, reproductive and sexual health and improving diagnostics.** Extensive experience working with communities on reducing alcohol harm and other outreach programs.Ajak WA, Simat SF, Eng HS, **Lasimbang HB**, Lin TP (2017). Characterisation, Proliferation and differentiation potential of long term cultured Wharton's Jelly derived mesenchymal stem cells. **Biomedical Reseach and Therapy** 4 (S):133.

a. Fiona Macniesia Thomas, Kumar V, Simat SF, **Lasimbang HB** (2017). Telomerase activity, telomerase length and P53 mutation detection on cellular senescence of Human Amnion Mesenchymal StemCells (HAMCs). **Biomedical Research & Therapy** 4 (S): 131.

b. James S, Eckerman L, Shoesmith W, **Lasimbang HB**, Joseph A (2017). Using the diamond dialogue to explore community ambivalence towards changing alcohol use and strengthen community action. **J Addict Res Ther.** 8:4 (Suppl). doi: 10.4172/2155-6105-C1-030.

c. **Lasimbang HB**, Tong WT, Low WY (2016). Migrant workers in Sabah, East Malaysia: The importance of legislation and policy to uphold equity on sexual and reproductive health and rights. **Best Pract. Res. Clin. Obstet. Gynaecol.** 32, 10. doi:10.1016/j.bpobgyn.2015.08.015 (IF: 2.291).

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

University Community Transformation Centre Lasimbang (PI)
Produk Minuman Halia untuk Meningkatkan Ekonomi dan Kesihatan Komuniti Daerah Tambunan
Role: PI

University Malaysia Sabah. "Knowledge, Attitude, and behaviour regarding of Comprehensive Sexuality Education among First Year Students of UMS"
Role: Co-researcher

United National Children Fund (UNICEF) Lasimbang (PI)
Maternal and child malnutrition in Sabah
Role: PI

University Malaysia Sabah Lasimbang (PI)
Effectiveness of community support training program for alcohol harm reduction
Role: PI

Completed Research Support

SGK0022-SKK-2015 Lasimbang (PI) 01/07/2015-30/06/2017
University Sabah Malaysia
Pap Smear reporting in tertiary hospital and maternal child health clinics of Kota Kinabalu, Sabah
Role: PI

FK-MHC/1(UMS-15) Lasimbang (PI) 01/12/2015-01/12/2017
University Sabah Malaysia
Alcohol Intervention Tool-kit: Empowering the Indigenous Communities of Sabah to Reduce Alcohol-related Harm
Role: PI

RACE0019-SKK-2014 Lasimbang (PI) 01/26/2015-01/25/2017
University Malaysia Sabah
Cellular NUteraction Between Human Amnion Mesenchymal Stem Cells and Human Dermal Fibroblasts
Role: PI

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BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Lee, Heng Gee

eRA COMMONS USER NAME (credential, e.g., agency login):

POSITION TITLE: Infectious Disease Consultant (Sabah State and Queen Elizabeth Hospital)

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University of Auckland, New Zealand	MBChB	03/2002	Bachelor of Medicine, Bachelor of Surgery
Royal College of Physicians of the United Kingdom	MRCP (UK)	03/2011	Internal Medicine
National University Hospital, Singapore	Infectious Disease Fellowship	03/2017	Infectious Disease

A. Personal Statement

I have 17 years of working experience as a clinician in the Malaysian Ministry of Health and the Sabah State Health Department. I am currently the Sabah State Infectious Disease Consultant and the Head of the Infectious Disease Unit in Queen Elizabeth Hospital, Kota Kinabalu, Sabah, Malaysia. I was involved in the recruitment of patients for the USAID PREDICT Human Syndromic Surveillance in 2018.

B. Positions and Honors

Positions and Employment

2002 -10 Medical Officer, Sabah State Health Department, Ministry of Health of Malaysia
2011 - Internal Medicine Specialist, Queen Elizabeth Hospital, Kota Kinabalu, Sabah, Malaysia
2017 - Head of Infectious Disease Unit, Queen Elizabeth Hospital, Kota Kinabalu, Sabah, Malaysia
2018 - Infectious Disease Consultant, Sabah State Health Department

Other Experience and Professional Membership

2011 - Member of the Royal College of Physicians, MRCP (UK), MRCP (London)
2014 - Member of the Malaysian Society for HIV Medicine (MASHM)
2017 - Associate Member of the Infectious Diseases Society of America (IDSA)
2017 - Associate Member of the HIV Medicine Association (HIVMA)
2017 - Member of the Malaysian Medical Association (MMA)

Honors

2005 Ministry of Health of Malaysia Excellent Service Awards
2009 Ministry of Health of Malaysia Excellent Service Awards
2015 Ministry of Health of Malaysia Excellent Service Awards

C. Contributions to Science

1. **USAID PREDICT Human Syndromic Surveillance in 2018.** Objective is to detect novel viruses that are causing diseases in patients without known etiology.

2. Research on the etiologies of central nervous system infections in Kota Kinabalu, Sabah.

a. **Lee HG**, William T, Menon J, Ralph AP, Ooi EE, Hou Y, Sessions O, Yeo TW (2016). Tuberculous meningitis is a major cause of mortality and morbidity in adults with central nervous system infections in Kota Kinabalu, Sabah, Malaysia: an observational study. **BMC Infect. Dis.** 16: 296

D. Additional Information: Research Support and/or Scholastic Performance

Not applicable

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BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Rajahram, Giri Shan

eRA COMMONS USER NAME (credential, e.g., agency login): (b) (6)

POSITION TITLE: Infectious Disease Physician

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Science University of Malaysia	MD	08/2006	Medicine
Royal College of Physician London	MRCP	07/2011	Medicine
Asia Pacific Society of Infection Control	Certification in Infection Control	06/2014	Tropical Medicine
Liverpool School of Tropical Medicine	DTM&H (with distinction)	02/2018	Tropical Medicine
Royal College of Physician London	Leadership Accreditation	06/2018	Leadership and Management

A. Personal Statement

I am an infectious disease consultant for Sabah State Health Department and an infectious disease physician working in the only tertiary referral center in Sabah, serving a population of 3 million people managing various complex and emerging infectious diseases. I am an integral partner from the Ministry of Health Malaysia, involved in collaborative research with partners from Menzies School of Health Research, Australia to further the understanding of epidemiology, pathophysiology and clinical management of zoonotic *plasmodium knowlesi* malaria. I have also been involved with local and international partners, examining emerging infectious disease threats in the region including the PREDICT project. Among others, I have authored scientific papers describing cases of *Streptococcus suis* and one of the few detailed post-mortem cases of fatal zika virus infections in an adult.

1. Cooper DJ, **Rajahram GS**, William T, Jelip J, Maohammad R, Benedict J, Alaza DA, Malacova E, Yeo TW, Grigg MJ, Anstey NM, Barber BE (2019). Plasmodium knowlesi malaria in Sabah, Malaysia, 2015-2017: ongoing increase in incidence despite near-elimination of the human-only Plasmodium species **Clin Infect Dis.** pii: ciz237. doi: 10.1093/cid/ciz237.
2. **Rajahram GS**, Hale G, Bhatanagar J, Hui J, Thayan R, William T, Kum Tong W, Tambayah PA, Yeo TW (2019). Postmortem evidence of disseminated Zika virus infection in an adult patient. **Int J Infect Dis.** pii: S1201-9712(19)30060-8. doi: 10.1016/j.ijid.2019.01.047.
3. **Rajahram GS**, Cooper DJ, William T, Grigg MJ, Anstey NM, Barber BE (2019). Deaths from Plasmodium knowlesi malaria: case series and systematic review. **Clinical Infectious Diseases** ciz011, https://doi.org/10.1093/cid/ciz011.
4. Grigg MJ, William T, Barber BE, **Rajahram GS**, Menon J, Schimann E, Piera K, Wilkes CS, Patel K, Chandna A, Drakeley CJ, Yeo TW, Anstey NM (2018). Age-Related Clinical Spectrum of Plasmodium knowlesi Malaria and Predictors of Severity. **Clinical Infectious Diseases** doi.org/10.1093/cid/ciy065.

B. Positions and Honors

Positions and Employment

Infectious Disease and General Med. Consultant Queen Elizabeth Hospital, Kota Kinabalu, Sabah
Head of Unit, Infection Control, Queen Elizabeth Hospital 2, Sabah
Deputy Head, Department of Medicine, Queen Elizabeth Hospital 2, Sabah
Adjunct Clinical Lecturer University Malaysia Sabah
Sabah State Technical Expert for Infection Control and Infectious Diseases
Former Head of Unit Neurology, Queen Elizabeth Hospital
Former Deputy Head, Department of Medicine Keningau Hospital

Honors

2010 Excellent Service Award, Ministry of Health Malaysia
2014 Malaysian Government Merit Scholarship, for Infectious Disease Training
2014 Travel Grant, Asia Pacific Malaria Elimination Network (APMEN)
2016 Travel Grant, National Institute of Health, United States of America
2016 Excellent Service Award, Ministry of Health Malaysia
2017 Travel Grant, Malaysia Society of HIV Medicine, Malaysia
2017 Travel Grant, Asia Pacific AIDS and Co-Infection Conference
2017 Merit Scholarship Award Liverpool School of Tropical Medicine, United Kingdom
2018 Honorary Fellow, Menzies School of Health Research
2019 Endeavor Executive Leadership Award by the Government of Australia

C. Contributions to Science

1. **Advancing the understanding of epidemiology, pathophysiology and clinical management of *plasmodium knowlesi* malaria**, an emerging zoonotic malaria in collaboration with international partners from Menzies, which has resulted in publications and policy changes both nationally in Malaysia and international in World Health Organization (WHO) guidelines in clinical management of *plasmodium knowlesi* malaria.
   a. Grigg MJ, William T, Barber BE, GS Rajahram et al (2018). Artemether-lumefantrine versus chloroquine for the treatment of uncomplicated Plasmodium knowlesi malaria in Sabah, Malaysia (CAN KNOW): an open-label randomized controlled trial. Clinical Infectious Diseases 66(2):229–236, DOI: 10.1093/cid/cix779.
   b. Grigg MJ, William T, Menon J, Barber BE, Wilkes CS, GS Rajahram et al. Age-related clinical spectrum of malaria in children and adults infected with Plasmodium knowlesi compared with human-only Plasmodium species: A prospective district hospital study in Sabah; Clinical Infectious Diseases, ciy065, Mac 2018 https://doi.org/10.1093/cid/ciy065.
   c. Barber BE, Rajahram GS, William T, Yeo TW, Anstey NJ (2017). World Malaria Report: Time to acknowledge knowlesi malaria. Malaria Journal 16:135DOI: 10.1186/s12936-017-1787.
   d. Rajahram GS, Hameed AA, Menon J, William T (2017). Case Report: Two Human Streptococcus Suis Infections in Borneo, Sabah, Malaysia. BMC Infectious Diseases 17:188 DOI 10.1186/s12879-017-2294.
2. **Community engagement and participation.** Dr Rajahram is the Vice-President Medical Society of Queen Elizabeth Hopsital and the Treasurer of Infectious Disease Society of Sabah. He makes regular public speaking appearances on Infectious Disease and Tropical Medicine locally and nationally for both health professionals and general public. He is also involved as Medical Coordinating Director for the Mobile Court Initiative which serves remote and difficult to access areas in Sabah with multi-agency service provision an initiative by Rtd Chief Justice of Malaysia, Tan Sri Richard Malanjum.

a. Tan JS, Ambang T, Azlina A-A, **Rajahram GS**, Wong KT, Goh KJ (2016). Congenital myasthenic syndrome due to novel CHAT mutations in an ethnic kadazandusun family. **Muscle & Nerve** 53(5):822-6. doi: 10.1002/mus.25037.

b. Lim KS, Tan AH, Lim CS, Chua KH, Lee PC, Ramli N, **Rajahram GS**, Hussin FT, Wong KT, Bhattacharjee MB, Ng CC (2015). R54C mutation of NOTCH3 gene in the first Rungus family with CADASIL. **PLoS One** 13;10(8):e0135470. doi: 10.1371/journal.pone.0135470.

3. **Professional involvement.** Dr Rajahram was Convenor of the 3rd and upcoming 4th Borneo Scientific Meeting on Tropical Infectious Diseases 2019 and organizing organising committee member for the first two meetings. He has contributed as an author in clinical cases of *plasmodium knowlesi* malaria in Medical Parasitology a Textbook, R Mahmud Y Lim, A Amir, Springer International Publication 2017 ISBN 978-3-319-68794-0. He is also involved in contributing to the Malaysian National HIV guidelines; Chapter on Treatment Failure (2018), (b) (4)

a. **Rajahram GS**, Barber BE, William T, Grigg MJ, Menon J, Yeo TW, Anstey NM (2016). Falling Plasmodium knowlesi malaria death rate among adults despite rising incidence, Sabah, Malaysia, 2010-2014. **Emerg. Infect. Dis.** 22(1).

b. Grigg MJ, William T, Menon J, Barber BE, Wilkes CS, **Rajahram GS**, Edstein MD, Auburn S Price RN, Yeo TW, Anstey NM (2016). Efficacy of artesunate-mefloquine against high-grade chloroquine-resistant Plasmodium vivax malaria in Malaysia: an open-label randomised controlled trial. **Clin. Infect. Dis.** doi:10.1093/cid

c. **Rajahram GS**, Barber BE, Tan WW, Yeo T, William T (2013). Case Report: Fatal Plasmodium knowlesi malaria following an atypical clinical presentation and delayed diagnosis. **Med J Malaysia** 68(1):71-72.

d. **Rajahram GS**, Barber BE, William T, Menon J, Anstey NM, Yeo TW (2012). Deaths due to Plasmodium knowlesi malaria in Sabah, Malaysia: association with reporting as Plasmodium malariae and delayed parenteral artesunate. **Malaria Journal** 11:284.

e. **International standing:** Co-opted invited observer for WHO Expert Consultation Meeting, Kota Kinabalu, Sabah, 2017 and invited panelist to the Environment & Social Ecology of Human Infectious Diseases (ESEI), Medical Research Council (JK) Showcase Event at Royal Society in London, March 2018.

D. Additional Information: Research Support and/or Scholastic Performance

n/a

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BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Sekaran, Jayaseelan

eRA COMMONS USER NAME (credential, e.g., agency login): (b) (6)

POSITION TITLE: Senior Medical Officer

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University Malaya, Malaysia	BMMS	2006	Medicine
Irish College of General Practitioners, Seremban, Malaysia	LFOM	On-going	Occupational Medicine

A. Personal Statement

I have been running the Lintang Health Clinic in Sungai Siput for Orang Asli populations in the District of Kuala Kangsar since 2016. I worked with Tom Hughes and EcoHealth Alliance on the PREDICT project as the community POC to help liaise with the communities, identify participants, and manage the District Health team to collect samples. I am also responsible for returning results from this study to the participants. I have an interest in Infectious Disease and feel that the population I sever will strongly benefit from this study.

B. Positions and Honors

Positions and Employment

2006 -07 Housemanship, Teluk Intan Hospital, Perak, Malaysia.
2007 -16 Senior Medical Officer, Teluk Intan Hospital, Perak, Malaysia. Internal medicine.
2016 - Senior Medical Officer, Lintang Health Clinic, Kuala Kangsar District Health Office, Perak, Malaysia

Other Experience and Professional Membership

2018 Volunteer Treating Doctor, Refugee Relief Mission to Cox Bazaar, Bangladesh
2018 Team Leader, Forward Medical Team and Mobile Clinic, Tsunami Mission to Palu, Sulawesi, Indonesia

Honors

2019 Outstanding Award for Relief Mission, Islamic Medical Association of Malaysia

C. Contributions to Science

1. Examining neural tube defects in relation to nutrition.

a. J.J. Ho, L. Vyveganathan and **J. Sekaran.** Consumption of cereal flour in a Malaysian population: Flour fortification to prevent neural tube defect may be feasible in a rice-eating country. **Ecology of Food and Nutrition**. 2006 (45): 53-60.

D. Additional Information: Research Support and/or Scholastic Performance

n/a

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BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Tan, Cheng Siang

eRA COMMONS USER NAME (credential, e.g., agency login): cstan

POSITION TITLE: Senior Lecturer, Head

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Universiti Putra Malaysia, Malaysia	B.S. (hons)	09/2000	Biotechnology (Bacteriology, AMR)
Universiti Malaysia Sarawak, Malaysia	NSF Fellowship	12/2003	Virology (HFMD/EV71)
Universiti Malaysia Sarawak, Malaysia	M.S.	09/2004	Virology (HFMD/EV71)
Newcastle University, United Kingdom	Ph.D.	05/2012	Virology (hRSV)
Ministry of Public Health, Thailand	SEAOHUN Fellowship 2017	12/2017	One Health

A. Personal Statement

I have nearly 20 years of laboratory experience on human viruses. I have started off with the sentinel surveillance of Hand, foot and mouth Disease (HFMD) from 2000-2004 providing molecular screening on swabs obtained from public hospitals and sentinel clinics. Results were made available to the Department of Public Health and State's Disaster Management Committee for outbreak management. I was tasked to develop a serological assay for the detection of Enterovirus 71. I have received the prestigious National Science Fellowship (NSF) Award from the Ministry of Science, Technology and Environment for my work on EV71 in Sarawak. I was also involved with the screening of suspected SARS-CoV specimens from Sarawak General Hospital (SGH) using molecular techniques but fortunately none were confirmed positive during that time. No manuscript was published on the work on SARS-CoV due to negative results but the experience of donning and doffing extra amount of PPE, setting up administrative and the maximizing the use of engineering controls to work safety in the laboratory become an invaluable experience for a virologist such as myself. Thereafter, I pursued my doctorate degree in Newcastle University, UK under the supervision of Emeritus Professor Geoffrey Toms. My project was to study the protective nature of maternal antibodies against human respiratory syncytial virus (RSV). I have to work closely with the research nurse to obtain in nasoparyngeal swabs and blood serum from hRSV infected infants. All work related with my MSc and PhD were tissue culture, molecular biology and serology intensive. Whilst heading the Centre for Tropical and Emerging Diseases, I have worked closely with zoologists from my UNIMAS to study the seroprevalence of hantavirus in both rodents captured from residential and forested areas of Sarawak. The work involved setting up traps in strategic locations, capturing the animal, obtaining specimens and ethically euthanizing the animal. I have collaborated with Southampton University, UK funded by Newton Fund to study the nasal carriage of *Streptococcus pneumoniae* in the Malaysian population in hope to provide disease burden data to influence the adoption of the pneumococcal vaccine in Malaysia. The newest project is

in Human Papillomavirus (HPV) and cervical cancer. We are trying to define the molecular epidemiology of HPV in Sarawak and at the same time provide HPV DNA test for the rural communities. The work involves explaining the study to the women, obtaining informed consent and obtaining the specimen. Participating women are also visually screened for cervical intraepithelial neoplasia (CIN) using visual inspection using acetic acid (VIA). This work is still at its infancy and 2 manuscripts are already in the pipeline. Recently, we have acquired the careHPV system (Qiagen), packed it in boxes and took a flight to Bario, a remote town at the northeast of Sarawak and set the portable laboratory there to screen the women for HPV infection and also providing them with cervical examination.

1. **Tan CS**, Cardosa MJ (2007). High-titred neutralizing antibodies to human enterovirus 71 preferentially bind to the N-terminal portion of the capsid protein VP1. **Archives of virology** 152(6) 1069-1073.
2. Perera D, Podin Y, Akin W, **Tan CS**, Cardosa MJ (2004). Incorrect identification of recent Asian strains of Coxsackievirus A16 as human enterovirus 71: improved primers for the specific detection of human enterovirus 71 by RT PCR. **BMC infectious diseases** 4 (1):11.
3. Hamdan NE, Ng YL, Lee WB, **Tan CS**, Khan FA, Chong YL (2017). Rodent species distribution and hantavirus seroprevalence in residential and forested areas of Sarawak. **Malaysia Tropical Life Sciences Research** 28 (1):151-159.
4. Tricarico, S, McNeil HC, Cleary DW, Head MG, Lim V, Yap IKS, Wie CC, **Tan CS**, Norazmi MN, Aziah I, Cheah ESG, Faust SN, Jefferies JMC, Roderick PJ, Moore M, Yuen HM, Newell ML, McGrath N, Doncaster CP, Kraaijeveld AR, Webb JS, Clarke SC (2017). Pneumococcal conjugate vaccine implementation in middle-income countries." **Pneumonia** 9(1): 6.

B. Positions and Honors

Positions and Employment

2000 -04 National Science Fellow, Universiti Malaysia Sarawak
2004 -06 Chemistry educator, Lodge Private School
2006 -12 Lecturer, Universiti Malaysia Sarawak
2012 - Senior lecturer, Universiti Malaysia Sarawak

Honors

2014 Excellence Award, Universiti Malaysia Sarawak
2016 Affiliate Young Scientists Network-Academy Science of Malaysia
2017 Certified Professional of the Month, International Federations of Biosafety Associations (IFBA)
2017 SEAOHUN Fellow
2018 Registered Biosafety Professional (RBP), Malaysian Biosafety and Biosecurity Association

C. Contributions to Science

1. **Ventilation engineering**. In collaboration with our Faculty of Engineering, our team have reengineered to air inlet in the type2 Class A2 Biosafety Cabinet (BSC) which will lengthen the lifespan of the HEPA filter in the BSC and distribute the air pressure more evenly on the HEPA filter while in operation.

2. **Developed and filed a patent protection on an algorithm to measure the antibiotic's inhibition zone**, consulting the database and provide instant results by the use of a standard mobile phone. This product has won Gold Medal in UNIMAS Innovation and Technology Expo 2016 and Silver Medal in the 28th International Invention, Innovation and Technology Exhibition 2017. *Patent pending.*

3. **Pioneering biosafety and biosecurity in Malaysia**. My contribution is internationally recognized and was awarded the Certified Professional of the Month in 2017 by the International Federation of Biosafety Associations. I currently hold 4 of 5 professional certification from IFBA, deemed the most certified biorisk management professional in Malaysia. I am also the national biorisk management trainer and conduct the annual Malaysian Advanced Biosafety Officer Training (MABOT) funded by CRDF Global, supported by

Sandia National Laboratories and Department of State, US. I have worked closely with the Ministry of Health Malaysia and the Ministry of Defense Malaysia to develop the national biosafety and biosecurity guidelines and policies.

a. Ibrahim MD, Mohtar MZ, Alias AA, Wong LK, Yunos YS, Rahman MRA, Zulkharnain A, **Tan CS**, Thayan R (2017). Airflow optimization for energy efficient blower of biosafety cabinet class II A2. **Journal of Physics: Conference Series** 822(1)012022.
b. Zalini Y, et al. (2018). National Laboratory Biosecurity Assessment and Monitoring Checklist (in the framework of the biological weapons convention) STRIDE, Ministry of Defense Malaysia. P. 1-31.
c. Biosafety and Biosecurity Sub-committee, Laboratory Technical Advisory Committee (LTAC) (2015) Malaysia Laboratory Biosafety and Biosecurity Policy and Guideline, Ministry of Health Malaysia. 1-26.
d. https://www.internationalbiosafety.org/index.php/professional-certification/ifba-professional-certifications/certified-professional-of-the-month/581-cheng-siang-tan
e. Ryu S., Kim B. I., Lim JS., Tan C.S. and Chun BC. (2017) One Health Perspectives on Emerging Public Health Threats. J Prev Med Public Health 50(6):411-414.

D. Additional Information: Research Support and/or Scholastic Performance

Completed Research Support (last 3 years only)

F05/SGS/1638/2018 2018
Special Grant Scheme (SGS), Universiti Malaysia Sarawak internal grant
A study on the epidemiology of HPV subtypes among women with abnormal pap smears in Sarawak General Hospital

F05/SpGS/1564/2017 2017
Special Grant Scheme (SGS), Universiti Malaysia Sarawak internal grant
Bioprospecting of bacteriolytic bacteriophages infecting *Pseudomonas aeruginosa*

RAGS/ST01(1)/1314/2015(08 2015
Research Acculturation Grant Scheme (RAGS), Ministry of Higher Education, Malaysia
A pilot study of bacterial diversity related to periodontal disease among Sarawak children

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BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Anwarali Khan, Faisal Ali

eRA COMMONS USER NAME (credential, e.g., agency login): (b) (6)

POSITION TITLE: Lecturer

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Universiti Malaysia Sarawak	B.S. (Hons)	05/2004	Biotechnology
Texas Tech University	M.S.	05/2008	Zoology
Texas Tech University	Ph.D.	05/2013	Zoology

A. Personal Statement

I am interested in the systematics and molecular evolution of Southeast Asian mammals, particularly bats. I aim to understand the diversity of several genera in these groups, looking for common patterns in their distributions and origins. This allows me to understand the extent to which biogeography of Southeast Asia has shaped the genetic diversity of mammals in this region. Currently, my lab is examining the evolution of Roundleaf bats, Horseshoe bats, and several groups of rodents. We are studying multiple transmission lines (paternal, maternal and autosomal markers) along with behavioral characteristic such as echolocation, and we are using geometric morphometric technique to identify taxonomic units. My hope is that this research will provide a better understanding of the mode of evolution and diversification for bats and rodents in Southeast Asia. I am also keen to move forward with the advancement of the genomic field, by incorporating bioinformatics to better utilize natural history collections. I hope to use this new tool to better understand the microbial fauna carried by mammalian hosts.

1. Runting RK, Griscom BW, Struebig MJ, Satar M, Meijaard E, Burivalova Z, Cheyne SM, Deere NJ, Game ET, Putz FE, Wells JA, Wi ting A, Ancrenaz M, Ellis P, **Khan FAA**, Leavitt SM, Marshall AJ, Possingham HP, Watson JEM, Venter O (2019). Larger gains from improved management over sparing–sharing for tropical forests. **Nature Sustainability** 2(1), 53-61.
2. Mazlan N, Abd-Rahman MR, Tingga RCT, Abdullah MT, **Khan FAA** (2019). Population Genetics Analyses of the Endangered Proboscis Monkey from Malaysian Borneo. **Folia Primatologica** 90(3), 139-152.
3. Murray SW, **Khan FAA**, Kingston T, Zubaid A, Campbell P (2018). A new species in the *Hipposideros bicolor* group (Chiroptera: Hipposideridae) from Peninsular Malaysia. **Acta Chiropterologica** 20:1, 1-29.
4. **Khan FAA**, Phillips CD, Baker RJ (2013). Timeframes of Speciation, Reticulation, and Hybridization in the Bulldog Bat Explained Through Phylogenetic Analyses of All Genetic Transmission Elements. **Systematic Biology** 63(1):96–110.

B. Positions and Honors

Positions and Employment

2004 -06 Tutor, Universiti Malaysia Sarawak, Sarawak, Malaysia
2008 -13 Teaching Assistant, Texas Tech University, Lubbock TX
2013 - Lecturer, Universiti Malaysia Sarawak, Sarawak, Malaysia
2013 - Research Associate, Museum of Texas Tech, Texas Tech University, Lubbock, TX
2014 - Research Fellow, Universiti Malaysia Terengganu, Malaysia
2016 - Principal at Rafflesia Student Residential College, UNIMAS
2017 -18 Deputy Dean (Student Affair and Alumni), FRST, UNIMAS
2018 Deputy Director (Department of Alumni Relation), Centre for Student Development, UNIMAS

Other Experience and Professional Membership

2006 - Life Member, American Society of Mammalogists
2006 - Life Member, Texas Society of Mammalogists
2011 Southeast Asia Bat Conservation Research Unit-member (SEABCRU) – member/Steering Committee.
2006 -12 Genetic Society of Malaysia, (PGM) (membership no: PGM 0835) – life member.
Texas Tech University Association of Biologist (TTUAB) – member (January 2006-May 2013), Vice President for 2007 – 2008 sessions., Board of Directors – 2010-2012
2016 Young Scientist Network-Academy Sciences Malaysia 2016 (YSN-ASM2016)
2013- Associate Editor: Borneo Journal of Resource Science and Technology (UNIMAS Publisher)
2015 -17 Reviewer (Member in Editorial Board) - Journal of Wildlife and Parks
2016- Subject Editor (Mammals): Checklist-the journal of biodiversity data
2015- Southeast Asia Section: IUCN Bat Specialist Group Newsletter
2018- Review Editor: Journal of Bat Research and Conservation

Honors

2016 - Young Scientist Network-Academy Sciences Malaysia 2016 (YSN-ASM2016) (1st December 2016 - 31 December 2019)
2016 Excellence Service Award 2015 / Anugerah Perkhidmatan Cemerlang 2015, UNIMAS
2015 UNIMAS Research and Development Expo 2015

1. Value of acoustic measures in identifying cryptic bat species: A Myth or reality? (Silver) – Prepared acoustic call CD, Website for echolocation calls, Prepared echolocation field guide book for bats of Malaysia
2. Connecting wildlife survey to tourism through LIDAR images: Wind Cave field guide (Bronze) – Prepared website for wind cave 3D maps
3. Value of acoustic survey in detecting elusive Tarsier: Description of their call and genetic structure (Bronze) – Prepared website with distribution and genetic data

2012 Texas Tech Association of Biologist Symposium Award
Organized by TTUAB at Texas Tech University, Lubbock, USA
Best presentation in Systematics and Evolution – 1st place (USD 200)
2010 Michelle C. Knapp Memorial Scholarship 2010
Recognition on mammalogy studies and field work (USD 500)
2010 Helen Hodges Educational Charitable Trust Scholarship
Recognition on academic and research achievement (USD 1250)
2010 Texas Society of Mammalogists Award
Best presentation on studies pertaining to mammalian cytology, evolution, and systematics – (USD 100)
2008 Seventh Annual Graduate Student Research Poster Award

Organized by Graduate School at Texas Tech University
Best poster award – 3rd place (USD 75)

2007 First International South East Asia Bat Conference Award
Best presenter award – Books

2007 British Ecological Society Grant
To attend the First International South East Asia Bat Conference at Phuket, Thailand-Registration and hotel fee paid

2007 TTUAB Graduate Forum Award
Organized by TTUAB at Texas Tech University, Lubbock, USA
Best presentation in Systematics and Evolution – 3rd place (USD 100)

2004 Malaysian Ministry of Higher Education Scholarship
For both Masters and PhD study at Texas Tech University, Lubbock, Texas, USA. Scholarship covers tuition fee and living allowance for six years.

C. Contributions to Science

1. **Studies on the systematics and evolution of mammals.** Different climatic conditions and geologic settings have been seen as the major signature in promoting diversification in mammals. Different types of molecular techniques allow us to capture this variation and understand when all of this happens. Further, new analyses allow us to test for the potential pitfall in analyzing data from different group of mammals. The following manuscripts are the flagship manuscripts for the last 5 years.
   a. Esselstyn JA, Evans BJ, Sedlock JL, **Khan FAA**, Heaney LR (2012). Single-locus species delimitation: A test of the mixed Yule-coalescent model, with an empirical application to Philippine round-leaf bats. **Proceedings of Royal Society of London**. 279:3678-3686.
   b. **Khan FAA**, Solari S, Swier VJ, Larsen PA, Abdullah MT, Baker RJ (2010). Systematics of Malaysian woolly bats (Vespertilionidae: *Kerivoula*) inferred from mitochondrial, nuclear, karyotypic, and morphological datasets. **Journal of Mammalogy**. 19(5):1058-1072.

2. **Assessing bat diversity across Malaysia.** The actual bat diversity in Malaysia may be underestimated, as there are several new species recently described which were unknown due to their cryptic morphology. New species are the result of incorporating: molecular methods with greater resolution, electronically recorded acoustic calls, and efficient field techniques such as harp traps, to properly describe species diversity and status. Different hypotheses have been proposed to facilitate speciation processes in Southeast Asian bats (e.g. geographic isolation, habitat fragmentation, adaptation to different echolocation calls, etc.).
   a. **Khan FAA**, Shazali N, Latip N, Azhar I (2019). Into the Heart of Borneo: Mammals of Upper Baleh, Sarawak. **Journal of Sustainability Science and Management** 14(2).
   b. Murray SW, **Khan FAA**, Kingston T, Zubaid A, Campbell P (2018). A new species in the *Hipposideros bicolor* group (Chiroptera: Hipposideridae) from Peninsular Malaysia. **Acta Chiropterologica** 20:1, 1-29.
   c. Morni MA, Tahir NF, Rosli QS, William-Dee J, Azhar I, Azuan R, Zahidin MA, Abdullah MT, **Khan FAA** (2016). New record of the endemic *Rhinolophus chiewkweeae* (Chiroptera: Rhinolophidae) to the east coast of Peninsular Malaysia in Terengganu with noteworthy records on their ecology, genetics, and taxonomy. **Raffles Bulletin of Zoology** 64: 242–249.
   d. Lim L, Csorba G, Wong CM, Zubaid A, Rahman SPH, Kumaran JV, **Khan FAA**, Huang JCC, Najimudin N, Görföl T (2016). The systematic position of *Hypsugo macrotis* (Chiroptera: Vespertilionidae) and a new record from Peninsular Malaysia. **Zootaxa** 4170(1): 169-177.

3. **Studies on the mammalian ecology.** Undestanding mammalian ecology is vital in order to develop effective conservation plans. My research group has actively looked into using techniques such as direct observation and LIDAR technology. The information collected from these techniques provides critical long-term

management data that is used to monitor the well-being of mammals. We also collaborate with other research groups to better understand the impacts of logging on mammals in Borneo.

a. Mohd-Ridwan AR, Tahir NF, Eshak MH, Csorba G, Görföl T, **Khan FAA**, Mohd-Azlan J (2018). Bats Assemblage and Lunar Phase Effect on Bat Activity at Mixed Dipterocarp Forest, Gunung Gading National Park, Sarawak, Borneo. **Sains Malaysiana** 47(7)(2018): 1349–1357. http://dx.doi.org/10.17576/jsm-2018-4707-01.
b. Rajasegaran P, Shazali N, **Khan FAA** (2018). Microclimate and Physiological Effects in the Roosts of Cave Dwelling Bats: Implications in the roost selection and the conservation in Sarawak, Malaysian Borneo. **Zoological Science** 35(6):521-527.
c. Shazali N, Chew TH, Shamsir MS, Tingga RCT, Mohd-Ridwan AR, **Khan FAA** (2017). Accessing Bat Roosts using LiDAR System at Wind Cave Nature Reserve in Sarawak, Malaysian Borneo. **Acta Chiropterologica** 19(1): 199-210.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

Royal Society and ASM/MIGHT (Royal Society-Newton Mobility Grant) 2017 - 2020
Applying DNA sequencing to guano deposits to assess the ecological consequences of forest loss
Role: PI

UMS-UNIMAS Collaboration Research Grant 2017 - 2019
Proboscis monkey assessment through predictive abundance modeling and microbiome analysis on populations from disturbed and fragmented habitat landscapes in Sabah and Sarawak, Malaysian Borneo (UMS-UNIMAS)
Role: PI

[redacted] (b) (4) 2018 - 2020
The potential of utilizing Visual Technologies as a research practice in zoological studies via Practice-led investigation: a Case study on Bat s Behavior and Characteristic
Role: Co-PI

Ministry of Education (MoE) (Fundamental Research Grant Scheme) 2017 - 2019
Diversity and Molecular Characterization of Fungal Communities in Speleothem, cavern water, dead arthropods, and bat guano substrates from Limestone Caves of Malaysian Borneo
Role: Co-PI

Completed Research Support (last 3 years only)

Ministry of Education (Niche Research Grant Scheme) 2014 - 2018
Biodiversity of Western Sarawak – Life from Headwaters to the Coast
Species of conservation importance – phylogeny and ecology
Role: Co-PI

Ministry of Education (Niche Research Grant Scheme) 2014 - 2018
Biodiversity of Western Sarawak – Life from Headwaters to the Coast
Species response to landscape change in Western Sarawak Ministry of Education (Niche Research Grant Scheme)
Role. Co-PI

OMB No. 0925-0001 and 0925-0002 (Rev 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES**

NAME: Hamzah, Nadia Diyana

eRA COMMONS USER NAME (credential, e.g., agency login):

POSITION TITLE: Medical Officer

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
UCSI University, Kuala Lumpur	MD	2015	General Medicine
Hospital Umum Sarawak	Resident	2018	Housemenship

A. Personal Statement

I am a Medical Officer that is passionate about community health, and serves rural communities that do not have as much access to medical care as suburban and urban areas. While serving the rural communities as Medical Officer, I have overseen educational programs at the local schools focusing on preventative medicine and community health.

B. <u>Positions and Employment</u>

2018 - Medical Officer (Rural Area Service)

C. Contribution to Science

1. Providing medical support to rural areas. I frequently attend emergency calls in the local communities I serve and leverage evidence-based expertise to interpret patient symptoms and rest results.

D. Additional Information: Research Support and/or Scholastic Performance

n/a

OMB No. 0925-0001 and 0925-0002 (Rev. 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Ahmed, Kamruddin

eRA COMMONS USER NAME (credential, e.g., agency login): (b) (6)

POSITION TITLE: Director & Professor

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University of Dhaka	M.B.B.S.	01/1986	Medicine
Institute of Tropical Medicine, Nagasaki University	D.T.M.	08/1988	Tropical Medicine
Nagasaki University	Ph.D.	03/1992	Microbiology

A. Personal Statement

During my carrier in the academia I have gained research experiences on different aspects of infectious diseases, and the scientific management experiences to support this proposed work that involves international interdisciplinary teams working on field survei lance in wild mammals, human behavioral risk surveys and clinical sampling, development of novel diagnostic approaches, and viral characterization *in vitro* and *in vivo*. I am Professor, Department of Pathobiology and Medical Diagnostics, and Director, Borneo Medical and Health Research Centre, Faculty of Medicine and Health Sciences, Universiti Malaysia Sabah that involves in teaching and conducts research on communicable diseases, outbreak investigations and ethnomedicine. My research background is focused on understanding the epidemiology, pathogenesis, and diagnostics of infectious agents particularly emerging infectious diseases. This includes etiology of viral diarrhea and encephalitis; molecular epidemiology of viruses from diarrhea, encephalitis and rabies; identifying novel virus or virus variants in humans and animals; zoonotic infections such as rabies, leptospirosis and brucellosis; developing new diagnostics for rabies and biomarker for encephalitis.

1. Matsumoto T, Sato M, Nishizono A and **Ahmed K*** (2019) A novel bat-associated circovirus identified in northern Hokkaido, Japan. **Arch. Virol.** Doi:10.1007/s00705-019-04286-x.
2. Yahiro T, Takaki M, Chandrasena TGAN, Rajindrajith S, Iha H and **Ahmed K*** (2018) Human-porcine reassortant rotavirus generated by multiple reassortant events in a Sri Lankan child with diarrhea. **Infect. Gen. Evol.** 65: 170-186.
3. Yahiro T, Wangchuk S, Tshering K, Bandhari P, Zangmo S, Dorji T, Tshering K, Matsumoto T, Nishizono A, Soderlund-Venermo M and **Ahmed K*** (2014) Novel human bufavirus genotype 3 in children with severe diarrhea, Bhutan. **Emerg. Infect. Dis.** 20: 1037-1039.
4. Matsumoto T, **Ahmed K***, Wimalaratne O, Nanayakkara S, Perera D, Karunanayake D and Nishizono A (2011) Novel sylvatic rabies virus variant in endangered golden palm civet, Sri Lanka. **Emerg. Infect. Dis.** 17: 2346-2349.

B. Positions and Honors

Positions and Employment

1986 -87 In service Trainee, Mymensingh Medical College Hospital, Bangladesh

1987 -88 Medical Officer, Samorita Hospital, Dhaka, Bangladesh
1988 Visiting Scientist, Dept. of Internal Medicine, Institute of Trop. Med., Nagasaki University, Japan
1992 -95 Guest Research Fellow, Dept. of Internal Medicine, Institute of Trop. Med., Nagasaki University, Japan
1995 Lecturer (CoE), Dept. of Internal Medicine, Institute of Trop. Med., Nagasaki University, Japan
1995 -97 Assistant Professor, Dept. of Microbiology, Faculty of Medicine, Kuwait University, Kuwait. Consultant Microbiologist, Dept. of Microbiology, Mubarak Al-Kabir Hospital, Kuwait
1997 -98 Lecturer (CoE), Dept. of Internal Med., Institute of Trop. Med., Nagasaki University, Japan
1998 -01 Research fellow, Dept. of Internal Med., Institute of Trop. Med., Nagasaki University, Japan
2001 -04 Visiting Associate Professor, Dept. of Mole, Bio. and Genetics, Bilkent University, Turkey
2004 -06 Lecturer, Division of Molecular Epidemiology, Department of Molecular Microbiology and Immunology, Nagasaki University School of Medicine, Nagasaki, Japan
2006 -16 Associate Professor, Department of Microbiology, Faculty of Medicine (Research Promotion Institute), Oita University, Japan
2016 - Professor, Department of Pathobiology and Medical Diagnostics, Faculty of Medicine and Health Sciences, Universiti Malaysia Sabah, Kota Kinabalu, Sabah, Malaysia
2017 - Director, Borneo Medical and Health Research Centre, Faculty of Medicine and Health Sciences, Universiti Malaysia Sabah, Kota Kinabalu, Sabah, Malaysia

Other Experience and Professional Membership

2014 - Member Editorial Board, Tropical Medicine and Health (TMH), published by the Japanese Society of Tropical Medicine
2018 - Member Editorial Board, Borneo Journal of Medical Sciences (BJMS), published by Universiti Malaysia Sabah
2016 -17 Member, Research Clinic Series 2016 and 2017 Screening Panel
2016 Member, Human Genome and Clinical Genetics Laboratory Project Monitoring Team 2016
2016 Member, MD Curriculum Review Panel 2016 for MM60130-Transformative year
2015 -16 Fellow, Development and Health Research Unit
2016 -18 Fellow, Research and Publication Cluster
2016 -17 Fellow, Tuberculosis Unit, Faculty of Medicine and Health Sciences

Honors

1992 -93 Recipient of Inoue Fellowship from Inoue Science Foundation, Tokyo, Japan
1994 -95 Recipient of JSPS Fellowship for Foreigners from Japan Society for the Promotion of Science, Japan
1998 - Fellow of Australasian College of Tropical Medicine from Australasian College of Tropical Medicine, Queensland, Australia
2010 - Executive Board Member of Japanese Society of Tropical Medicine from January.
2016 -17 Leadership in Research Award from the Faculty of Medicine and Health Sciences, Universiti Malaysia Sabah
2016 -17 Dean's Special Award from the Faculty of Medicine and Health Sciences, Universiti Malaysia Sabah
2016 -18 Publication Award from the Faculty of Medicine and Health Sciences, Universiti Malaysia Sabah
2018 Gold Medal, Research and Design Completion of Universiti Malaysia Sabah in Research, Health and Medical Sciences.
2018 Outstanding Research Award, Faculty of Medicine and Health Sciences, Universiti Malaysia, Sabah.

C. Contribution to Science

1. Research on the molecular epidemiology of rabies virus in Asian countries. Rabies is the most fatal among all the infectious diseases with 100% mortality rate, however 100% protective if vaccine is used properly Therefore proper epidemiology, strains detection in different animals and variants detection is of utmost importance. Although rabies death toll is highest in Asian countries however studies are scarce from this region. My group studied the molecular epidemiology in Thailand, Bangladesh, Bhutan, Laos and Sri Lanka. We found a wide range of genotypes of rabies viruses are circulating in not only dogs but among cats and a wide range of wild animals. Rabies in bat is well recognized in the Americas however we first time confirmed rabies in an Asian bat. We also detected rabies for the first time in civet. We also showed that the strain is a variant of circulating rabies virus indicating genetic changes are occurring which may jeopardize vaccination.

a. Matsumoto T, Nanayakkara S, Perera D, Ushijima S, Wimalaratne O, Nishizono A, **Ahmed K*** (2017) Terrestrial animal-derived rabies virus in a juvenile Indian flying fox in Sri Lanka. **Jpn. J. Infect. Dis.** 70: 637-695.
b. **Ahmed K*,** Phommachanh P, Vorachith P, Matsumoto T, Lamaningao P, Mori D, Takaki M, Douangngeum B, Khambounheuang B and Nishizono A (2015) Molecular epidemiology of rabies viruses circulating in two rabies endemic provinces of Laos, 2011 – 2012: regional diversity in Southeast Asia. **PLoS Negl. Trop. Dis**.9(3): e0003645.
c. Karunanayake D, Matsumoto T, Wimalaratne O, Nanayakkara S, Perera D, Nishizono A and **Ahmed K*** (2014) Twelve years of rabies surveillance in Sri Lanka, 1999–2010. **PLoS Negl. Trop. Dis.** 8: e3205.
d. Jamil KM, **Ahmed K*,** Hossain M, Matsumoto T, Ali MA, Hossain S, Hossain S, Islam A, Nasiruddin M and Nishizono A (2012) Arctic-like rabies virus, Bangladesh. **Emerg. Infect. Dis.** 18: 2021-2024.

2. Detection of animal-human reassortant of rotaviruses in human infections. Rotavirus gastroenteritis was designated as the first emerging infectious disease. Although there is species specificity regarding the genotype distribution of rotavirus, however, in several instances strains can jump from animals to humans or can form human-animal reassortant virus. These strains are challenge for the current rotavirus vaccination strategy. We have documented several events of human-animal reassortants during our research in several Asian countries.

a. Yahiro T, Takaki M, Chandrasena TGAN, Rajindrajith S, Iha H and **Ahmed K*** (2018) Human-porcine reassortant rotavirus generated by multiple reassortant events in a Sri Lankan child with diarrhea. **Infect. Gen. Evol.** 65: 170-186.
b. **Ahmed K*,** Anh DD and Nakagomi O (2007) Rotavirus G5P[6] in a child with diarrhea, Vietnam. **Emerg. Infect. Dis.**13: 1232-1235.
c. **Ahmed K.** Nakagomi T and Nakagomi O (2007) Molecular identification of a novel G1 VP7 gene carried by a human rotavirus with a super-short RNA pattern. **Virus Genes.** 35: 141-145.
d. Uchida R, Pandey BD, Sherchand JB, **Ahmed K,** Yokoo M, Nakagomi T, Cuevas LE, Cunliffe NA, Hart CA and Nakagomi O (2006) Molecular epidemiology of rotavirus diarrhea among children and adults in Nepal: detection of G12 strains with P[6] or P[8] and a G11P[25] strain. **J. Clin. Microbiol.** 44: 3499-3505.

3. Improved diagnostic kits for zoonotic infections. Diagnosis of diseases is hampered by unavailability of user friendly, economical, rapid and robust diagnostic kits in the remote areas of Asia and Africa where the zoonotic diseases are more. Every year about 55,000 people die of rabies however it is known that many cases go undiagnosed because of the lack of diagnostic facilities in many areas. My group developed immunochromatography kit for diagnosis of rabies which is easy to use, robust and with high sensitivity and specificity. In many developing countries host response after vaccination cannot be evaluated due to the

unavailability of cell culture facilities. We also developed an immunochromatography based kit to detect the level of neutralizing antibody after rabies vaccination to determine whether the immune response is protective.

a. Nishizono A, Yamada K, Khawplod P, Shiota S, Perera D, Matsumoto T, Wimalaratne O, Mitui MT, **Ahmed K** (2012) Evaluation of an improved rapid neutralizing antibody detection test (RAPINA) for qualitative and semiquantitative detection of rabies neutralizing antibody in humans and dogs. **Vaccine.** 30: 3891-3896.
b. **Ahmed K*,** Wimalaratne O, Dahal N, Khawplod P, Nanayakkara S, Rinzin K, Perera D, Karunanayake D, Matsumoto T and Nishizono A (2012) Evaluation of a monoclonal antibody-based rapid immunochromatographic test for the direct detection of rabies virus in the brain of humans and animals. **Am. J. Trop. Med. Hyg.** 86: 736-740.
c. Shiota S, Mannen K, Matsumoto T, Yamada K, Yasui T, Takayama K, Kobayashi Y, Khawplod P, Gotoh K, **Ahmed K,** Iha H and Nishizono A (2009) Development and evaluation of a rapid neutralizing antibody test for rabies. **J. Virol. Methods.** 161: 58-62.

4. Detection of novel virus. A large number of viruses in animals and humans have not yet been discovered. However, these viruses in animals have the potential to spill over to humans and cause infections. There are several infectious diseases in humans where the etiology is unknown. We discovered one novel virus in bat which has the potential to spill over to humans. We also identified novel viruses causing infections in humans.

a. Matsumoto T, Sato M, Nishizono A and **Ahmed K*** (2019) A novel bat-associated circovirus identified in northern Hokkaido, Japan. **Arch. Virol.** Doi:10.1007/s00705-019-04286-x.
b. Phan TG, Mori D, Deng X, Rajindrajith S, Ranawaka U, Ng TFF, Bucardo-Rivera F, Orlandi P, **Ahmed K,** Delwart E (2015) Small circular single stranded DNA viral genomes in unexplained cases of human encephalitis, diarrhea, and in untreated sewerage. **Virol.** 482: 98-104.
c. Yahiro T, Wangchuk S, Tshering K, Bandhari P, Zangmo S, Dorji T, Tshering K, Matsumoto T, Nishizono A, Soderlund-Venermo M and **Ahmed K*** (2014) Novel human bufavirus genotype 3 in children with severe diarrhea, Bhutan. **Emerg. Infect. Dis.** 20: 1037-1039.
d. Mori D, Ranawaka U, Yamada K, Rajindrajith S, Miya K, Perera HKK, Matsumoto T, Dassanayake M, Mitui MT, Mori H, Nishizono A, Söderlund-Venermo M, **Ahmed K*** (2013) Human bocavirus in patients with encephalitis, Sri Lanka, 2009–2010. **Emerg. Infect. Dis.** 19: 1859-1862.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

FRGS0457-2017 Ahmed (PI) 08/2017 – 08/2020
Fundamental Research Grant from Malaysian Ministry of Higher Education
A study on the evolution of novel rotavirus with virulency traits and high transmissibility circulating among the children with diarrhea in Sabah.
Role: PI

TRGS009-2016 Zainal (PI) 12/2016 – 11/2019
Transdisciplinary Research Grant from Malaysian Ministry of Higher Education
Whole genome sequence analyses to find out the relationship of *Mycobacterium tuberculosis* strains circulating in Sabah to understand the spread of tuberculosis.
Role: Co-PI

TRGS008-2016 Zainal (PI) 12/2016 – 11/2019
Transdisciplinary Research Grant from Malaysian Ministry of Higher Education
Evaluating molecular diagnosis of Mycobacterium tuberculosis for formulating policy of tuberculosis diagnosis in Sabah.
Role: Co-PI

OMB No. 0925-0001 and 0925-0002 (Rev. 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

NAME: Yeo, Tsin Wen

eRA COMMONS USER NAME (credential, e.g., agency login): (b) (6)

POSITION TITLE: Associate Professor, Infectious Diseases Physician

EDUCATION/TRAINING:

INSTITUTION AND LOCATION	DEGREE	Completion Date	FIELD OF STUDY
National University of Singapore	MBBS	05/1993	Bachelor of Medicine and Surgery
University of Hawaii Residency Program	ABIM Certificate	05/2001	Adult Internal Medicine
University of Utah	ABIM Certificate	05/2004	Infectious Diseases
Charles Darwin University	Ph.D.	11/2008	Malaria and Infectious Diseases

A. Personal Statement:

I am an infectious diseases clinician-scientist based in Singapore and my research is focused on diagnosis, epidemiology, pathogenesis and clinical management of tropical and emerging infectious diseases My research has been conducted in the field in low and middle income countries in South East Asia including Indonesia, Myanmar, Malaysian Borneo and Bangladesh as well as in Tanzania, Africa. In Indonesia, Bangladesh and Tanzania, my research has been conducted on clinical management and vascular pathogenesis of malaria including drug-resistant parasites in district hospitals and outpatient clinics. These studies were done in collaboration with the Indonesian Ministry of Health, Oxford University and Duke University. In Myanmar, the research has been conducted with the National Tuberculosis Reference Laboratory on the molecular epidemiology, transmission, diagnosis, and clinical therapeutics of multi-drug resistant tuberculosis in Yangon. In Malaysian Borneo, I have collaborated with the Malaysian Ministry of Health and the London School of Hygiene and Tropical Medicine on a novel emerging zoonotic malaria, *Plasmodium knowlesi*, which is increasing in incidence and is now the most common cause of malaria in Malaysia due to changes in land use. These studies have included multi-disciplinary studies involving entomologists, social scientists, geospatial experts, parasitologists and economists. Results from several of these studies have been used in the development of World Health Organization guidelines for malaria. In Malaysian Borneo, I have also collaborated on multiple clinical studies on central nervous system infections (including encephalitis) in both adults and children, as well as studies to delineate the etiologies of acute undifferentiated febrile illness in adults.

In Singapore, I am currently a clinician scientist, practicing adult infectious disease physician and designated lead researcher for emerging viral and infectious disease at the National Centre for Infectious Diseases, the designated facility for management of outbreaks. I have been involved in the national response and research related to the Zika outbreak in Singapore in 2016 and well as the travel related case of Monkeypox in 2019. I currently also have ongoing research projects looking at the pathogenesis and clinical management of dengue in Singapore and Malaysia. I am also the deputy director of the research training office of the National Centre for Infectious Diseases, whose role is to co-ordinate pandemic research in Singapore.

B. Positions and Honors

Positions and Employment

1993 -98 Medical Officer, Ministry of Health, Singapore
1998 -01 Internship and Residency in University of Hawaii Internal Medicine Residency Program
2001 -04 Fellowship in Infectious Disease at the University of Utah Medical Center
2004 -08 PhD student at Menzies School of Health Research/ Charles Darwin University from (Supervisor Professor Nicholas Anstey)
2008 - Senior Research Fellow at Menzies School of Health Research, Australia
2010 -14 Infectious Diseases Physician, Royal Darwin Hospital, Australia,
2014 - Associate Professor, Lee Kong Chian School of Medicine, Singapore
2014 - Infectious Disease Physician, National Centre for Infectious Diseases, Singapore

Other Experience and Professional Membership

Member, Infectious Diseases Society of America
Member, American Society of Tropical Medicine and Hygiene
Member, Singapore Infectious Society
Member, Australian Society of Infectious Diseases
Research Theme Leader, Emerging Viral and Infectious Disease Research, National Centre for Infectious Diseases, Singapore
Deputy Director of Research Training Office, National Centre for Infectious Diseases, Singapore
Member, Singapore Ministry of Health Infectious Disease Research Taskforce

Awards and Honors

2001 Award for Best Resident, University of Hawaii Internal Medicine Residency Program
2006 Young Investigator Travel Award from the American Society of Tropical Medicine and Hygiene
2011 Northern Territory Research and Innovation Awards-Chief Ministers Award, Australia
2016 Clinician Scientist Award, Ministry of Health, Singapore

C. Contributions to Science

1. Research on the epidemiology, risk factors, clinical management of the emerging zoonotic malaria, *Plasmodium knowlesi*. In collaboration with Malaysian investigators, we have detailed the increasing incidence of human knowlesi malaria in Malaysian Borneo with currently over 3000 cases annually, despite the near elimination of the human malarias such as *P. falciparum* and *P. vivax*. Collaborating with investigators, I have also been detailing the rise of this parasite in other areas of South East Asia including Sumatra, Indonesia. In an inter-disciplinary study with other scientists, we have also detailed that change in land use and local ecology leading to a change in simian and vector behavior is a main driver of the increasing incidence. Clinical studies including randomized controlled trials have also led to rigorous data for evidence based clinical management of complicated and uncomplicated knowlesi malaria. The results from these studies have also been used in World Health Organization guidelines on the management of malaria.

a. Barber BE, William T, Grigg MJ, Menon J, Auburn S, Marfurt J, Anstey NM, **Yeo TW** (2013). A prospective comparative study of knowlesi, falciparum and vivax malaria in Sabah, Malaysia: high proportion of severe disease from Plasmodium knowlesi and P. vivax but no mortality with early referral and artesunate therapy. **Clinical Infectious Diseases** 56: 383-97.
b. William T, Menon J, Rajahram G, Chan L, Ma G, Donaldson S, Khoo S, Frederick C, Jelip J, Anstey NM, **Yeo TW** (2011). Severe Plasmodium knowlesi malaria in a tertiary care hospital, Sabah, Malaysia. **Emerging Infectious Diseases** 17; 1248-55.
c. Grigg MJ, William T, Menon J, Dhanaraj P, Barber BE, Wilkes CS, von Seidlein L, Rajahram GS, Pasay C, McCarthy JS, Price RN, Anstey NM, **Yeo TW** (2016). Artesunate-mefloqine vs chloroquine for

treatment of uncomplicated Plasmodium knowlesi malaria in Malaysia (ACT-KNOW): an open-label randomized controlled trial. **Lancet Infectious Disease** 16:180-8.

2. Delineating the Role of the Host Vascular Endothelium on the Pathogenesis of Malaria and Dengue.
I have done clinical and translational research to further characterize the role of the host vascular endothelium on the pathogenesis of severe disease in falciparum, vivax and knowlesi malaria. This has led to several novel findings which have led to translational studies of adjunctive agents to attenuate vascular damage and dysfunction in critical infections such as malaria and dengue. These findings have recently also been shown by other investigators to be relevant in other viral hemorrhagic pathogens such as Ebola.

a. **Yeo TW**, Lampah DA, Gitawati R, Tjitra E, Kenangalem E, McNeil Y, Darcy C, Lopansri B, Granger DL, Weinberg JB, Price RN, Duffull SB, Celermajer DS, Anstey NM (2007). Impaired nitric oxide bioavailability and L-arginine reversible endothelial dysfunction in adults with falciparum malaria. **Journal of Experimental Medicine** 204:2693-2704.
b. **Yeo TW**, Weinberg JB, Lampah DA, Kenangalem E, Bush P, Chen Y, Price RN, Young S, Zhang HY, Millington D, Granger DL, Anstey NM (2019). Glycocalyx Breakdown is Associated with Severe Disease and Fatal Outcome in Plasmodium falciparum Malaria. **Clin Infect Dis**
c. Tang TH, Alonso S, Ng LF, Thein TL, Pang VJ, Leo YS, Lye DC, **Yeo TW** (2017). Increased Serum Hyaluronic Acid and Heparan Sulfate in Dengue Fever: Association with Plasma Leakage and Disease Severity. **Scientific Reports** 10;7:46191.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

National Medical Research Council, Singapore 2016-2020
Clinician-Scientist Award
The Role of the Endothelial Glycocalyx, Mast Cells and Vascular Nitric Oxide in the Pathogenesis of Dengue.

National Research Foundation 2018-2022
Singapore MIT Alliance for Research and Technology
Antimicrobial Resistance Interdisciplinary Research Group
This is a translational research program with 17 named investigators aimed at addressing the growing threat of resistance to antimicrobial drugs.

Ministry of Education, Singapore
Tier 1 Grant,
Co-Investigator on Tier 1 grant with Prof Peter Preiser and Assoc Prof Zbynek Bozdech from School of Biological Sciences, NTU. Molecular mechanisms driving the adaptation of Plasmodium knowlesi to humans

National Health Medical Research Council of Australia Yeo (CI-B) 2016-2019
A multi-center double-blind RCT on community-acquired pneumonia in Indigenous children and a developing country: Improving clinical outcomes and identifying systemic biomarkers

NIH RO1AI116472-01 William (PI) 2015-2019
Incidence, Epidemiology and Clinical Features of *Plasmodium knowlesi* malaria in Sabah, East Malaysia
Role: Co-I

Completed Research Support (last 3 years only)

Ministry of Health, Singapore Infectious Diseases Initiative
Bridging Grant
The Viral Determinants of Acute Encephalitis in Children in Sabah, Malaysia

National Health Medical Research Council of Australia Yeo (CI-B) 2016-2018
Targeting microvascular dysfunction in severe malaria

NIH 5RO1AI041764-12 Weinberg (PI) 2016-2018
Arginine, Nitric Oxide and Severe Malaria
Role: Clinical Investigator

NIH 1RO1HL130763-01 Yeo (Co-PI) 2016-2018
Nitric Oxide and Microvascular Dysfunction in Severe Malaria

OMB No 0925-0001 and 0925-0002 (Rev 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Hickey, Andrew Christopher

eRA COMMONS USER NAME (credential, e.g., agency login):

POSITION TITLE: USPHS O-4, Research Science Officer

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Colorado State University; Fort Collins, C	B.S.	05/2001	Environmental Health and Political Science
Emory University; Atlanta, GA	M.P.H.	05/2003	Epidemiology
Uniformed Services University of the Health Sciences; Bethesda, MD	Ph.D.	05/2010	Emerging Infectious Diseases (Virology)
Boston University/National Emerging Infectious Diseases Laboratory; Boston, MA	Postdoctoral	04/2013	Emerging Infectious Diseases (Virology)

A. Personal Statement

The HIV/STD Research Program (HSRP) is a joint enterprise of the US CDC and Thailand Ministry of Public Health. HSRP investigates clinical and behavioral interventions to reduce HIV and STI transmission among men who have sex with men (MSM) and transgender women (TGW) at high risk of acquisition. HSRP's Laboratory section provides both clinical laboratory and microbiology capacity for clinical trials/investigations as well as original investigations focused on HIV/STI prevention. I started my current role in Bangkok, Thailand in May 2016, where I oversee laboratory operations, provide scientific oversight/guidance, mentor staff, support publication/presentation of results, and coordinate operations/analysis within HSRP and our collaborators. I have led HSRP laboratory activities for all network studies for the past three years, including MTN-026 and HPTN-083. Prior to joining HSRP, I developed and managed multi-site and international research studies leading to publication. I have more than 10 years of laboratory research experience in molecular techniques, microbiology, virology, and *in vivo* studies. Much of my research focused on the development and characterization of clinical interventions/medical countermeasures for emerging viral diseases, including *in* vivo efficacy testing. I provided scientific mentorship laboratory personnel and oversight for research and public health laboratory programs during the response to infectious disease, including the introduction of a novel diagnostic for clinical practice. I contributed (first or co-authorship) to published 17 research articles (additional publications in preparation) and more than 16 professional presentations. I have a strong interest in translational research of clinical interventions for infectious diseases, particularly viral diseases. I have the motivation, experience, and training to successfully execute the laboratory studies as well as contribute to the scientific development of the proposed project.

B. Positions and Honors

Positions and Employment

2006 -09 PhD Candidate, Henry M. Jackson Foundation for the Advancement of Military Medicine/Uniformed Services University of the Health Sciences, Bethesda, MD

2009 -13 Postdoctoral Fellow, Boston University School of Medicine/National Emerging Infectious Diseases Laboratory, Boston, MA

2013 -16 Biosurveillance Analyst, National Biosurveillance Integration Center, DHS, Washington, DC

2016 - Chief, HIV/STD Laboratory Research Section, HIV/STD Research Program, Thailand MOPH –US CDC Collaboration (TUC) Bangkok, Thailand; 2018-present: Lead Silom Community Clinic (non-network component) CRS

Other Experience and Professional Memberships

2006 - American Association for the Advancement of Science (AAAS)

2006 - American Society for Microbiology (ASM)

2006 - American Society of Virology (ASV)

2013 -16 Viral Hemorrhagic Fevers Integrated Program Team, Public Health Emergency Medical Countermeasures Enterprise, Assistant Secretary for Preparedness and Response, HHS

2014, 15 International Society for Disease Surveillance Annual Conference

2014 -16 Emerging Infectious Diseases Workgroup, Public Health Emergency Medical Countermeasures Enterprise, Assistant Secretary for Preparedness and Response, HHS

2015 Novel Medical Countermeasures Development Targeting Filovirus Pathogenesis and Resistance Study Section, Defense Threat Reduction Agency

2015 -16 Smallpox Integrated Program Team, Public Health Emergency Medical Countermeasures Enterprise, Assistant Secretary for Preparedness and Response, HHS

Honors

2003 Achievement Medal for achieving Immigration Health Service program objectives, USPHS

2005 Unit Commendation Medal for infectious disease surveillance and case referrals, USPHS

2014 Citation for improving NBIC biosurveillance reporting, USPHS

2014 Unit Commendation Medal for USPHS Ensemble, USPHS

2014 Commendation Medal for national and international subject matter analysis support, USPHS

2015 Commendation Medal for West Africa Ebola response, USPHS

2016 Humanitarian Assistance Award (Monrovia Medical Unit), Assoc. of Military Surgeons of the US

2017 National Center for Immunization and Respiratory Diseases, CDC, Certificate of Excellence

2017 Certificate of Appreciation - EGASP and Support to CDC Thailand, U.S. Department of State

2018 Certificate of Appreciation - HSRP laboratory and global leadership in HIV prevention research, U.S. Department of State, U.S. Embassy Bangkok

2018 Excellence in Laboratory Quality, U.S. Department of State, U.S. Embassy Bangkok

2019 Excellence in Laboratory Quality, Division of HIV/AIDS Prevention, U.S. Centers for Disease Control and Prevention

2019 Best laboratory performance, 2018 – HPTN-083, HIV Prevention Trials Network

C. Contributions to Science

1. **The development of non-human primate (NHP) models for emerging viral infections to study acute infection and evaluate experimental medical countermeasures.** This research path began with Hendra and Nipah viruses; as the NHP model was required to meet the criteria established under the FDA two-animal rule for medical countermeasures to highly-pathogenic viruses. I developed and performed the molecular studies to characterize Nipah virus pathogenesis in NHPs, the first NHP model for a Henipavirus, as well as molecular assays used to develop the NHP model of Hendra virus infection. I managed and

performed a long-term study of the humoral responses to flaviviruses. This was the first NHP study examining antibody persistence over an extended period as well as only report to directly compare the acute infection and humoral responses to all four Dengue virus serotypes. I directed and performed an *in vivo* efficacy study of a novel EV-71 virus-like particle vaccine developed by our collaborators. These projects contributed novel tools for characterizing acute infection, further characterized host responses to these infectious agents, and established reproducible models for important viral illnesses.

a. Lim PY*, **Hickey AC*** (*authors contributed equally), Jamiluddin MF, Hamid S, Kramer J, Santos R, Bossart KN, Cardosa MJ (2015). Immunogenicity and performance of an enterovirus 71 virus-like-particle vaccine in nonhuman primates. **Vaccine** 33(44):6017-24.
b. **Hickey AC**, Koster JA, Thalmann CM, Hardcastle K, Tio PH, Cardosa MJ, Bossart KN (2013). Serotype-specific host responses in rhesus macaques after primary dengue challenge. **Am J Trop Med Hyg**. 89(6):1043-57.
c. Geisbert TW, Daddario-DiCaprio KM, **Hickey AC**, Smith MA, Chan YP, Wang LF, Mattapallil JJ, Geisbert JB, Bossart KN, Broder CC (2010). Development of an acute and highly pathogenic nonhuman primate model of Nipah virus infection. **PLoS One** 5(5):e10690.
d. Rockx B, Bossart KN, Feldmann F, Geisbert JB, **Hickey AC**, Brining D, Callison J, Safronetz D, Marzi A, Kercher L, Long D, Broder CC, Feldmann H, Geisbert TW (2010). A novel model of lethal Hendra virus infection in African green monkeys and the effectiveness of ribavirin treatment. **J Virol.** 84(19):9831-9.

2. **The development of an experimental sub-unit vaccine and antibody therapeutic for Hendra and Nipah viruses, two highly-lethal emerging viruses.** The sub-unit G vaccine and monclonal antibody therapy are the the most well-characterized experimental countermeasure and furthest advanced in the development process. The sub-unit Henipavirus G vaccine has been deployed as a standard equine vaccine in Australia and the monoclonal antibody has now been administered, under FDA's compassionate use provision, to more than 11 individuals exposed to Hendra virus.
   a. Bossart KN, Rockx B, Feldmann F, Brining D, Scott D, LaCasse R, Geisbert JB, Feng YR, Chan YP, **Hickey AC**, Broder CC, Feldmann H, Geisbert TW (2012). A Hendra virus G glycoprotein subunit vaccine protects African green monkeys from Nipah virus challenge. **Sci Transl Med.** 4(146):146ra07.
   b. Bossart KN, Geisbert TW, Feldmann H, Zhu Z, Feldmann F, Geisbert JB, Yan L, Feng YR, Brining D, Scott D, Wang Y, Dimitrov AS, Callison J, Chan YP, **Hickey AC**, Dimitrov DS, Broder CC, Rockx B (2011). A neutralizing human monoclonal antibody protects african green monkeys from hendra virus challenge. **Sci Transl Med.** 3(105):105ra3.
   c. Bossart KN, Zhu Z, Middleton D, Klippel J, Crameri G, Bingham J, McEachern JA, Green D, Hancock TJ, Chan YP, **Hickey AC**, Dimitrov DS, Wang LF, Broder CC (2009). A neutralizing human monoclonal antibody protects against lethal disease in a new ferret model of acute nipah virus infection. **PLoS Pathog.** 5(10):e1000642.

3. **I developed the largest monoclonal antibody panel specific for Henipavirus Attachment (G) Glycoproteins and used the panel to identify protective epitopes as well as structural features associated with the viral fusion mechanism.** These monoclonal antibodies were developed using the same soluble Henipavirus G determinants included in experimental Henipavirus subunit vaccine(s) and were used to demonstrate a conserved antigenic structure between the soluble and native G glycoprotein. These studies identified protective epitopes not previously documented in the literature (publication in preparation) and the first to describe receptor-independent protective epitopes of Henipavirus G. I devised and performed molecular studies to show extensive structural changes in the G glycoprotein following receptor binding and found some of these changes present in unbound soluble G (additional publications in preparation). This discovery suggests soluble G assumes an intermediate receptor-bound structural configuration and could explain why crystal structures of paramyxovirus G glycoproteins have not exhibited

significant changes when co-cyrstalized with receptor. Refining the paramyxovirus fusion model can identify opportunities for developing clinical therapies to Henipaviruses and structures/functions common to other viruses that use a Type I viral fusion mechanism, such as HIV and Ebola virus.

a. Borisevich V, Lee B, **Hickey AC**, DeBuysscher B, Broder CC, Feldmann H, Rockx B (2016). Escape From Monoclonal Antibody Neutralization Affects Henipavirus Fitness In Vitro and In Vivo. ***J Infect Dis.*** 213(3):448-55.
b. **Hickey AC**, Broder CC (2009). The Mechanism of Henipavirus Fusion: Examining the Relationships between the Attachment and Fusion Glycoproteins. ***Virologica Sinica*** 24(2):110-20.
c. Bishop KA, **Hickey AC**, Khetawat D, Patch JR, Bossart KN, Zhu Z, Wang LF, Dimitrov DS, Broder CC (2008). Residues in the stalk domain of the Hendra virus G glycoprotein modulate conformational changes associated with receptor binding. ***J Virol.*** 82(22):11398-409.
d. Bishop KA, Stantchev TS, **Hickey AC**, Khetawat D, Bossart KN, Krasnoperov V, Gill P, Feng YR, Wang L, Eaton BT, Wang LF, Broder CC (2007). Identification of Hendra virus G glycoprotein residues that are critical for receptor binding. ***J Virol.*** 81(11):5893-901.

4. I developed multi-site collaborative studies to identify emerging viruses and further define the epidemiology. I worked with a team of epidemiologists and laboratorians to use molecular techniques, including next generation sequencing, to uncover the epidemiologic relationships of a cluster of Ebola infections near Monrovia, Liberia. These data were used to improve the public health intervention and control further spread of the virus. I developed a reliable and adaptable assay for identifying Henipavirus-specific antibody responses and deployed the assay for field studies, uncovering serologic evidence of sporadic exposure to Nipah/Nipah-like virus among bats in China and school children in rural Thailand (publication in preparation). Notably, this was the northern most detection of the virus and the first identification of Henipaviruses in insectivorious bats. I contributed to serology screening to determine the incidence and rate of re-infection with human Metapneumovirus, a common childhood respiratory infection. While developing a Dengue research project, I discovered abnormal properties of a sylvatic Dengue virus isolate isolated from a Malaysian individual with severe disease. Studies of this isolate in NHPs elicited illnesses among animals previously challenged with another Dengue virus serotype and NHP antibody responses suggested the isolate was antigenically divergent to the other Dengue serotypes (publication in preparation). The unique attributes of this Dengue virus isolate have been confirmed by additional groups. These studies have contributed a better understanding of the viral ecology and occurrence of important paramyxo-, flavi-, and filoviruses.

a. Dokubo EK, Wendland A, Mate SE, Ladner JT, Hamblion EL, Raftery P, Blackley DJ, Laney AS, Mahmoud N, Wayne-Davies G, Hensley L, Stavale E, Fakoli L, Gregory C, Chen TH, Koryon A, Roth-Allen D, Mann J, **Hickey AC**, Saindon J, Badini M, Baller A, Clement P, Bolay F, Wapoe Y, Wiley MR, Logue J, Dighero-Kemp B, Higgs E, Gasasira A, Williams DE, Dahn B, Kateh F, Nyenswah T, Palacios G, Fallah MP (2018). Persistence of Ebola virus after the end of widespread transmission in Liberia: an outbreak report. ***Lancet Infectious Diseases*** 18(9):1015-1024.
b. Li Y, Wang J, **Hickey AC**, Zhang Y, Li Y, Wu Y, Zhang H, Yuan J, Han Z, McEachern J, Broder CC, Wang LF, Shi Z (2008). Antibodies to Nipah or Nipah-like viruses in bats, China. ***Emerg Infect Dis.*** 14(12):1974-6.
c. Pavlin JA, **Hickey AC**, Ulbrandt N, Chan YP, Endy TP, Boukhvalova MS, Chunsuttiwat S, Nisalak A, Libraty DH, Green S, Rothman AL, Ennis FA, Jarman R, Gibbons RV, Broder CC (2008). Human metapneumovirus reinfection among children in Thailand determined by ELISA using purified soluble fusion protein. ***J Infect Dis.*** 198(6):836-42.

URL to a list of published work:
https://www.ncbi.nlm.nih.gov/pubmed/?term=%22Hickey+AC%22

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

NIH RO1 Kelley (PI) 2019-2023
Project title: Understanding the rectal mucosal effects of cross-sex hormone therapy among U.S. and Thai transgender women
Role: Site Investigator / CDC Principle Investigator

NIH RO1 Beyrer (PI) 2015-2020
Project title: Effectiveness and Cost Effectiveness of a Combination HIV Preventive Intervention with and without daily oral Truvada® pre-exposure prophylaxis (PrEP) with adherence support among young men who have sex with men (YMSM) and transgender women (TGW) aged 18-26 in Bangkok and Pattaya, Thailand
Role: Site Investigator / CDC Principle Investigator

HPTN-083 network trial 2016-
Project title: A Phase 2b/3 Double Blind Safety and Efficacy Study of Injectable Cabotegravir Compared to Daily Oral Tenofovir Disoproxil Fumarate/Emtricitabine (TDF/FTC), for Pre-Exposure Prophylaxis in HIV-Uninfected Cisgender Men and Transgender Women who have Sex with Men
Role: Laboratory lead

Completed Research Support (last 3 years only)

MTN-026 network trial 2016-2018
Project title: A Randomized, Double Blind, Placebo-Controlled, Phase 1 Safety and Pharmacokinetic Study of Dapivirine Gel (0.05%) Administered Rectally to HIV-1 Seronegative Adults
Role: CRS Laboratory Lead

CDC - Advanced Molecular Diagnostics 2016-2017
Project title: *Development and evaluation of a rapid point-of-care NAT for accurate diagnosis of HIV-1 infection*
Role: Site PI

OMB No. 0925-0001 and 0925-0002 (Rev. 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Field, Hume Ernest

eRA COMMONS USER NAME (credential, e.g., agency login): (b) (6)

POSITION TITLE: Honorary Professor, School of Veterinary Science, University of Queensland, Australia. Principal Scientist and Director, Jeppesen Field Consulting, Australia.

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University of Queensland, Australia	BVSc	12/1976	Veterinary Science
Griffith University, Australia	MSc	02/1981	Environmental Science
Australian College of Veterinary Scientists	Member by examination	07/2004	Epidemiology
University of Queensland, Australia	Ph.D.	12/2005	Emerging Disease Ecology (Hendra virus)

A. Personal Statement

My strong research background with a suite of emerging zoonoses associated with wildlife will positively support the success of the proposed project. My hybrid professional skills enable me to take a cross-disciplinary approach to the surveillance of wildlife populations, the identification of the origins of novel agents, and the elaboration of infection dynamics in reservoir and spillover host populations. I am recognized as an authority on EIDs associated with bats, having worked with the US Centers for Disease Control, the World Health Organization, and the UN Food and Agriculture Organization to find the origins of Nipah virus in Malaysia, SARS in China, and Reston ebolavirus in the Philippines. More recently, as Principal Research Scientist at the Queensland Centre for Emerging Infections Diseases, I was co-PI on government and university-funded grants to elaborate Hendra virus infection and immune dynamics in the reservoir population, enabling more effective spillover risk management. The current proposal complements and substantially expands this approach in proposing to novel and powerful tools to understand how host immune dynamics and heterogeneity in immune response affect the timing, location, and severity of disease outbreaks in wildlife, and risk of spillover from wildlife to human populations. As a company Director, I also have strong management skills that translate to effective team, project, budget and report management. My affiliations with the University of Queensland and the University of Malaysia, Sabah support EID research capacity building. I have a strong publication record, with over 120 peer-reviewed papers and numerous book chapters.

1. Chua K, Bellini W, Rota P, Harcourt B, Tamin A, Lam S, Ksiazek T, Rollin P, Zaki S, Shieh. W-J, Goldsmith C, Gubler D, Roehrig J, Eaton B, Gould A, Olson J, **Field HE**, Daniels P, Ling A, Peters C, Anderson L, Mahy B (2000). Nipah virus: A recently emergent deadly paramyxovirus. **Science** 288:1432-1435

2. Li W, Shi Z, Yu M, Ren W, Smith C, Epstein JH, Wang H, Crameri G, Hu Z, Zhang H, Zhang J, McEachern J, **Field HE**, Daszak P, Eaton BT, Zhang S & Wang L-F (2005). Bats are natural reservoirs of SARS-like coronaviruses. **Science** 310: 676-679.

3. **Field HE,** MacKenzie J, Daszak P (2007). Henipaviruses: emerging paramyxoviruses associated with fruit bats. Wildlife and Zoonotic Diseases: The Biology, Circumstances, and Consequences of Cross-Species Transmission. Eds. MacKenzie, J.S. et al. **Curr. Topics Microbiol. Immunol.** 315: 133-159.
4. Jayme SI, **Field HE**, de Jong C, Olival KJ, Marsh G et al. (2015). Molecular evidence of Ebola Reston virus infection in Philippine bats. **Virol. J.** 12:107.

B. Positions and Honors

Positions and Employment

2000 -09 Principal Epidemiologist (Emerging Infectious Diseases), Queensland Department of Agriculture. Brisbane, Australia
2009 -10 Visiting Professor for Zoonoses, University of Malaysia, Sarawak
2010 -14 Principal Research Scientist, Queensland Centre for Emerging Infections Diseases. Brisbane, Australia
2014 - Director and Principal Scientist, Jeppesen Field Consulting. Brisbane, Australia
2016 - Honorary Professor, University of Queensland. Brisbane Australia

Other Experience and Professional Memberships

2003 WHO Adviser on SARS (China)
2003 FAO Consultant on SARS (China)
2010 OIE/FAO/WHO Emerging Diseases at the human-animal interface (Italy)
2010 FAO Ebola Reston Origin Project (Philippines)
2010 OIE Rabies Code Working Group (Italy)
2013 Expert Working Group on Emerging Rabies (Taiwan)
2015 -18 Deputy Chair, Board of Wildlife Health Australia (Australia)
2015 - Research Advisor, Development and Health Research Unit, University of Sabah (Malaysia)
2016 -18 Board Member, International Association of Ecosystem Health
2016 -18 Expert Working Group, Hendra virus Risk Management (Australia)

C. Contributions to Science

1. **Hendra virus research.** My role in identifying species of bats (Chiroptera) as the natural reservoir of Hendra virus was a pivotal breakthrough in the subsequent realization of the unique role of this taxa as reservoirs for highly lethal zoonoses. The early work provided a model for the investigation of the origins of wildlife associated EIDS and facilitated effective surveillance strategies; the later work elaborated spatiotemporal patterns and informed more targeted risk mitigation strategies.
   a. Halpin K, Young P, **Field HE**, Mackenzie J. (2000). Isolation of Hendra virus from pteropid bats: a natural reservoir of Hendra virus. **J. Gen. Virol.** 81(8): 1927-32.
   b. **Field HE**, de Jong C, Melville D, Smith C, Smith I, Broos A, Kung YH, McLaughlin A, Zeddeman A (2011). Hendra virus infection dynamics in Australian fruit bats. **PLoS One** 6: e28678.
   c. Edson D, **Field HE**, McMichael L, Vidgen M, Goldspink L et al. (2015). Routes of Hendra Virus Excretion in Naturally-Infected Flying-Foxes: Implications for Viral Transmission and Spillover Risk. **PLoS One** 15:e0140670.
   d. **Field HE**, Jordan D, Edson D, Morris S, Melville D, Parry-Jones K, Broos A, Divljan A, McMichael L, Davis R, Kung N, Kirkland P, Smith C. (2015). Spatiotemporal Aspects of Hendra Virus Infection in Pteropid Bats (Flying-Foxes) in Eastern Australia. **PLoS One** 10: e0144055.
2. **Origins and drivers of Nipah virus.** Beyond identifying the origins of the virus, the Nipah virus research focused on elaborating the ecology of infection in the natural host and drivers for emergence. Our

collaborative and cross-disciplinary approach to the research across human health, livestock health and environmental components has been widely adopted. The work provided a basis for subsequent focus on immunology, phylogenetics, ecological modelling and diagnostic test development.

a. Yob JM, **Field HE**, Rashdj AM, Morrissy C, van der Heide B, Rota P, bin Adzhar A, White J, Daniels P, Jamaluddin A, Ksiazek TJohara MY (2001). Nipah Virus Infection in Bats (Order Chiroptera) in Peninsular Malaysia. **Emerg. Infect. Dis.** 7(3):439-41.

b. Sohayati AR, Hassan L, Sharifah SH, Lazarus K, Zaini CM, Epstein JH, Shamsyul NN, **Field HE**, Arshad SS, Abdul Aziz J, Daszak P, Henipavirus Ecology Research Group (2011). Evidence for Nipah virus recrudescence and serological patterns of captive Pteropus vampyrus. **Epidemiol. Infect.** 139(10):1570-9.

c. Pulliam JRC, Epstein JH, Dushoff J, Rahman SA, Bunning M, HERG, Jamaluddin AA, Hyatt AD, **Field HE**, Dobson AP & Daszak P and the Henipavirus Ecology Research Group (HERG). (2012). Agricultural intensification, priming for persistence, and the emergence of Nipah virus: a lethal bat-borne zoonosis. **J. Roy. Soc. Interface** 9:89-101

3. **Origins and drivers of SARS emergence.** The early epidemiological investigation of SARS cases undertaken by our WHO team showed that the earliest human cases were associated with wet markets, and lead to the identification of civets and other traded species as the source of human infection. However, these species were not the natural reservoirs and as part of an international team, I played a key role in focusing research on bats in which we subsequently found ancestral SARS-like coronaviruses. This finding precipitated global surveillance of bats and lead to the discovery of a suite of coronaviruses in the taxa, and promoted broader pathogen discovery focus on bats.

   a. Xu RH, He JF, Evans MR, Peng GW, **Field HE**, Yu DW, Lee CK, Luo HM, Lin WS, Lin P, Li LH, Liang WJ, Lin JY, Schnur A (2004). Epidemiologic clues to SARS origin in China. **Emerg. Infect. Dis.** 10:1030-1037.

   b. Wang L-F, Shi Z, Zhang S, **Field HE,** Daszak P, Eaton BT (2006). A review of bats and SARS: virus origin and genetic diversity. **Emerg. Infect. Dis.** 12: 1834-1840.

   c. Cui J, Han N, Streicker D, Li G, Tang X, Shi Z, Hu Z, Zhao G, Fontane, A, Yi G, Wang L, Jones G, **Field HE,** Daszak P, Zhang S (2007). Evolutionary relationships between bat coronaviruses and their hosts. **Emerg. Infect. Dis.** 13: 1526-1532.

   d. Wood JLN, Leach M, Waldman L, MacGregor H, Fooks AR, Jones KE, Restif O, Dechmann D, Hayman DTS, Baker KS, Peel AJ, Kamins AO, Fahr J, Ntiamoa-Baidu Y, Suu-Ire R, Breiman RF, Epstein JH, **Field HE**, Cunningham AA (2012). A framework for the study of zoonotic disease emergence and its drivers: spillover of bat pathogens as a case study. **Phil. Trans. Roy. Soc. B.** 367:2881-2892.

D. Additional Information: Research Support and/or Scholastic Performance

Not applicable

OMB No. 0925-0001 and 0925-0002 (Rev 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Zambrana-Torrelio, Carlos

eRA COMMONS USER NAME (credential, e.g., agency login):

POSITION TITLE: Associate Vice President for Conservation and Health

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Universidad Mayor de San Andres - Bolivia	Licenciado	11/2002	Biology
Universidad de Puerto Rico - Rio Piedras	M.S.	12/2010	Ecology and Evolution
Sapienza - Università di Roma	Ph.D.	09/2017	Environmental and Evolutionary Biology

A. Personal Statement

I have over 15 years' experience linking biodiversity conservation, land use planning, environmental change and disease emergence via multi-institutional collaborative consortia, as well as over 10 years of experience managing projects internationally. I made significant contributions to the development of the research on ecosystem health, especially as it relates to biodiversity loss, land use change, disease emergence and their economic implications. I have published peer-reviewed papers in Nature, Nature Comm., Lancet, PNAS, mBio and others. I have advised the Convention on Biological Diversity (CBD), the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services Intergovernmental Panel of Biodiversity and Ecosystem Services (IPBES), the United Nations – System of Environmental-Economic Accounting (UN-SEEA) and I chair the International Union of Conservation Nature (IUCN) Task Force on Human Health and Ecosystems Management. Over the past ten years, I supervised students and technical teams in Argentina, Bolivia, Malaysia, Mexico, Venezuela and the USA. I am is a key member of the Modeling and Analytics Team of the PREDICT Consortium, under the cooperative agreement for USAID's Emerging Pandemic Threats Program. I have designed and implemented the Deep Forest Project that evaluates how increasing land-use development affects biodiversity which in turn changes viral dynamics that could lead to disease emergence. This project has been implemented in Brazil, Malaysia and Uganda. Similarly, Dr. Zambrana-Torrelio is Key Personnel of the USAID Infectious Disease Emergence and Economics of Altered Landscapes (IDEEAL) team that examines how land-use change and economics of disease emergence can be used by local and regional decision makers.

B. Positions and Honors

Positions and Employment

1999 -02 Research Associate, Centro de Analisis Espacial – Bolivia
2002 -03 Researcher, Wildlife Conservation Society
2003 - Research Associate, Bolivian Bat Conservation Program
2006 Consultant, NatureServe
2008 - Research Associate, Institute of Molecular Biology and Biotechnology, Bolivia
2010 -13 Research Scientist, EcoHealth Alliance
2014 -17 Senior Research Scientist, EcoHealth Alliance
2017 - Associate VP for Conservation & Health, EcoHealth Alliance

Other Experience and Professional Membership

2019 - Chair IUCN Task Force Human Health and Ecosystem Management (2019 - 2022)

Honors

2006 Alwyn H. Gentry Fellowship – Missouri Botanical Garden
2007 WWF Russell E. Train Education for Nature Program FellowshiP
2009 Dissertation fellowship. Decanato de Estudios Graduados e Investigacion University of Puerto Rico

C. Contributions to Science

1. **Applications of ecological niche modeling in disease systems.** Ecological niche modeling (ENM) is widely employed in ecology to predict species' potential geographic distributions in relation to their environmental constraints. This method is increasingly employed to prioritize geographic areas for disease surveillance and control under the assumption that the distribution of hosts is directly related to the distribution of pathogens. I applied ENMs to predict the potential impact of future climate change on the distribution of Henipaviruses. We showed that Henipaviruses' hosts could potentially expand to new geographic areas in Africa and Southeast Asia. I further explored the main assumption of ENMs in disease ecology: host distribution corresponds to pathogen distribution. Hosts may occur where parasites are absent, and even when infection occurs, disease may be absent. I developed an ecological framework to model the geography of disease transmission under the an ENM approach. This theoretical framework: (i) addresses the selection of an appropriate modeling approach and highlights the importance of including biologically sound predictor variables; (ii) proposes the concept of a microscale parasitic niche defined by host traits to identify relevant parasite–host associations; and (iii) integrates traditional parasite ENM with the proposed microscale niche to better understand geographic distributions and improve fine-scale predictions of disease transmission risk.

   a. Daszak P, **Zambrana-Torrelio C**, Bogich TL, Fernández M, Epstein JH, Murray KA, Hamilton H (2013). Interdisciplinary approaches to understanding disease emergence: the past, present, and future drivers of Nipah virus emergence. **PNAS** 110:3681–3688.

   b. Johnson EE, Escobar LE, **Zambrana-Torrelio C*** (2019). An Ecological Framework for Modeling the Geography of Disease Transmission. **Trends in Ecology & Evolution** 34:655-668.

2. **Linking biodiversity, human health and ecosystems.** Human health is intimately interconnected with biodiversity and the health of our ecosystems. There are different ways in which biodiversity can provide health and wellbeing to humans, including psychological (e.g. mental health), physiological (e.g. food provision), and traditional and modern medicines. Another important benefit from biodiversity to human health is the capacity to regulate the transmission and prevalence of some infectious diseases. Over the past 5 years I have worked with environmental economists, disease ecologists and biodiversity researchers and developed an optimal land use planning framework that assess the costs and benefits of developing land. This framework allows to determine the optimal land conversion rate when considering the losses of ecosystem services and also the economic damages of disease emergence. I have tested this framework in Sabah, Malaysia and our results showed that the Malaysian government could potentially lose $US 748 million due to excessive land conversion over the next 30 years by not considering the economic damages of malaria.

   a. **Zambrana-Torrelio C**, Lee KD, Hughes T, Murray KA, Loh E, Epstein JH, Schar D, Daszak P (2015). Land use change and economic cost of emerging infectious diseases, Montpellier: International Congress for Conservation Biology.

b. Machalaba C, Smith KM, Awada L, Berry K, Berthe F, Bouley TA, Bruce M, Cortiñas Abrahantes J, El Turabi A, Feferholtz Y, Flynn L, Fournié G, Andre A, Grace D, Jonas O, Kimani T, Le Gall F, Miranda JJ, Peyre M, Pinto J, Ross N, Rüegg SR, Salerno RH, Seifman R, **Zambrana-Torrelio C**, Karesh WB (2017). One Health Economics to confront disease threats. **Trans R Soc Trop Med Hyg**. 111:235–237.

3. **Impacts of land use change on the ecology of emerging infectious diseases.** The majority of emerging infectious diseases since 1940 were caused by zoonotic pathogens. Over the past 5 years I developed and implemented a systematic sampling methodology to address the ecological factors that drive zoonotic disease emergence due to land-use change. Land-use change has been attributed to around 1/5 of all novel disease emergence events and around half of all zoonotic diseases. Land-use changes could modify the risk of cross-species transmission ("spillover") by perturbing the dynamics of pathogens in wildlife hosts and/or by bringing novel host-pathogen pairs (including humans) into unprecedented contact. This project was implemented across a range of biogeographical regions including the Neotropical region (Brazil), Afrotropical (Uganda) and the Oriental region (Malaysian Borneo). Sampling was focused on two high-risk groups: bats and rodents.

   a. Anthony SJ, Islam A, Johnson C, Navarrete-Macias I, Liang E, Jain K, Hitchens PL, Che X, Soloyvov A, Hicks AL, Ojeda-Flores R, **Zambrana-Torrelio C**, Ulrich W, Rostal MK, Petrosov A, Garcia J, Haider N, Wolfe N, Goldstein T, Morse SS, Rahman M, Epstein JH, Mazet JK, Daszak P Lipkin WI (2015). Nonrandom patterns in viral diversity. **Nature Comm** 6:8147.

   b. Anthony SJ, Epstein JH, Murray KA, Navarrete-Macias I, **Zambrana-Torrelio C**, Solovyov A, Ojeda-Flores R, Arrigo NC, Islam A, Ali Khan S, Hosseini P, Bogich TL, Olival KJ, Sanchez-Leon MD, Karesh W, Goldstein T, Luby SP, Morse SS, Mazet JAK, Daszak P, Lipkin WI (2013). A strategy to estimate unknown viral diversity in mammals. **MBio** 4(5): e00598-13.

   c. Hosseini PR, Murray KA, Loh E, **Zambrana-Torrelio C**, Gilardi KVK, Goldstein T, Johnson CK, Mazet JAK, Daszak P (2013). Land-use change and pathogen emergence: Differential implication of factors driving emergence across land-use gradients. Ecological Society of America 98th Annual meeting.

   d. Murray KA, Preston N, Allen T, **Zambrana-Torrelio C**, Hosseini PR, Daszak P (2015). Global biogeography of human infectious diseases. **PNAS** 12:12746-12751.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

USAID Emerging Pandemic Threats Mazet (PI) 10/01/14 – 09/30/19
PREDICT-2
The goal is to conduct surveillance for novel pathogens in wildlife, livestock and people; characterize human risk behavior; analyze EID risk; and design interventions in >20 countries
Role: Senior Personal

Completed Research Support

USAID 1414374 (RDMA, Thailand) Daszak (CoP) 10/01/13 - 03/30/19
Infectious Disease Emergence and Economics of Altered Landscapes (IDEEAL)
Cooperative agreement to analyze how land use change affects economics of disease risk in SE Asia.
Role: Senior Personal

OMB No. 0925-0001 and 0925-0002 (Rev. 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Hemachudha, Pasin

eRA COMMONS USER NAME (credential, e.g., agency login): (b) (6)

POSITION TITLE: Physician

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
King's College London, United Kingdom	BSc	06/2012	Biomedical Science
Barts and The London, London, United Kingdom	MD	06/2017	Medicine
Royal Free Hospital, London, United Kingdom	Residency	08/2018	Internship

A. Personal Statement

I am an early career medical doctor and Thai national, who graduated from medicine and biomedical sciences in 2017 with ongoing interests in neurology infectious disease and immunology. I recently joined Thai Red Cross Emerging Infectious Diseases in 2018 as a research physician and have become involved with emerging infectious disease Since joining have been involved in Zika technical workshop and clinical section editor for Zika operational guideline in Southeast Asian countries, leading to my first lead-authored paper below. I have participated in multi-sectoral collaboration at the animal human ecosystem interface in Thailand, and the infectious disease emergence and economic of altered landscapes and environmental economics workshop led by EcoHealth Alliance. I have been working with the USAID-PREDICT project for the last 6 months to lead analysis of clinical data and linking this to observed virus detections.

I am also a full-time clinician now based at the Queen Savang Vadhana Memorial Hospital in Chonburi, Thailand. If we are funded to develop our EID-SEARCH research program, I am excited to include our hospital as one of our clinical sites under Specific Aim 3 of the research proposal.

B. Positions and Honors

Positions and Employment

2017 - 18 Foundation year doctor, The Royal Free Hospital London, UK
2018 - Thai Red Cross Emerging Infectious Disease Health Sciences, Thailand
2019 - Queen Savang Vadhana Memorial Hospital, The Thai Red Cross Society, Thailand

C. Contributions to Science

1. Publications

a. Hemachudha P, Wacharapluesadee S, Buathong R, Petcharat S, Bunprakob S, Ruchiseesarod C, Roeksomtawin P, Hemchudha T. (2019). Lack of Transmission of Zika Virus Infection to Breastfed Infant. Clinical Medical Insights – Case Reports, 12:UNSP 1179547619835179.

2. Reviewer for Biomedical Journal Case Report.

OMB No. 0925-0001 and 0925-0002 (Rev. 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

NAME: Lin, Ingrid Ting Pao

eRA COMMONS USER NAME:

POSITION TITLE: Clinical Specialist

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	COMPLETION DATE	FIELD OF STUDY
Kursk State Medical University	B.S.	2002	Pre-Medical
Kursk State Medical University	MD	2009	Medicine
Universiti Sains Malaysia	MMED	2018	Internal Medicine

A. Personal Statement

Positions and H I have 8 years of working experience as a medical officer and clinician in Sarawak Hospitals. I am currently the lead Clinical Specialist in the Department of Medicine at Hospital Miri in Sarawak, Malaysia. I was involved in the recruitment of patients for the USAID PREDICT Human Syndromic Surveillance in 2018.

B. Positions and Honors

Positions and Employment

2011 -12 Medical Officer, Hospital Daerah Bau, Kuching, Sarawak
2012- 14 Medical Officer, Internal Medicine, Hospital Raja Perempuan Zainab II, Kota Bharu
2014 -18 Medical Officer, Internal Medicine, Hospital Universiti Sains Malaysia, Kubang Kerian
2018 - Clinical Specialist, Department of Medicine, Hospital Miri, Sarawak

Other Experience and Professional Memberships

2016 Certification, Good Clinical Practice Certification
2016 Certification, Bioethics and Communication Skills
2016 Certification, Basic Statistics and Research Methodology
2017 Certification, Intermediate Statistics and Research Methodology
2019 Reviewer, British Medical Journal Case Reports

Honors

2013 Anugerah Perkhidmatan Cemerlang 2013 from Jabatan Kesihatan Negeri Kelantan
2016 3rd Place, 3rd Malaysian Parkinson's and Movement Disorder Teaching course
2019 2nd Place in 4th Northern Zone Sarawak Research Day 2019 Poster Presentation

C. Contribution to Science

1. **I have presented at many different major conferences and conventions on various communicable and non-communicable diseases across Malaysia.**
    a. "Risk Factors of In-Hospital Mortality of Tuberculosis Patients in Hospital Raja Perempuan Zainab II". (*Oral Poster Presentation*), National TB and Lung Diseases Conference, 2014."
    b. "Acute abdomen, a rare occurrence in MELAS syndrome" (*Oral Poster Presentation*), MyNeuro2017 Conference
    c. "Predictive Factors of First-year Mortality in Newly Diagnosed ESRD patients commencing on Hemodialysis in Kelantan". (*Oral Poster Presentation*) 34th Annual Congress of Malaysian Society of Nephrology 2018.
    d. "A First Reported Case of Successful Chronic Lead Extraction with Lead Extractor-Evolution". (*Oral Poster Presentation*), 11th Asia Pacific Cardiology Update 2018

2. **I am a published author and have contributed to the general medical field through the findings of my research papers.**
    a. **Ting IP**, Halim SA, Adnan A, Jaafar H. (2017). Status epilepticus as the initial presentation of antibody-negative Goodpasture's syndrome. **British Medical Journal**
    b. **Ting IP**, Adnan A, Imran K, Alfatah AW (2018). Predictive Factors of First-Year Mortality in Newly Diagnosed End-Stage Renal Disease Patients Commencing on Hemodialysis in Kelantan, Malaysia. **J Nephrol Forecast**; 1(1).;1004.

3. **I have been an invited speaker at several different hospitals in Malaysia on various medical topics.**
    a. Management of Hypertension, Bilik Mesyuarat Lama, Hospital Bau, 2011
    b Recognizing Revere Dengue, Hospital Miri weekly CME, 2019
    c. Heart Disease in Preganancy and Postpartum, Bilik Mesyuarat Klinik Kesihatan Tudan, 2019
    d. Thyroid Disorder in Pregnancy, Bil k Mesyuarat Klinik Kesihatan Tudan, 2019

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

(b) (4) Lin (PI) 2019-2020

Impact of on-site herpes simplex virus molecular diagnostics on the laboratory diagnosis and case management of suspected viral encephalitis in Central Sarawak using den Bruel's framework of diagnostic test evaluation

Completed Research Support

Lin (PI) 2016-2018

Predictive Factors of First-Year Mortality in Newly Diagnosed End-Stage Renal Disease Patients Commencing on Hemodialysis in Kelantan, Malaysia as Principal investigator

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 1

ORGANIZATIONAL DUNS*: 0770900660000

Budget Type*: ● Project ○ Subaward/Consortium

Enter name of Organization: EcoHealth Alliance

Start Date*: 03-01-2020 **End Date*:** 02-28-2021 **Budget Period:** 1

A. Senior/Key Person

Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 . Dr	Peter		Daszak	Ph.D	PD/PI		[redacted]					(b) (4), (b) (6)
2 . Dr	Kevin		Olival	Ph.D	Co-Investigator							
3 . Dr	Carlos		Zambrana-Torrelio		Co-Investigator							
4 . Dr	Alice		Latinne		Bioinformat cian							
5 . Dr	Kendra		Phelps		Field Scientist							
6 . Dr	Patrick		Dawson		Epidemiologist							
7 . Ms.	Hongying		Li		Epidemiologist							
8 . Dr	Aleksei		Chmura		Senior Program Manager							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name:

Total Senior/Key Person 256,075.51

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Data Scientist	[redacted]					(b) (4), (b) (6)
1	Epidemiologist						
1	Program Manager						
3	**Total Number Other Personnel**					**Total Other Personnel**	**113,489.98**
						Total Salary, Wages and Fringe Benefits (A+B)	**369,565.49**

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 1

ORGANIZATIONAL DUNS*: 0770900660000
Budget Type*: ● Project ○ Subaward/Consortium
Organization: EcoHealth Alliance

Start Date*: 03-01-2020 **End Date*:** 02-28-2021 **Budget Period:** 1

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**
Additional Equipment: File Name:	

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	15,592.00
2. Foreign Travel Costs	56,633.00
Total Travel Cost	**72,225.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget (C-E) (Funds Requested)

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 1

ORGANIZATIONAL DUNS*: 0770900660000
Budget Type*: ● Project ○ Subaward/Consortium
Organization: EcoHealth Alliance

Start Date*: 03-01-2020 **End Date*:** 02-28-2021 **Budget Period:** 1

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	7,917.50
2. Publication Costs	
3. Consultant Services	15,000.00
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	708,280.27
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
8 . Shipping	27,000.00
Total Other Direct Costs	**758,197.77**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**1,199,988.26**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . Facilities and administrative costs	32.0	616,708.01	197,346.56
2 . Foreign Subcontractual & Consortium IDC	8 0	708,280 27	40,662.42
3 . Henry Jackson IDC	52 0	74,999.99	39,372.03
4 . University of North Carolina IDC	55.5	125,000.00	69,375.00
		Total Indirect Costs	**346,756.01**

Cognizant Federal Agency (Agency Name, POC Name, and POC Phone Number)	EcoHealth Alliance: DOD Dept. of Navy, Shea Kersey, +1.703.696.2055

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**1,546,744.27**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	1,546,744.27

L. Budget Justification*	File Name: EHA_EIDRC_2019_budget_Justification_FINAL.pdf (Only attach one file)

RESEARCH & RELATED Budget (F-K) (Funds Requested)

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 2

ORGANIZATIONAL DUNS*: 0770900660000

Budget Type*: ● Project ○ Subaward/Consortium

Enter name of Organization: EcoHealth Alliance

Start Date*: 03-01-2021 **End Date*:** 02-28-2022 **Budget Period:** 2

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1	Dr	Peter		Daszak	Ph.D	PD/PI		[redacted]					(b) (4), (b) (6)
2	Dr	Kevin		Olival	Ph.D	Co-Investigator							
3	Dr	Carlos		Zambrana-Torrelio		Co-Investigator							
4	Dr	Alice		Latinne		Bioinformatician							
5	Dr	Kendra		Phelps		Field Scientist							
6	Dr	Patrick		Dawson		Epidemiologist							
7	Ms.	Hongying		Li		Epidemiologist							
8	Dr	Aleksei		Chmura		Senior Program Manager							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name:

Total Senior/Key Person 256,075.51

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Data Scientist	[redacted]					(b) (4), (b) (6)
1	Epidemiologist						
1	Program Manager						
3	**Total Number Other Personnel**					**Total Other Personnel**	113,489.98
						Total Salary, Wages and Fringe Benefits (A+B)	369,565.49

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 2

ORGANIZATIONAL DUNS*: 0770900660000
Budget Type*: ● Project ○ Subaward/Consortium
Organization: EcoHealth Alliance

Start Date*: 03-01-2021 **End Date*:** 02-28-2022 **Budget Period:** 2

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**
Additional Equipment: File Name:	

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	15,592.00
2. Foreign Travel Costs	56,633.00
Total Travel Cost	**72,225.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget (C-E) (Funds Requested)

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 2

ORGANIZATIONAL DUNS*: 0770900660000
Budget Type*: ● Project ○ Subaward/Consortium
Organization: EcoHealth Alliance

Start Date*: 03-01-2021 **End Date*:** 02-28-2022 **Budget Period:** 2

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	7,917.50
2. Publication Costs	
3. Consultant Services	15,000.00
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	708,280.27
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
8 . Shipping	27,000.00
Total Other Direct Costs	**758,197.77**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**1,199,988.26**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . EcoHealth Alliance IDC	32.0	491,708.01	157,346.56
2 . Foreign Subcontractual & Consortium IDC	8 0	708,280 27	40,662.42
3 . Henry Jackson IDC	52 0	74,999.99	39,372.03
4 . University of North Carolina IDC	55.5	125,000.00	69,375.00
		Total Indirect Costs	**306,756.01**

Cognizant Federal Agency DOD Dept. of Navy, Shea Kersey, +1.703.696 2055
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**1,506,744.27**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	1,506,744.27

L. Budget Justification*	File Name: EHA_EIDRC_2019_budget_Justification_FINAL.pdf (Only attach one file)

RESEARCH & RELATED Budget (F-K) (Funds Requested)

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 3

ORGANIZATIONAL DUNS*: 0770900660000

Budget Type*: ● Project ○ Subaward/Consortium

Enter name of Organization: EcoHealth Alliance

Start Date*: 03-01-2022 **End Date*:** 02-28-2023 **Budget Period:** 3

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1	Dr	Peter		Daszak	Ph.D	PD/PI		[redacted]					(b) (4), (b) (6)
2	Dr	Kevin		Olival	Ph.D	Co-Investigator							
3	Dr	Carlos		Zambrana-Torrelio		Co-Investigator							
4	Dr	Alice		Latinne		Bioinformatician							
5	Dr	Kendra		Phelps		Field Scientist							
6	Dr	Patrick		Dawson		Epidemiologist							
7	Ms.	Hongying		Li		Epidemiologist							
8	Dr	Aleksei		Chmura		Senior Program Manager							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name:

Total Senior/Key Person 256,075.51

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Data Scientist	[redacted]					(b) (4), (b) (6)
1	Epidemiologist						
1	Program Manager						
3	**Total Number Other Personnel**					**Total Other Personnel**	113,489.98
						Total Salary, Wages and Fringe Benefits (A+B)	369,565.49

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 3

ORGANIZATIONAL DUNS*: 0770900660000
Budget Type*: ● Project ○ Subaward/Consortium
Organization: EcoHealth Alliance

Start Date*: 03-01-2022 **End Date*:** 02-28-2023 **Budget Period:** 3

C. Equipment Description		
List items and dollar amount for each item exceeding $5,000		
Equipment Item		**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file		
	Total Equipment	**0.00**
Additional Equipment: File Name:		

D. Travel		Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)		15,592.00
2. Foreign Travel Costs		56,633.00
	Total Travel Cost	**72,225.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget (C-E) (Funds Requested)

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 3

ORGANIZATIONAL DUNS*: 0770900660000
Budget Type*: ● Project ○ Subaward/Consortium
Organization: EcoHealth Alliance

Start Date*: 03-01-2022 **End Date*:** 02-28-2023 **Budget Period:** 3

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	7,917.50
2. Publication Costs	
3. Consultant Services	15,000.00
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	708,280.27
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
8 . Shipping	27,000.00
Total Other Direct Costs	**758,197.77**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**1,199,988.26**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . EcoHealth Alliance IDC	32.0	491,708.01	157,346.56
2 . Foreign Subcontractual & Consortium IDC	8 0	708,280 27	40,662.42
3 . Henry Jackson IDC	52 0	74,999.99	39,372.03
4 . University of North Carolina IDC	55.5	125,000.00	69,375.00
		Total Indirect Costs	**306,756.01**

Cognizant Federal Agency (Agency Name, POC Name, and POC Phone Number): DOD Dept. of Navy, Shea Kersey, +1.703.696 2055

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**1,506,744.27**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	1,506,744.27

L. Budget Justification*	File Name: EHA_EIDRC_2019_budget_Justification_FINAL.pdf (Only attach one file)

RESEARCH & RELATED Budget (F-K) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA AI-19-028 . Received Date: 2019-06-28T16:02.40 000-04.00

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 4

ORGANIZATIONAL DUNS*: 0770900660000

Budget Type*: ● Project ○ Subaward/Consortium

Enter name of Organization: EcoHealth Alliance

Start Date*: 03-01-2023 **End Date*:** 02-29-2024 **Budget Period:** 4

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1	Dr	Peter		Daszak	Ph.D	PD/PI		[redacted]					(b) (4), (b) (6)
2	Dr	Kevin		Olival	Ph.D	Co-Investigator							
3	Dr	Carlos		Zambrana-Torrelio		Co-Investigator							
4	Dr	Alice		Latinne		Bioinformatician							
5	Dr	Kendra		Phelps		Field Scientist							
6	Dr	Patrick		Dawson		Epidemiologist							
7	Ms.	Hongying		Li		Epidemiologist							
8	Dr	Aleksei		Chmura		Senior Program Manager							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name:

Total Senior/Key Person 256,075.51

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Data Scientist	[redacted]					(b) (4), (b) (6)
1	Epidemiologist						
1	Program Manager						
3	**Total Number Other Personnel**					**Total Other Personnel**	**113,489.98**
						Total Salary, Wages and Fringe Benefits (A+B)	**369,565.49**

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 4

ORGANIZATIONAL DUNS*: 0770900660000
Budget Type*: ● Project ○ Subaward/Consortium
Organization: EcoHealth Alliance

Start Date*: 03-01-2023 **End Date*:** 02-29-2024 **Budget Period:** 4

C. Equipment Description		
List items and dollar amount for each item exceeding $5,000		
Equipment Item		**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file		
	Total Equipment	**0.00**
Additional Equipment: File Name:		

D. Travel		Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)		15,592.00
2. Foreign Travel Costs		56,633.00
	Total Travel Cost	**72,225.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget (C-E) (Funds Requested)

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 4

ORGANIZATIONAL DUNS*: 0770900660000
Budget Type*: ● Project ○ Subaward/Consortium
Organization: EcoHealth Alliance

Start Date*: 03-01-2023 **End Date*:** 02-29-2024 **Budget Period:** 4

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	7,917.50
2. Publication Costs	
3. Consultant Services	15,000.00
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	708,280.27
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
8 . Shipping	27,000.00
Total Other Direct Costs	**758,197.77**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**1,199,988.26**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . EcoHealth Alliance IDC	32.0	491,708.01	157,346.56
2 . Foreign Subcontractual & Consortium IDC	8 0	708,280 27	40,662.42
3 . Henry Jackson IDC	52 0	74,999.99	39,372.03
4 . University of North Carolina IDC	55.5	125,000.00	69,375.00
		Total Indirect Costs	**306,756.01**

Cognizant Federal Agency DOD Dept. of Navy, Shea Kersey, +1.703.696 2055
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**1,506,744.27**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	1,506,744.27

L. Budget Justification* File Name:
EHA_EIDRC_2019_budget_Justification_FINAL.pdf
(Only attach one file)

RESEARCH & RELATED Budget (F-K) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA AI-19-028 . Received Date: 2019-06-28T16:02.40 000-04.00

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 5

ORGANIZATIONAL DUNS*: 0770900660000

Budget Type*: ● Project ○ Subaward/Consortium

Enter name of Organization: EcoHealth Alliance

Start Date*: 03-01-2024 **End Date*:** 02-28-2025 **Budget Period:** 5

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1	Dr	Peter		Daszak	Ph.D	PD/PI		[redacted]					(b) (4), (b) (6)
2	Dr	Kevin		Olival	Ph.D	Co-Investigator							
3	Dr	Carlos		Zambrana-Torrelio		Co-Investigator							
4	Dr	Alice		Latinne		Bioinformatician							
5	Dr	Kendra		Phelps		Field Scientist							
6	Dr	Patrick		Dawson		Epidemiologist							
7	Ms.	Hongying		Li		Epidemiologist							
8	Dr	Aleksei		Chmura		Senior Program Manager							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name:

Total Senior/Key Person 256,075.51

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Data Scientist	[redacted]					(b) (4), (b) (6)
1	Epidemiologist						
1	Program Manager						
3	**Total Number Other Personnel**					**Total Other Personnel**	**113,489.98**
						Total Salary, Wages and Fringe Benefits (A+B)	**369,565.49**

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 5

ORGANIZATIONAL DUNS*: 0770900660000
Budget Type*: ● Project ○ Subaward/Consortium
Organization: EcoHealth Alliance

Start Date*: 03-01-2024 **End Date*:** 02-28-2025 **Budget Period:** 5

C. Equipment Description		
List items and dollar amount for each item exceeding $5,000		
Equipment Item		**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file		
	Total Equipment	**0.00**
Additional Equipment: File Name:		

D. Travel		Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)		15,592.00
2. Foreign Travel Costs		56,633.00
	Total Travel Cost	**72,225.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget (C-E) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA AI-19-028 . Received Date: 2019-06-28T16:02.40 000-04.00

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 5

ORGANIZATIONAL DUNS*: 0770900660000
Budget Type*: ● Project ○ Subaward/Consortium
Organization: EcoHealth Alliance

Start Date*: 03-01-2024 **End Date*:** 02-28-2025 **Budget Period:** 5

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	7,917.50
2. Publication Costs	
3. Consultant Services	15,000.00
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	708,280.27
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
8 . Shipping	27,000.00
Total Other Direct Costs	**758,197.77**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**1,199,988.26**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . EcoHealth Alliance IDC	32.0	491,708.01	157,346.56
2 . Foreign Subcontractual & Consortium IDC	8 0	708,280 27	40,662.42
3 . Henry Jackson IDC	52 0	74,999.99	39,372.03
4 . University of North Carolina IDC	55.5	125,000.00	69,375.00
		Total Indirect Costs	**306,756.01**

Cognizant Federal Agency (Agency Name, POC Name, and POC Phone Number): DOD Dept. of Navy, Shea Kersey, +1.703.696 2055

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**1,506,744.27**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	1,506,744.27

L. Budget Justification* File Name:
EHA_EIDRC_2019_budget_Justification_FINAL.pdf
(Only attach one file)

RESEARCH & RELATED Budget (F-K) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA AI-19-028 . Received Date: 2019-06-28T16:02.40 000-04.00

ECOHEALTH ALLIANCE BUDGET JUSTIFICATION

A. Senior/Key Personnel:

The PD/PI, Dr. Peter Daszak, will commit (b) (4), (b) (6) per year in each year of this budget. Dr Daszak has over 20 years of experience in building international collaborations and leading emerging infectious disease surveillance work in southeast Asia PI Daszak will meet with Co-PIs, Key Personnel, and senior governmental officials to initiate the project work. He will then work with the Co-PIs to coordinate the wide array of partners involved in this collaboration and promote stakeholder engagement. He will be primarily responsible for overseeing the project, general management, communication and collaboration with subaward partners, as well as contributing to data analysis and manuscript writing.

Co-Investigator, Dr. Kevin Olival, will commit (b) (4), (b) (6) per year in each year of this budget. Dr. Olival has more than 10 years of experience managing international multidisciplinary field and lab-based research projects focused on the dynamics of high consequence (e.g. select agent) zoonotic viruses in wildlife reservoirs and spillover into human populations. He will work on the management team to coordinate field and team training, sampling methodology, study implementation, and data management. Dr. Olival will oversee the analysis, field, and lab teams and lead the design and implementation of the sampling fieldwork; facilitate overall project management; and train and oversee field teams. Dr. Olival will also oversee modeling and analyses, participate in regular conference calls, and help write manuscripts and reports.

Co-Investigator, Dr. Carlos Zambrana-Torrelio, will commit (b) (4), (b) (6) per year in each year of this budget. Dr. Zambrana-Torrelio has more than 8 years of experience leading international teams analyzing emerging infectious disease emergence. He will oversee the Data Analytics team lead modeling and data analysis work, and assist with manuscript writing.

Bioinformatician, Dr. Alice Latinne, will commit (b) (4), (b) (6) per year in each year of this budget. Dr. Latinne will assist in with phylogenetic and phylogeographic analyses and manuscript writing.

Field Scientist, Dr Kendra Phelps, will commit (b) (4), (b) (6) per year in each year of this budget. Dr. Phelps is a disease biologist with a strong field-based research and expertise in vector-borne diseases and eco-epidemiology. Dr. Phelps will manage study implementation, coordinate fieldwork in Thailand and Malaysia, and assist in training field work teams. Dr. Phelps will be responsible for wildlife surveillance and sampling.

Epidemiologist, Dr. Patrick Dawson will commit (b) (4), (b) (6) per year in each year of this budget. Dr. Dawson will oversee epidemiological work in Thailand and Malaysia, design the human surveillance study in coordination with partners, and conduct epidemiologic analysis and biostatistical modeling. He will assist with the development of human data collection instruments testing, and implementation; advise on data storage, data analyses, and manuscript writing He will also provide training for field teams conducting human subjects research. He will assist in managing permissions for human subjects, including IRB.

Epidemiologist, Ms. Hongying Li, will commit (b) (4), (b) (6) per year in each year of this budget. Ms. Li will assist with the development of human data collection instruments, testing, and implementation, and advise on data storage, data analyses, and manuscript writing. Ms. Li will participate in human sampling and field work in Malaysia and Thailand.

Dr. Aleksei Chmura, Senior Program Manager, will commit (b) (4), (b) (6) per year in each year of this budget. Dr. Chmura has over 13 years of experience managing international research projects in Asia. He will maintain EcoHealth Alliance and subaward contracts, budgets, project reporting, and financial reporting as well as advise field activities and assist with data analysis and manuscript drafting.

B. Other Personnel

Data Scientist, Ms. Emma Mendelsohn, will commit (b) (4), (b) (6) per year in each year of this budget. Ms. Mendelsohn assist with modeling work and data analyses. She will also advise on data management, statistical approaches, and computational work. Ms. Mendelsohn will also assist in modelling and analytics, manuscript generation, and data cleaning, as well as with the development of project reports.

Epidemiologist, Ms. Stephanie Martinez, will commit (b) (4), (b) (6) per year in each year of this budget. Ms. Martinez will assist with field sampling efforts as well as human data collection and analyses.

Program Manager, Mr. Luke Hamel, will commit (b) (4), (b) (6) per year in each year of this budget. Mr. Hamel will coordinate regular calls, annual meetings, reports, draft subcontracts, and set-up project databases. advise field activities, assist with statistical analysis, and manuscript writing.

Fringe benefits for Year 1 are calculated for EcoHealth Alliance's federally approved rate of 35.4% of base salary and is included in all subsequent years.

C. Equipment
No Equipment costing more than $5,000 will be purchased

D. Travel
Domestic Travel
Travel support is requested to support eight (8) personnel - PI (Daszak) and Co-Investigators (Olival, Zambrana-Torrelio, Dawson, Baric, Sims, Liang, and Broder) - to attend a 1-day kick-off meeting in Year 01 hosted by NIH in the Bethesda Maryland area and annual 2-day meetings in Years 02-05 also to be hosted by NIH. Co-Investigators will stay an extra day after the kick-off meeting in DC to meet and coordinate project planning and roll-out. Travel is estimated at $10,184 per year and calculated at $251 for maximum lodging per night and $76 for MIE per day with $57 (75%) for first and last days of travel. Round trip train fare from NYC/Boston to Washington DC is estimated at $361. Taxis to/from train stations are estimated at $55 per trip. Total costs are estimated as follows: 8 people three days, two nights: lodging ($251 x 2 nights x 8 people) + MIE ($76 x 1 day x 8 people + $57 x 2 days x 8 people) + taxis ($55 x 4 trips to/from NYC/BOS/WAS train stations x 8 people).

Additional domestic travel support is requested for four (4) personnel - PD (Daszak) and Co-Investigators (Olival, Zambrano-Torellio, and Dawson) to attend and present on research results annually at the annual American Society for Tropical Medicine and Hygiene and the American Public Health Association meetings. 2 night and 3 day travel to Washington, DC is calculated as follows: $251 for hotels ($251 x 2 nights x 4 people); $76 for meals and incidentals with $57 (75%) for first and last days of travel ($76 x 1 days x 4 people + $57 x 2 days x 4 people); $350 for round-trip airfare ($350 x 4 people); $100 for taxis to/from NYC airports and $55 for taxis to/from Conference venue and airports ($100 x 2 x 4 people + $55 x 2 x 4 people).

International Travel
To facilitate collaboration, present results, ensure quality training, sample collection, and data analyses, annual meetings of the PI, Co-Investigators, and other personnel will be held in Thailand, Singapore, and Malaysia Respective Consortium budgets include travel and venue expenses to support personnel and lab/field team participation. We request support for round-trip flights from New York to Bangkok to Singapore and to Malaysia (all in one trip) for the annual meetings for 6 Senior/Key Personnel (Daszak, Olival, Zambrana-Torrelio, Latinne, Li, and Chmura) at $1,800 each. Eight (8) nights and nine (9) days of hotels, meals, and incidentals for travel to Bangkok (Thailand), Kuala Lumpur (Peninsular Malaysia), Singapore, Kuching (Malaysia), and Kota Kinabalu (Malaysia) for six (6) Senior/Key Personal are calculated at $24,303 per year: hotels at average of $193 per night and meals and incidentals at $96 per day. Taxis to/from NYC airport are calculated at $110 x 2 rides and taxis to/from in-country airports are calculated at $15 x 2 rides. Daily taxis are estimated at $20 per day per person.

Field, Wildlife, and Data Management/Analysis Scientists will also participate in annual meetings. These personnel will spend an additional week (7 days and 6 nights) respectively in Malaysia (Peninsular Malaysia, Sabah, and Sarawak) Thailand, and Singapore. We request support for round-trip flights from New York to Bangkok to Singapore and to Malaysia (all in one trip) for the 2 Personnel (Dawson and Phelps or Mendelsohn and Martinez) at $1,800 each. A total of 28 days and 27 nights of hotels, meals, and incidentals for travel to Bangkok (Thailand), Kuala Lumpur (Peninsular Malaysia), Singapore, Kuching (Malaysia), and Kota Kinabalu (Malaysia) for six (6) Senior/Key Personal are calculated at $26,350 per year. Per diems and other costs are

well below US Government per diem rates to save costs and as these locations will be outside urban centers. We calculate average hotel nightly costs at $92 per night and meals and incidentals at $65 per day. Taxis to/from NYC airport are calculated at $110 x 2 rides and taxis to/from in-country airports are calculated at $15 x 2 rides. Daily taxis are estimated at $20 per day per person.

Additional travel support is requested for four (2) personnel - PD (Daszak) and Co-Investigator (Olival) to attend and present on research results annually at the IMED Vienna or other international meetings. 3 night and 4 day international travel to the conference venue is calculated as follows: $221 for hotels ($221 x 3 nights x 2 people); $122 for meals and incidentals w th $92 (75%) for first and last days of travel ($122 x 2 days x 2 peop e + $92 x 2 days x 2 people); $1 500 for round-trip airfare ($1,500 x 2 people); $110 for taxis to/from NYC airports and $55 for taxis to/from Conference venue and airports ($110 x 2 x 2 people + $55 x 2 x 2 people).

E. Participant/Trainee Support Costs
There are no participant/trainee support costs.

F. Other Direct Costs
Materials & Supplies
We request $7,000 in Year 1 for two (2) laptops for the Program Manager (TBD) and Epidemiologist (Li). Costs for Apple MacBook Pros are estimated at $3,500 including MS Office licenses, adaptor cables, and Applecare/insurance. We also request $917.50 per year in each year to cover software and reference materials, and acquisition of datasets.

Consultant Services
We request (b) (4), (b) (6) in each year of this proposed project to engage Senior Veterinary Officer and Epidemiologist Dr. Hume Field. Dr. Field has over 20 years of experience working in Southeast Asia on wildlife disease surveillance. Most recently he was the Principal Research Scientist at the Australian Queensland Centre for Emerging Infectious Diseases where he was co-PI on numerous international government and university-funded projects which sought to elaborate zoonotic disease infections. He works closely with the US Centers for Disease Control, the World Health Organization, and the UN Food and Agriculture Organization. His work directly resulted in the finding of the origins of Nipah virus in Malaysia, SARS in China, and Reston ebolavirus in the Philippines. Dr. Field will participate in training field teams, provide support and recommendation on project evaluation and consultation on drafting high-impact, quality peer-review scientific manuscripts based upon project findings.

Publication Costs
We request $7,000 per year for only Years 2 to 5 for open access fees required to publish research findings in peer-reviewed journals such as *Nature*, *Public Library of Science*, and other journals. We estimate two publications per year at $3,500 in open access fees each.

Subawards/Consortium/Contractual Costs
We are requesting consortium/contractual support for our five partners in all years of our proposed project: Chulalongkorn University Hospital Thailand, Conservation Medicine Malaysia, Duke-National University Singapore Medical School, Uniformed Services Univers ty (via Henry M. Jackson Foundation), and the University of North Carolina at Chapel Hill. We have fully detailed these direct and indirect costs in their respective sub-award budgets.

Shipping
We will be shipping biological samples from Thailand and Malaysia to our collaborators at the National Emerging Infectious Diseases Laboratories (NEIDL) in Boston USA. Shipping box and all taxes are estimated at $3,000 per shipment. We estimate 3 shipments of samples ($3,000 x 3 = $9,000) will be sent every year from each country (Singapore, Thailand, and Malaysia: $9,000 x 3 = $27,000) throughout the duration of our project.

H. Indirect Costs

We are requesting the EcoHealth Alliance federally approved indirect cost rate of 32% on all applicable direct costs. The cognizant agency is the US Department of Defense Department of the Navy. Our Indirect is also applied only on the first $25,000 for each consortium/contractual agreement in each year. As there are 5 consortium/contractual agreements, a total of $40,000 is requested as indirect costs on consortium/subaward agreements only in Year 1. This and all consortium indirect costs are not included as part of direct cost calculations. In years 2-5 no indirect will be taken on consortium/contractual agreement subcontracts.

RESEARCH & RELATED BUDGET - Cumulative Budget

	Totals ($)	
Section A, Senior/Key Person		1,280,377.55
Section B, Other Personnel		567,449.90
Total Number Other Personnel	15	
Total Salary, Wages and Fringe Benefits (A+B)		1,847,827.45
Section C, Equipment		0 00
Section D, Travel		361,125 00
1. Domestic	77,960.00	
2. Foreign	283,165.00	
Section E, Participant/Trainee Support Costs		0 00
1. Tuition/Fees/Health Insurance	0.00	
2. Stipends	0.00	
3 Travel	0.00	
4. Subsistence	0.00	
5. Other	0.00	
6. Number of Participants/Trainees	0	
Section F, Other Direct Costs		3,790,988.85
1. Materials and Supplies	39,587 50	
2. Publication Costs	0.00	
3. Consultant Services	75,000.00	
4. ADP/Computer Services	0 00	
5. Subawards/Consortium/Contractual Costs	3,541,401.35	
6. Equipment or Facility Rental/User Fees	0.00	
7. Alterations and Renovations	0.00	
8. Other 1	135,000 00	
9. Other 2	0.00	
10. Other 3	0 00	
Section G, Direct Costs (A thru F)		5,999,941 30
Section H, Indirect Costs		1,573,780 05
Section I, Total Direct and Indirect Costs (G + H)		7,573,721 35
Section J, Fee		0 00
Section K, Total Costs and Fee (I + J)		7,573,721 35

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA AI-19-028 Received Date 2019-06-28T16:02 40.000-04:00

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 1

ORGANIZATIONAL DUNS*: 6598088360000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: Chulalongkorn University

Start Date*: 03-01-2020 **End Date*:** 02-28-2021 **Budget Period:** 1

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	Supaporn		Wacharapluesadee	Ph.D	Co-Investigator		[redacted]					(b) (4), (b) (6)
2 .	Dr.	Thiravat		Hemachudha	Ph.D	Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name:

Total Senior/Key Person (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Lab & Field Technician	[redacted]					(b) (4), (b) (6)
1	Lab Technician						
1	Field Technician						
1	Program Manager						
4	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)

Total Salary, Wages and Fringe Benefits (A+B)

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 1

ORGANIZATIONAL DUNS*: 6598088360000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Chulalongkorn University

Start Date*: 03-01-2020 **End Date*:** 02-28-2021 **Budget Period:** 1

C. Equipment Description		
List items and dollar amount for each item exceeding $5,000		
Equipment Item		**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file		
	Total Equipment	**0.00**
Additional Equipment: File Name:		

D. Travel		Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)		43,495.00
2. Foreign Travel Costs		7,601.00
	Total Travel Cost	**51,096.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget (C-E) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA AI-19-028 . Received Date: 2019-06-28T16:02.40 000-04.00

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 1

ORGANIZATIONAL DUNS*: 6598088360000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Chulalongkorn University

Start Date*: 03-01-2020 **End Date*:** 02-28-2021 **Budget Period:** 1

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	88,001.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
8 . Annual Meeting (Facilities, Meals)	3,660.00
9 . Maintenance Costs	1,525.00
Total Other Direct Costs	**93,186.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**199,948.66**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . Facilities and administrative costs	8.0		15,995.89
		Total Indirect Costs	**15,995.89**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**215,944.55**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	215,944.55

L. Budget Justification*	File Name. Chulalongkorn EIDRC 2019_Justification.pdf (Only attach one file.)

RESEARCH & RELATED Budget (F K) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date: 2019-06-28T16:02.40 000-04.00

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 2

ORGANIZATIONAL DUNS*: 6598088360000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: Chulalongkorn University

Start Date*: 03-01-2021 **End Date*:** 02-28-2022 **Budget Period:** 2

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	Supaporn		Wacharapluesadee	Ph.D	Co-Investigator		[redacted]					(b) (4), (b) (6)
2 .	Dr.	Thiravat		Hemachudha	Ph.D	Co-Investigator		[redacted]					

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name:

Total Senior/Key Person (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Lab & Field Technician	[redacted]					(b) (4), (b) (6)
1	Lab Technician						
1	Field Technician						
1	Program Manager						
4	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)

Total Salary, Wages and Fringe Benefits (A+B) [redacted]

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 2

ORGANIZATIONAL DUNS*: 6598088360000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Chulalongkorn University

Start Date*: 03-01-2021 **End Date*:** 02-28-2022 **Budget Period:** 2

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**
Additional Equipment: File Name:	

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	43,495.00
2. Foreign Travel Costs	7,601.00
Total Travel Cost	**51,096.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget (C-E) (Funds Requested)

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 2

ORGANIZATIONAL DUNS*: 6598088360000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Chulalongkorn University

Start Date*: 03-01-2021 **End Date*:** 02-28-2022 **Budget Period:** 2

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	88,001.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
8 . Annual Meeting (Facilities, Meals)	3,660.00
9 . Maintenance Costs	1,525.00
Total Other Direct Costs	**93,186.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**199,948.66**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . Facilities and administrative costs	8.0		15,995.89
		Total Indirect Costs	**15,995.89**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**215,944.55**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	215,944.55

L. Budget Justification*	File Name. Chulalongkorn EIDRC 2019_Justification.pdf (Only attach one file.)

RESEARCH & RELATED Budget (F K) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date: 2019-06-28T16:02.40 000-04.00

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 3

ORGANIZATIONAL DUNS*: 6598088360000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: Chulalongkorn University

Start Date*: 03-01-2022 **End Date*:** 02-28-2023 **Budget Period:** 3

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	Supaporn		Wacharapluesadee	Ph.D	Co-Investigator		[redacted]					(b) (4), (b) (6)
2 .	Dr.	Thiravat		Hemachudha	Ph.D	Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name: **Total Senior/Key Person** (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Lab & Field Technician	[redacted]					(b) (4), (b) (6)
1	Lab Technician						
1	Field Technician						
1	Program Manager						
4	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)

Total Salary, Wages and Fringe Benefits (A+B) (b) (4), (b) (6)

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 3

ORGANIZATIONAL DUNS*: 6598088360000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Chulalongkorn University

Start Date*: 03-01-2022 **End Date*:** 02-28-2023 **Budget Period:** 3

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**
Additional Equipment: File Name:	

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	43,495.00
2. Foreign Travel Costs	7,601.00
Total Travel Cost	**51,096.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget (C-E) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA AI-19-028 . Received Date: 2019-06-28T16:02.40 000-04.00

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 3

ORGANIZATIONAL DUNS*: 6598088360000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Chulalongkorn University

Start Date*: 03-01-2022 **End Date*:** 02-28-2023 **Budget Period:** 3

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	88,001.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
8 . Annual Meeting (Facilities, Meals)	3,660.00
9 . Maintenance Costs	1,525.00
Total Other Direct Costs	**93,186.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**199,948.66**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . Facilities and administrative costs	8.0		15,995.89
		Total Indirect Costs	**15,995.89**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**215,944.55**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	215,944.55

L. Budget Justification*	File Name. Chulalongkorn EIDRC 2019_Justification.pdf (Only attach one file.)

RESEARCH & RELATED Budget (F K) (Funds Requested)

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 4

ORGANIZATIONAL DUNS*: 6598088360000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: Chulalongkorn University

Start Date*: 03-01-2023 **End Date*:** 02-29-2024 **Budget Period:** 4

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	Supaporn		Wacharapluesadee	Ph.D	Co-Investigator		[redacted]					(b) (4), (b) (6)
2 .	Dr.	Thiravat		Hemachudha	Ph.D	Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name: **Total Senior/Key Person** (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Lab & Field Technician	[redacted]					(b) (4), (b) (6)
1	Lab Technician						
1	Field Technician						
1	Program Manager						
4	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)

Total Salary, Wages and Fringe Benefits (A+B) (b) (4), (b) (6)

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 4

ORGANIZATIONAL DUNS*: 6598088360000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Chulalongkorn University

Start Date*: 03-01-2023 **End Date*:** 02-29-2024 **Budget Period:** 4

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**
Additional Equipment: File Name:	

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	43,495.00
2. Foreign Travel Costs	7,601.00
Total Travel Cost	**51,096.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget (C-E) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA AI-19-028 . Received Date: 2019-06-28T16:02.40 000-04.00

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 4

ORGANIZATIONAL DUNS*: 6598088360000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Chulalongkorn University

Start Date*: 03-01-2023 **End Date*:** 02-29-2024 **Budget Period:** 4

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	88,001.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
8 . Annual Meeting (Facilities, Meals)	3,660.00
9 . Maintenance Costs	1,525.00
Total Other Direct Costs	**93,186.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**199,948.66**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . Facilities and administrative costs	8.0		15,995.89
		Total Indirect Costs	**15,995.89**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**215,944.55**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	215,944.55

L. Budget Justification*	File Name. Chulalongkorn EIDRC 2019_Justification.pdf (Only attach one file.)

RESEARCH & RELATED Budget (F K) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date: 2019-06-28T16:02.40 000-04.00

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 5

ORGANIZATIONAL DUNS*: 6598088360000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: Chulalongkorn University

Start Date*: 03-01-2024 **End Date*:** 02-28-2025 **Budget Period:** 5

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	Supaporn		Wacharapluesadee	Ph.D	Co-Investigator		[redacted]					(b) (4), (b) (6)
2 .	Dr.	Thiravat		Hemachudha	Ph.D	Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name: **Total Senior/Key Person** (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Lab & Field Technician	[redacted]					(b) (4), (b) (6)
1	Lab Technician						
1	Field Technician						
1	Program Manager						
4	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)

Total Salary, Wages and Fringe Benefits (A+B)

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 5

ORGANIZATIONAL DUNS*: 6598088360000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Chulalongkorn University

Start Date*: 03-01-2024 **End Date*:** 02-28-2025 **Budget Period:** 5

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**
Additional Equipment: File Name:	

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	43,495.00
2. Foreign Travel Costs	7,601.00
Total Travel Cost	**51,096.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget (C-E) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA AI-19-028 . Received Date: 2019-06-28T16:02.40 000-04.00

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 5

ORGANIZATIONAL DUNS*: 6598088360000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Chulalongkorn University

Start Date*: 03-01-2024 **End Date*:** 02-28-2025 **Budget Period:** 5

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	88,001.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
8 . Annual Meeting (Facilities, Meals)	3,660.00
9 . Maintenance Costs	1,525.00
Total Other Direct Costs	**93,186.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**199,948.66**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . Facilities and administrative costs	8.0		15,995.89
		Total Indirect Costs	**15,995.89**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**215,944.55**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	215,944.55

L. Budget Justification*	File Name. Chulalongkorn EIDRC 2019_Justification.pdf (Only attach one file.)

RESEARCH & RELATED Budget (F K) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date: 2019-06-28T16:02:40 000-04.00

CHULALONGKORN HOSPITAL BUDGET JUSTIFICATION, SUBAWARD

A. Senior/Key Personnel

Supaporn Wacharapluesadee, Co-Investigator will commit [redacted] (b) (4), (b) (6) to this project. Dr. Wacharapluesadee is a known expert in field surveillance in wild mammals, human behavioral risk surveys, and clinical sampling in Thailand. Dr. Wacharapluesadee will oversee all aspects of this project in Thailand and direct the activities of the Other Personnel. At a regular basis, Dr. Wacharapluesadee will meet with the PI and other Co-PIs to refine study protocols, report back results, and prepare publications. Dr. Wacharapluesadee has been working on the discovery and characterization of novel viruses from bats and other wildlife as well as clinical sampling for over 15 years and has worked extensively with and managing international and local interdisciplinary teams. Dr. Wacharapluesadee's laboratory was the first to correctly diagnose the first human MERS case in Thailand, which led to swift execution of containment measures preventing a MERS outbreak.

Thiravat Hemachudha, Co-Investigator will commit [redacted] (b) (4), (b) (6) to this project. Dr. Thiravat has over 20 years of internationally funded research in various fields, from immunological studies, to rabies pathology, to CNS infection pathology. Since 2008, Dr. Thiravat has been the director of the World Health Organization's Collaborating Centre for Research and Training on Viral Zoonoses. Dr. Thiravat will directly supervise and coordinate all the clinical hospital work under this project.

B. Other Personnel

TBD, Laboratory and Field Technician will commit [redacted] (b) (4), (b) (6) per year to this project to directly supervisor the lab and field technicians, and coordinate with Senior Personnel and collaborators for communication, reporting, and or organizing meetings and reports.

TBD, Laboratory Technician will commit [redacted] (b) (4), (b) (6) per year to run diagnostic assays, genomics, and virus isolation work as well as assisting with sample shipments, storage, and maintenance of cold chain

TBD, Field Technician will commit [redacted] (b) (4), (b) (6) per year to conduct field surveillance efforts and coordinate partner institution/site field teams

TBD, Program Manager will commit [redacted] (b) (4), (b) (6) per year to assisting all personnel and maintaining all administrative aspects of this proposal including equipment purchase and inventory, reporting minutes, setting up meetings, and coordinating annual in-country meetings.

Fringe Benefits

No fringe benefits are requested.

C. Equipment

No equipment over $5,000 will be purchased.

D. Travel

Domestic Travel.

Domestic travel costs are estimated at $43 495 per year for site surveillance and sampling visits. These costs are calculated as follows: $17,398 for four 1-week bat sampling trips per year (visiting each site twice per year); concurrent community sampling is estimated at the same cost $17,398. Sampling costs include field personnel, drivers, vehicle rental, and flights

Foreign Travel.

International travel costs are requested for 1 trip for Co-Investigator annually from Bangkok to USA (DC and NYC) for NIH kickoff (Year 1) and annual meetings (Years 2-5). Co-Investigator will fly roundtrip to NYC and take train to NIH annual meeting and return to NYC to EcoHealth Alliance Offices to meet with PI, Co-Investigators, and Research Scientists. Costs for one traveler are estimated at $251 NYC/DC hotel per diem ($251 x 6 nights = $1,506); $76/day for meals and incidental expenses with 75% applied on first and final days of travel ($76 x 6.5 days = $494); $1,400 round trip flight from Bangkok to NYC ($1,400 x 1 = $1,400); $192 for roundtrip train fare from NYC to Washington DC ($192 x 1 = $192); $30 per daily taxi rides in NYC and DC ($15 x 2 rides per day x 5 days = $150); $330 for to/from airport taxis in Bangkok and USA ($110 per ride in

NYC = $220 and $30 per ride in Bangkok = $60, total = $280).

Additional international travel support is requested for both Co-Investigators (2) to attend annual regional meetings in Singapore and Malaysia. These costs are estimated as follows: $200 for Singapore hotel per diem ($200 x 2 nights x 2 people = $800); $95 for meals and incidental expenses with 75% applied on first and final days of travel ($95 x 2.5 days x 2 people = $475); $150 roundtrip airfare from Bangkok to Singapore ($150 x 2 people = $300); $10 per daily taxi rides in Singapore ($10 x 2 people x 1 day = $20); $120 for to/from airport taxis in Bangkok and Singapore ($30 per ride in Bangkok and Singapore = $30 x 2 trips to/from airport x 2 people = $240). Trips to Malaysia for two Co-Investigators are estimated from Bangkok to Kuala Lumpur at: $186 for Singapore hotel per diem ($186 x 2 nights x 2 people = $372); $80 for meals and incidental expenses with 75% applied on first and final days of travel ($80 x 2.5 days x 2 people = $160); $150 roundtrip airfare from Bangkok to Kuala Lumpur ($150 x 2 people = $300); $10 per daily taxi rides in Kuala Lumpur ($10 x 2 people x 1 day = $20); $120 for to/from airport taxis in Bangkok and Kuala Lumpur ($30 per ride in Bangkok and Kuala Lumpur = $30 x 2 trips to/from airport x 2 people = $240).

E. Participant/Trainee Support Costs
No participant/trainee support costs are requested.

F. Other Direct Costs
Materials and Supplies.
Chulalongkorn University Hospital requests reimbursement of estimated laboratory costs. These are calculated based upon current annual costs and requested in each year of this proposed project. Costs include RNA extraction ($13,200.15) PCR reagents and sequencing ($44,000.50) and gloves, chemicals, plasticware, and other miscellaneous supplies ($13,200.15). In addition, NGS sequencing costs are estimated at ($17,600.20).

Annual Meeting
Chulalongkorn University Hospital will host an annual meeting of PI, Co-Investigators and other collaborators. Facilities fees are estimated at $3,666.00 and detailed as follows: $1,500.00 for room rental costs, AV, and University support; University Dining will charge a fixed fee for meals for 20 attendees at $36/day for the three days of the meeting ($36 x 3 days x 20 people = $2,166.00).

Maintenance Costs.
Reimbursement is requested in the amount of $1,525.00 for annual maintenance costs for laboratory PCR-sequencers and other equipment.

H. Indirect Costs (8%)
Chulalongkorn University Hospital requests reimbursement of the *de minimus* indirect cost recovery rate of 8% of modified or allowable direct costs.

RESEARCH & RELATED BUDGET - Cumulative Budget

	Totals ($)	
Section A, Senior/Key Person		133,333.30
Section B, Other Personnel		145,000.00
Total Number Other Personnel	20	
Total Salary, Wages and Fringe Benefits (A+B)		278,333.30
Section C, Equipment		0 00
Section D, Travel		255,480 00
1. Domestic	217,475.00	
2. Foreign	38,005 00	
Section E, Participant/Trainee Support Costs		0 00
1. Tuition/Fees/Health Insurance	0.00	
2. Stipends	0.00	
3 Travel	0.00	
4. Subsistence	0.00	
5. Other	0.00	
6. Number of Participants/Trainees	0	
Section F, Other Direct Costs		465,930 00
1. Materials and Supplies	440,005.00	
2. Publication Costs	0.00	
3. Consultant Services	0.00	
4. ADP/Computer Services	0 00	
5. Subawards/Consortium/Contractual Costs	0 00	
6. Equipment or Facility Rental/User Fees	0.00	
7. Alterations and Renovations	0.00	
8. Other 1	18,300 00	
9. Other 2	7,625.00	
10. Other 3	0 00	
Section G, Direct Costs (A thru F)		999,743 30
Section H, Indirect Costs		79,979 45
Section I, Total Direct and Indirect Costs (G + H)		1,079,722.75
Section J, Fee		0 00
Section K, Total Costs and Fee (I + J)		1,079,722 75

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA AI-19-028 Received Date 2019-06-28T16:02 40.000-04:00

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 1

ORGANIZATIONAL DUNS*: 5344092560000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: Conservation Medicine Ltd.

Start Date*: 03-01-2020 **End Date*:** 02-28-2021 **Budget Period:** 1

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Mr.	Thomas	J.	Hughes		Co-Investigator		[redacted]					(b) (4), (b) (6)

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name:

Total Senior/Key Person (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Lab Coordinator	[redacted]					(b) (4), (b) (6)
1	Lab Technician						
1	Field Coordinator						
1	Veterinarian						
2	Wildlife Rangers						
6	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)

Total Salary, Wages and Fringe Benefits (A+B) (b) (4), (b) (6)

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 1

ORGANIZATIONAL DUNS*: 5344092560000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Conservation Medicine Ltd.

Start Date*: 03-01-2020 **End Date*:** 02-28-2021 **Budget Period:** 1

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**
Additional Equipment: File Name:	

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	34,800.00
2. Foreign Travel Costs	4,807.50
Total Travel Cost	**39,607.50**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget (C-E) (Funds Requested)

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 1

ORGANIZATIONAL DUNS*: 5344092560000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Conservation Medicine Ltd.

Start Date*: 03-01-2020 **End Date*:** 02-28-2021 **Budget Period:** 1

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	63,660.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
Total Other Direct Costs	**63,660.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**208,331.63**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . US Federal Gov't de minimus rate	8.0	208,331.62	16,666.53
		Total Indirect Costs	**16,666.53**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**224,998.16**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	224,998.16

L. Budget Justification*	File Name
	CM EIDRC 2019 Subawardbudget_Justification_v02.pdf
	(Only attach one file.)

RESEARCH & RELATED Budget (F-K) (Funds Requested)

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 2

ORGANIZATIONAL DUNS*: 5344092560000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: Conservation Medicine Ltd.

Start Date*: 03-01-2021 **End Date*:** 02-28-2022 **Budget Period:** 2

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Mr.	Thomas	J.	Hughes		Co-Investigator		[redacted]					(b) (4), (b) (6)

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name:

Total Senior/Key Person (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Lab Coordinator	[redacted]					(b) (4), (b) (6)
1	Lab Technician						
1	Field Coordinator						
1	Veterinarian						
2	Wildlife Rangers						
6	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)

Total Salary, Wages and Fringe Benefits (A+B) (b) (4), (b) (6)

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 2

ORGANIZATIONAL DUNS*: 5344092560000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Conservation Medicine Ltd.

Start Date*: 03-01-2021 **End Date*:** 02-28-2022 **Budget Period:** 2

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**
Additional Equipment: File Name:	

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	34,800.00
2. Foreign Travel Costs	4,807.50
Total Travel Cost	**39,607.50**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget (C-E) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA AI-19-028 . Received Date: 2019-06-28T16:02.40 000-04.00

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 2

ORGANIZATIONAL DUNS*: 5344092560000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Conservation Medicine Ltd.

Start Date*: 03-01-2021 **End Date*:** 02-28-2022 **Budget Period:** 2

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	63,660.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
Total Other Direct Costs	**63,660.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**208,331.63**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . US Federal Gov't de minimus rate	8.0	208,331.62	16,666.53
		Total Indirect Costs	**16,666.53**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**224,998.16**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	224,998.16

L. Budget Justification*	File Name
	CM EIDRC 2019 Subawardbudget_Justification_v02.pdf
	(Only attach one file.)

RESEARCH & RELATED Budget (F-K) (Funds Requested)

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 3

ORGANIZATIONAL DUNS*: 5344092560000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: Conservation Medicine Ltd.

Start Date*: 03-01-2022 **End Date*:** 02-28-2023 **Budget Period:** 3

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Mr.	Thomas	J.	Hughes		Co-Investigator		[redacted]					(b) (4), (b) (6)

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name: **Total Senior/Key Person** [redacted] (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Lab Coordinator	[redacted]					(b) (4), (b) (6)
1	Lab Technician						
1	Field Coordinator						
1	Veterinarian						
2	Wildlife Rangers						
6	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)
						Total Salary, Wages and Fringe Benefits (A+B)	[redacted]

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 3

ORGANIZATIONAL DUNS*: 5344092560000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Conservation Medicine Ltd.

Start Date*: 03-01-2022 **End Date*:** 02-28-2023 **Budget Period:** 3

C. Equipment Description		
List items and dollar amount for each item exceeding $5,000		
Equipment Item		**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file		
	Total Equipment	**0.00**
Additional Equipment: File Name:		

D. Travel		Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)		34,800.00
2. Foreign Travel Costs		4,807.50
	Total Travel Cost	**39,607.50**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget (C-E) (Funds Requested)

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 3

ORGANIZATIONAL DUNS*: 5344092560000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Conservation Medicine Ltd.

Start Date*: 03-01-2022 **End Date*:** 02-28-2023 **Budget Period:** 3

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	63,660.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
Total Other Direct Costs	**63,660.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**208,331.63**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . US Federal Gov't de minimus rate	8.0	208,331.62	16,666.53
		Total Indirect Costs	**16,666.53**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**224,998.16**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	224,998.16

L. Budget Justification*	File Name
	CM EIDRC 2019 Subawardbudget_Justification_v02.pdf
	(Only attach one file.)

RESEARCH & RELATED Budget (F-K) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date: 2019-06-28T16:02:40 000-04:00

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 4

ORGANIZATIONAL DUNS*: 5344092560000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: Conservation Medicine Ltd.

Start Date*: 03-01-2023 **End Date*:** 02-29-2024 **Budget Period:** 4

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Mr	Thomas	J.	Hughes		Co-Investigator		[redacted]					(b) (4), (b) (6)

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name: **Total Senior/Key Person** (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Lab Coordinator	[redacted]					(b) (4), (b) (6)
1	Lab Technician						
1	Field Coordinator						
1	Veterinarian						
2	Wildlife Rangers						
6	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)
						Total Salary, Wages and Fringe Benefits (A+B)	

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 4

ORGANIZATIONAL DUNS*: 5344092560000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Conservation Medicine Ltd.

Start Date*: 03-01-2023 **End Date*:** 02-29-2024 **Budget Period:** 4

C. Equipment Description		
List items and dollar amount for each item exceeding $5,000		
Equipment Item		**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file		
	Total Equipment	**0.00**
Additional Equipment: File Name:		

D. Travel		Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)		34,800.00
2. Foreign Travel Costs		4,807.50
	Total Travel Cost	**39,607.50**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget (C-E) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA AI-19-028 . Received Date: 2019-06-28T16:02.40 000-04.00

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 4

ORGANIZATIONAL DUNS*: 5344092560000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Conservation Medicine Ltd.

Start Date*: 03-01-2023 **End Date*:** 02-29-2024 **Budget Period:** 4

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	63,660.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
Total Other Direct Costs	**63,660.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**208,331.63**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . US Federal Gov't de minimus rate	8.0	208,331.62	16,666.53
		Total Indirect Costs	**16,666.53**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**224,998.16**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	224,998.16

L. Budget Justification*	File Name
	CM EIDRC 2019 Subawardbudget_Justification_v02.pdf
	(Only attach one file.)

RESEARCH & RELATED Budget (F-K) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date: 2019-06-28T16:02:40 000-04:00

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 5

ORGANIZATIONAL DUNS*: 5344092560000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: Conservation Medicine Ltd.

Start Date*: 03-01-2024 **End Date*:** 02-28-2025 **Budget Period:** 5

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Mr.	Thomas	J.	Hughes		Co-Investigator		[redacted]					(b) (4), (b) (6)

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name:

Total Senior/Key Person (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Lab Coordinator	[redacted]					(b) (4), (b) (6)
1	Lab Technician						
1	Field Coordinator						
1	Veterinarian						
2	Wildlife Rangers						
6	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)
						Total Salary, Wages and Fringe Benefits (A+B)	

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 5

ORGANIZATIONAL DUNS*: 5344092560000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Conservation Medicine Ltd.

Start Date*: 03-01-2024 **End Date*:** 02-28-2025 **Budget Period:** 5

C. Equipment Description		
List items and dollar amount for each item exceeding $5,000		
Equipment Item		**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file		
	Total Equipment	**0.00**
Additional Equipment: File Name:		

D. Travel		Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)		34,800.00
2. Foreign Travel Costs		4,807.50
	Total Travel Cost	**39,607.50**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget (C-E) (Funds Requested)

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 5

ORGANIZATIONAL DUNS*: 5344092560000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Conservation Medicine Ltd.

Start Date*: 03-01-2024 **End Date*:** 02-28-2025 **Budget Period:** 5

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	63,660.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
Total Other Direct Costs	**63,660.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**208,331.63**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . US Federal Gov't de minimus rate	8.0	208,331.62	16,666.53
		Total Indirect Costs	**16,666.53**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**224,998.16**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	224,998.16

L. Budget Justification*	File Name
	CM EIDRC 2019 Subawardbudget_Justification_v02.pdf
	(Only attach one file.)

RESEARCH & RELATED Budget (F-K) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date: 2019-06-28T16:02:40 000-04:00

CHULALONGKORN HOSPITAL BUDGET JUSTIFICATION, SUBAWARD

A. Senior/Key Personnel
Thomas J. Hughes, Co-Investigator will commit (b) (4), (b) (6) to this project. Mr. Hughes is a known expert in field surveillance in wild mammals and human behavioral risk surveys, and clinical sampling in Malaysia. Mr. Hughes will oversee all aspects of this project in Malaysia and direct the activities of the other personnel. At a regular basis, Mr. Hughes will meet with the PI and other Co-PIs to refine study protocols, report back results, and prepare publications. Mr. Hughes has been working on the discovery and characterization of novel viruses from bats and other wildlife as well as clinical sampling for over 10 years and has worked extensively with and managing international and local interdisciplinary teams.

B. Other Personnel
TBD, Laboratory and Program Coordinator will commit (b) (4), (b) (6) per year to this project to conduct all laboratory assays and supervise the Laboratory Technician. The Laboratory Coordinator will work with Mr. Hughes and other Senior/Key Personnel and collaborators for communication, reporting, contracts as well as equipment purchases, inventory, minutes, setting up meetings, and coordinating annual in-country meetings.

TBD, Laboratory Technician will commit (b) (4), (b) (6) per year to run diagnostic assays and virus isolation work as well as assisting with sample shipments, storage, and maintenance of cold chain

TBD, Field Coordinator will commit (b) (4), (b) (6) per year to conduct field and clinic surveillance efforts and coordinate partner institution/site field teams. Field Coordinator will supervise the Field Veterinarian and Wildlife Rangers (2).

TBD, Field Veterinarian will commit (b) (4), (b) (6) per year to training and working with all field personnel and maintaining highest quality of sampling aspects of this proposal as well as safety for all human and non-human animals.

TBD, Field/Wildlife Rangers (2) will commit (b) (4), (b) (6) to assisting Field Coordinator and Field Veterinarian in collection, processing, storage, and shipping of field sampling efforts.

Fringe Benefits
No fringe benefits are requested.

C. Equipment
No equipment over $5,000 will be purchased.

D. Travel
Domestic Travel.
Domestic travel costs are estimated at $34 800 per year for site surveillance and sampling visits in Sabah, Sawarak, and Peninsular Malaysia. These costs are calculated as follows: $14,400 for 2 1-week bat sampling trips per year, i.e. visiting each site twice per year. Concurrent community sampling is estimated at the same cost $14,400. Sampling costs include field personnel, drivers, vehicle rental, and local flights as well as equipment for clinical surveillance ($6,000)

Foreign Travel.
International travel costs are requested for 1 trip for Co-Investigator Hughes to fly annually from Kuala Lumpur to USA (DC and NYC) for NIH kickoff (Year 1) and annual meetings (Years 2-5). Co-Investigator will fly roundtrip to NYC and take train to NIH annual meeting and return to NYC to EcoHealth Alliance Offices to meet with PI, Co-Investigators, and Research Scientists. Costs for one traveler are estimated at $251 NYC/DC hotel per diem ($251 x 6 nights = $1,506); $76/day for meals and incidental expenses with 75% applied on first and final days of travel ($76 x 6.5 days = $494); $1,400 round trip flight from Kuala Lumpur to NYC ($1,400 x 1 = $1,400); $192 for roundtrip train fare from NYC to Washington DC ($192 x 1 = $192); $30 per daily taxi rides in NYC and DC ($15 x 2 rides per day x 5 days = $150); $330 for to/from airport taxis in Kuala Lumpur and USA ($110 per ride in NYC = $220 and $30 per ride in Kuala Lumpur = $60, total = $280).

Additional international travel support is requested for both Co-Investigator Hughes to attend annual regional meetings in Singapore and Thailand. These annual costs to Singapore or Thailand are estimated as follows: $200 for Singapore hotel per diem ($200 x 2 nights x 1 people = $400); $95 for meals and incidental expenses with 75% applied on first and final days of travel ($95 x 2.5 days x 1 person = $237.50); $150 roundtrip airfare from Kuala Lumpur to Singapore or Thailand ($150 x 1 person = $150); $20 per day taxi rides in Singapore or Thailand ($20 x 1 person x 1 day = $20); $120 for to/from airport taxis in Kuala Lumpur and Singapore or Thailand ($30 per ride in Bangkok and Singapore = $30 x 2 trips to/from airport x 2 people = $240). Trips to Malaysia for Mr. Hughes is estimated from Bangkok to Kuala Lumpur at: $186 for Singapore or Bangkok hotel per diem ($186 x 2 nights x 1 person = $372); $80 for meals and incidental expenses with 75% applied on first and final days of travel ($80 x 2.5 days x 1 person = $200); $150 roundtrip airfare from Bangkok to Kuala Lumpur ($150 x 1 people = $150); $10 per daily taxi rides in Kuala Lumpur ($10 x 1 person x 1 day = $20); $120 for to/from airport taxis in Bangkok and Kuala Lumpur ($30 per ride in Bangkok and Kuala Lumpur = $30 x 2 trips to/from airport x 1 person = $240).

E. Participant/Trainee Support Costs
No participant/trainee support costs are requested.

F. Other Direct Costs
Laboratory Supplies.
Conservation Medicine requests reimbursement of estimated laboratory costs. These are calculated based upon current annual costs and requested in each year of this proposed project. Costs include RNA extraction ($12,000), PCR reagents and sequencing ($36,000) and gloves, chemicals, plasticware, and other miscellaneous supplies ($12,000).

Annual Meeting
Conservation Medicine Malaysia and partner institutions in Sabah, Sarawak, and Peninsular Malaysia will host annual meetings of PI, Co-Investigators and other collaborators. University facilities fees are estimated at $3,666.00 and detailed as follows: $1,500.00 for room rental costs, AV, and University support; University Dining will charge a fixed fee for meals for 20 attendees at $36/day for the three days of the meeting ($36 x 3 days x 20 people = $2,166.00).

H. Indirect Costs (8%)
Conservation Medicine Malaysia requests reimbursement of the *de minimus* indirect cost recovery rate for foreign organizations of 8% of modified or allowable direct costs.

RESEARCH & RELATED BUDGET - Cumulative Budget

	Totals ($)	
Section A, Senior/Key Person		271,890.00
Section B, Other Personnel		253,430.65
Total Number Other Personnel	30	
Total Salary, Wages and Fringe Benefits (A+B)		525,320.65
Section C, Equipment		0 00
Section D, Travel		198,037 50
1. Domestic	174,000.00	
2. Foreign	24,037 50	
Section E, Participant/Trainee Support Costs		0 00
1. Tuition/Fees/Health Insurance	0.00	
2. Stipends	0.00	
3 Travel	0.00	
4. Subsistence	0.00	
5. Other	0.00	
6. Number of Participants/Trainees	0	
Section F, Other Direct Costs		318,300 00
1. Materials and Supplies	318,300.00	
2. Publication Costs	0.00	
3. Consultant Services	0.00	
4. ADP/Computer Services	0 00	
5. Subawards/Consortium/Contractual Costs	0 00	
6. Equipment or Facility Rental/User Fees	0.00	
7. Alterations and Renovations	0.00	
8. Other 1	0 00	
9. Other 2	0.00	
10. Other 3	0 00	
Section G, Direct Costs (A thru F)		1,041,658 15
Section H, Indirect Costs		83,332.65
Section I, Total Direct and Indirect Costs (G + H)		1,124,990.80
Section J, Fee		0 00
Section K, Total Costs and Fee (I + J)		1,124,990 80

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA AI-19-028 Received Date 2019-06-28T16:02 40.000-04:00

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 1

ORGANIZATIONAL DUNS*: 5861922530000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: Duke NUS Medical School

Start Date*: 03-01-2020 **End Date*:** 02-28-2021 **Budget Period:** 1

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	Linfa		Wang		Co-Investigator		[redacted]					(b) (4), (b) (6)
2 .	Dr.	Danielle		Anderson		Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name:

Total Senior/Key Person (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
1	Post Doctoral Associates	[redacted]					(b) (4), (b) (6)
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)

Total Salary, Wages and Fringe Benefits (A+B) [redacted]

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 1

ORGANIZATIONAL DUNS*: 5861922530000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Duke NUS Medical School

Start Date*: 03-01-2020 **End Date*:** 02-28-2021 **Budget Period:** 1

C. Equipment Description		
List items and dollar amount for each item exceeding $5,000		
Equipment Item		**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file		
	Total Equipment	**0.00**
Additional Equipment: File Name:		

D. Travel		Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)		
2. Foreign Travel Costs		5,000.00
	Total Travel Cost	**5,000.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 1

ORGANIZATIONAL DUNS*: 5861922530000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Duke NUS Medical School

Start Date*: 03-01-2020 **End Date*:** 02-28-2021 **Budget Period:** 1

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	12,500.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
8 . Scientific services	14,500.00
Total Other Direct Costs	**27,000.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**100,000.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . Facilities and administrative costs	8.0		8,000.00
		Total Indirect Costs	**8,000.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**108,000.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	108,000.00

L. Budget Justification*	File Name: DUKE NUS EIDRC 2019 Subawardbudget Justification_v01-LW DEA_FINAL.pdf (Only attach one file)

RESEARCH & RELATED Budget (F K) (Funds Requested)

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 2

ORGANIZATIONAL DUNS*: 5861922530000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: Duke NUS Medical School

Start Date*: 03-01-2021 **End Date*:** 02-28-2022 **Budget Period:** 2

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	Linfa		Wang		Co-Investigator							(b) (4), (b) (6)
2 .	Dr.	Danielle		Anderson		Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name: **Total Senior/Key Person** (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
1	Post Doctoral Associates						(b) (4), (b) (6)
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)
						Total Salary, Wages and Fringe Benefits (A+B)	

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 2

ORGANIZATIONAL DUNS*: 5861922530000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Duke NUS Medical School

Start Date*: 03-01-2021 **End Date*:** 02-28-2022 **Budget Period:** 2

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**
Additional Equipment: File Name:	

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	
2. Foreign Travel Costs	5,000.00
Total Travel Cost	**5,000.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date: 2019-06-28T16:02.40 000-04.00

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 2

ORGANIZATIONAL DUNS*: 5861922530000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Duke NUS Medical School

Start Date*: 03-01-2021 **End Date*:** 02-28-2022 **Budget Period:** 2

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	11,410.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
8 . Scientific services	14,500.00
Total Other Direct Costs	**25,910.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**100,000.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . Facilities and Administrative costs	8.0		8,000.00
		Total Indirect Costs	**8,000.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**108,000.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	108,000.00

L. Budget Justification*	File Name: DUKE NUS EIDRC 2019 Subawardbudget Justification_v01-LW DEA_FINAL.pdf (Only attach one file)

RESEARCH & RELATED Budget (F K) (Funds Requested)

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 3

ORGANIZATIONAL DUNS*: 5861922530000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: Duke NUS Medical School

Start Date*: 03-01-2022 **End Date*:** 02-28-2023 **Budget Period:** 3

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	Linfa		Wang		Co-Investigator		[redacted]					(b) (4), (b) (6)
2 .	Dr.	Danielle		Anderson		Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name: **Total Senior/Key Person** (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
1	Post Doctoral Associates	[redacted]					(b) (4), (b) (6)
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)
						Total Salary, Wages and Fringe Benefits (A+B)	

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 3

ORGANIZATIONAL DUNS*: 5861922530000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Duke NUS Medical School

Start Date*: 03-01-2022 **End Date*:** 02-28-2023 **Budget Period:** 3

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**
Additional Equipment: File Name:	

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	
2. Foreign Travel Costs	5,000.00
Total Travel Cost	**5,000.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date: 2019-06-28T16:02.40 000-04.00

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 3

ORGANIZATIONAL DUNS*: 5861922530000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Duke NUS Medical School

Start Date*: 03-01-2022 **End Date*:** 02-28-2023 **Budget Period:** 3

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	10,329.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
8 . Scientific services	14,500.00
Total Other Direct Costs	**24,829.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**100,000.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . Facilities and Administrative costs	8.0		8,000.00
		Total Indirect Costs	**8,000.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**108,000.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	108,000.00

L. Budget Justification*	File Name: DUKE NUS EIDRC 2019 Subawardbudget Justification_v01-LW DEA_FINAL.pdf (Only attach one file)

RESEARCH & RELATED Budget (F K) (Funds Requested)

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 4

ORGANIZATIONAL DUNS*: 5861922530000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: Duke NUS Medical School

Start Date*: 03-01-2023 **End Date*:** 02-29-2024 **Budget Period:** 4

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	Linfa		Wang		Co-Investigator							(b) (4), (b) (6)
2 .	Dr.	Danielle		Anderson		Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name: **Total Senior/Key Person** (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
1	Post Doctoral Associates						(b) (4), (b) (6)
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)
						Total Salary, Wages and Fringe Benefits (A+B)	

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 4

ORGANIZATIONAL DUNS*: 5861922530000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Duke NUS Medical School

Start Date*: 03-01-2023 **End Date*:** 02-29-2024 **Budget Period:** 4

C. Equipment Description		
List items and dollar amount for each item exceeding $5,000		
Equipment Item		**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file		
	Total Equipment	**0.00**
Additional Equipment: File Name:		

D. Travel		Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)		
2. Foreign Travel Costs		5,000.00
	Total Travel Cost	**5,000.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget (C-E) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date: 2019-06-28T16:02.40 000-04.00

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 4

ORGANIZATIONAL DUNS*: 5861922530000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Duke NUS Medical School

Start Date*: 03-01-2023 **End Date*:** 02-29-2024 **Budget Period:** 4

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	9,236.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
8 . Scientific services	14,500.00
Total Other Direct Costs	**23,736.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**100,000.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . Facilities and administrative costs	8.0		8,000.00
		Total Indirect Costs	**8,000.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**108,000.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	108,000.00

L. Budget Justification*	File Name: DUKE NUS EIDRC 2019 Subawardbudget Justification_v01-LW DEA_FINAL.pdf (Only attach one file)

RESEARCH & RELATED Budget (F K) (Funds Requested)

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 5

ORGANIZATIONAL DUNS*: 5861922530000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: Duke NUS Medical School

Start Date*: 03-01-2024 **End Date*:** 02-28-2025 **Budget Period:** 5

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	Linfa		Wang		Co-Investigator							(b) (4), (b) (6)
2 .	Dr.	Danielle		Anderson		Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name:

Total Senior/Key Person (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
1	Post Doctoral Associates						(b) (4), (b) (6)
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)

Total Salary, Wages and Fringe Benefits (A+B) (b) (4), (b) (6)

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 5

ORGANIZATIONAL DUNS*: 5861922530000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Duke NUS Medical School

Start Date*: 03-01-2024 **End Date*:** 02-28-2025 **Budget Period:** 5

C. Equipment Description		
List items and dollar amount for each item exceeding $5,000		
Equipment Item		**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file		
	Total Equipment	**0.00**
Additional Equipment: File Name:		

D. Travel		Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)		
2. Foreign Travel Costs		5,000.00
	Total Travel Cost	**5,000.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date: 2019-06-28T16:02.40 000-04.00

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 5

ORGANIZATIONAL DUNS*: 5861922530000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: Duke NUS Medical School

Start Date*: 03-01-2024 **End Date*:** 02-28-2025 **Budget Period:** 5

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	8,141.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
8 . Scientific services	14,500.00
Total Other Direct Costs	**22,641.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**100,000.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . Facilities and administrative costs	8.0		8,000.00
		Total Indirect Costs	**8,000.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**108,000.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	108,000.00

L. Budget Justification*	File Name: DUKE NUS EIDRC 2019 Subawardbudget Justification_v01-LW DEA_FINAL.pdf (Only attach one file)

RESEARCH & RELATED Budget (F K) (Funds Requested)

DUKE-NATIONAL SINGAPORE UNIVERSITY BUDGET JUSTIFICATION, SUBAWARD

A. Senior/Key Personnel

Linfa Wang, PhD Co-Investigator will commit [redacted] (b) (4), (b) (6) to this project. Dr. Wang is a well-known expert in cross species transmission and pathogenesis of emerging bat viruses, including coronaviruses and henipaviruses and has been an international leader of the field for over 25 years. Dr. Wang will lead and supervise the Duke-NUS team to develop multiplex diagnostic platforms for testing of various field samples generated in this project.

Danielle Anderson, PhD Co-Investigator will commit [redacted] (b) (4), (b) (6) to this project. Dr. Anderson has over 15 years of research studying RNA virus replication and is the scientific director of the Duke-NUS ABSL3 facility. Dr Anderson will co-lead the Duke-NUS team with focus on international liaison and experiments involving animal samples.

B. Other Personnel

A research fellow will be hired and he/she will commit [redacted] (b) (4), (b) (6) to this project. The research fellow will be a skilled virologist/immunologist/molecular biologist and will develop the molecular and serology platforms to test the samples collected in this project. The RF will also be mainly responsible for data analysis, data presentation with the extended team of this large project and play a key role in manuscript preparation. In addition, the RF may also be required to supervise junior technical staff or students should the need arises.

Fringe Benefits.

Fringe benefits are included in the direct cost requested for each personnel. The rate is inclusive of employee benefits according to the Duke-NUS Medical School's HR policy. This includes 17% retirement for Singapore citizens, $855 (S$1,200) housing allowance for foreigners and $1,200 for health insurance.

C. Equipment

No equipment over $5,000 will be purchased.

D. Travel

Domestic travel. Not requested.

Foreign Travel. 1 trip for Co-Investigator(s) and additional personnel (1) to EHA in NYC (3-to-4-days) and NIH in DC (2-days) is estimated at $5,000.00 USD per person per year.

E. Participant/Trainee Support Costs

No participant/trainee support costs are requested.

F. Other Direct Costs

Materials and Supplies. A variety of culture media and serum ($3,000), DNA/RNA extraction and purification kits ($5,000), PCR reagents ($2000) an assortment of miscellaneous supplies (e.g., gloves, chemicals, plastcware, etc.)($2000) are needed during the course of the program to develop the serology assays and test the samples.

Other. Scientific services. Funds are requested to cover the costs of next-generation sequencing of the samples.

H. Indirect Costs (8%)

The facilities and administrative rate is at 8% of the total direct costs.

RESEARCH & RELATED BUDGET - Cumulative Budget

	Totals ($)	
Section A, Senior/Key Person		15,884.00
Section B, Other Personnel		335,000.00
Total Number Other Personnel	5	
Total Salary, Wages and Fringe Benefits (A+B)		350,884.00
Section C, Equipment		0 00
Section D, Travel		25,000 00
1. Domestic	0.00	
2. Foreign	25,000 00	
Section E, Participant/Trainee Support Costs		0 00
1. Tuition/Fees/Health Insurance	0.00	
2. Stipends	0.00	
3 Travel	0.00	
4. Subsistence	0.00	
5. Other	0.00	
6. Number of Participants/Trainees	0	
Section F, Other Direct Costs		124,116.00
1. Materials and Supplies	51,616.00	
2. Publication Costs	0.00	
3. Consultant Services	0.00	
4. ADP/Computer Services	0 00	
5. Subawards/Consortium/Contractual Costs	0 00	
6. Equipment or Facility Rental/User Fees	0.00	
7. Alterations and Renovations	0.00	
8. Other 1	72,500 00	
9. Other 2	0.00	
10. Other 3	0 00	
Section G, Direct Costs (A thru F)		500,000 00
Section H, Indirect Costs		40,000 00
Section I, Total Direct and Indirect Costs (G + H)		540,000.00
Section J, Fee		0 00
Section K, Total Costs and Fee (I + J)		540,000 00

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA AI-19-028 Received Date 2019-06-28T16:02 40.000-04:00

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 1

ORGANIZATIONAL DUNS*: 1446765660000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: The Henry M. Jackson Fdn. for the Adv'mt. of Mil. Med., Inc.

Start Date*: 03-01-2020 **End Date*:** 02-28-2021 **Budget Period:** 1

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1.		Christopher		Broder	PhD	Co-Investigator							(b) (4), (b) (6)
2.		Eric		Laing	PhD	Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name: **Total Senior/Key Person** (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Research Assistant						(b) (4), (b) (6)
1	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)
						Total Salary, Wages and Fringe Benefits (A+B)	

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 1

ORGANIZATIONAL DUNS*: 1446765660000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: The Henry M. Jackson Fdn. for the Adv'mt. of Mil. Med., Inc.

Start Date*: 03-01-2020 **End Date*:** 02-28-2021 **Budget Period:** 1

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**
Additional Equipment: File Name:	

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	3,500.00
2. Foreign Travel Costs	18,500.00
Total Travel Cost	**22,000.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget (C-E) (Funds Requested)

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 1

ORGANIZATIONAL DUNS*: 1446765660000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: The Henry M. Jackson Fdn. for the Adv'mt. of Mil. Med., Inc.

Start Date*: 03-01-2020 **End Date*:** 02-28-2021 **Budget Period:** 1

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	41,439.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
8 . AKTA Service Contract	4,500.00
Total Other Direct Costs	**45,939.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**74,999.99**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . USU Indirect Cost Rate FY20	30.45	74,999.99	22,837.50
2 . HJF Companywide G&A FY20	16 9	97,837.48	16,534.53
		Total Indirect Costs	**39,372.03**

Cognizant Federal Agency (Agency Name, POC Name, and POC Phone Number): USAMRAA, Jennifer C. Jackson, 301-619-2054

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**114,372.02**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	114,372.02

L. Budget Justification*	File Name. Budget_Justification_Broder_SE_Asia_(1).pdf (Only attach one file.)

RESEARCH & RELATED Budget (F-K) (Funds Requested)

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 2

ORGANIZATIONAL DUNS*: 1446765660000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: The Henry M. Jackson Fdn. for the Adv'mt. of Mil. Med., Inc.

Start Date*: 03-01-2021 **End Date*:** 02-28-2022 **Budget Period:** 2

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1.		Christopher		Broder	PhD	Co-Investigator							(b) (4), (b) (6)
2.		Eric		Laing	PhD	Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name: **Total Senior/Key Person** (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Research Assistant						(b) (4), (b) (6)
1	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)
						Total Salary, Wages and Fringe Benefits (A+B)	

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 2

ORGANIZATIONAL DUNS*: 1446765660000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: The Henry M. Jackson Fdn. for the Adv'mt. of Mil. Med., Inc.

Start Date*: 03-01-2021 **End Date*:** 02 28-2022 **Budget Period:** 2

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**

Additional Equipment: File Name:

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	3,500.00
2. Foreign Travel Costs	18,500.00
Total Travel Cost	**22,000.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget (C-E) (Funds Requested)

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 2

ORGANIZATIONAL DUNS*: 1446765660000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: The Henry M. Jackson Fdn. for the Adv'mt. of Mil. Med., Inc.

Start Date*: 03-01-2021 **End Date*:** 02-28-2022 **Budget Period:** 2

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	41,439.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
8 . AKTA Service Contract	4,500.00
Total Other Direct Costs	**45,939.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**74,999.99**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . USU Indirect Cost Rate FY20	30.45	74,999.99	22,837.50
2 . HJF Companywide G&A FY20	16 9	97,837.48	16,534.53
		Total Indirect Costs	**39,372.03**

Cognizant Federal Agency (Agency Name, POC Name, and POC Phone Number): USAMRAA, Jennifer C. Jackson, 301-619-2054

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**114,372.02**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	114,372.02

L. Budget Justification*	File Name. Budget_Justification_Broder_SE_Asia_(1).pdf (Only attach one file.)

RESEARCH & RELATED Budget (F-K) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date: 2019-06-28T16:02:40 000-04:00

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 3

ORGANIZATIONAL DUNS*: 1446765660000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: The Henry M. Jackson Fdn. for the Adv'mt. of Mil. Med., Inc.

Start Date*: 03-01-2022 **End Date*:** 02-28-2023 **Budget Period:** 3

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1.		Christopher		Broder	PhD	Co-Investigator							(b) (4), (b) (6)
2.		Eric		Laing	PhD	Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name: **Total Senior/Key Person** (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Research Assistant						(b) (4), (b) (6)
1	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)
						Total Salary, Wages and Fringe Benefits (A+B)	

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 3

ORGANIZATIONAL DUNS*: 1446765660000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: The Henry M. Jackson Fdn. for the Adv'mt. of Mil. Med., Inc.

Start Date*: 03-01-2022 **End Date*:** 02-28-2023 **Budget Period:** 3

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**
Additional Equipment: File Name:	

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	3,500.00
2. Foreign Travel Costs	18,500.00
Total Travel Cost	**22,000.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget (C-E) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA AI-19-028 . Received Date: 2019-06-28T16:02.40 000-04.00

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 3

ORGANIZATIONAL DUNS*: 1446765660000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: The Henry M. Jackson Fdn. for the Adv'mt. of Mil. Med., Inc.

Start Date*: 03-01-2022 **End Date*:** 02-28-2023 **Budget Period:** 3

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	41,439.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
8 . AKTA Service Contract	4,500.00
Total Other Direct Costs	**45,939.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**74,999.99**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . USU Indirect Cost Rate FY20	30.45	74,999.99	22,837.50
2 . HJF Companywide G&A FY20	16 9	97,837.48	16,534.53
		Total Indirect Costs	**39,372.03**

Cognizant Federal Agency (Agency Name, POC Name, and POC Phone Number): USAMRAA, Jennifer C. Jackson, 301-619-2054

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**114,372.02**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	114,372.02

L. Budget Justification*	File Name. Budget_Justification_Broder_SE_Asia_(1).pdf (Only attach one file.)

RESEARCH & RELATED Budget (F-K) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date: 2019-06-28T16:02:40 000-04:00

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 4

ORGANIZATIONAL DUNS*: 1446765660000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: The Henry M. Jackson Fdn. for the Adv'mt. of Mil. Med., Inc.

Start Date*: 03-01-2023 **End Date*:** 02-29-2024 **Budget Period:** 4

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1.		Christopher		Broder	PhD	Co-Investigator							(b) (4), (b) (6)
2.		Eric		Laing	PhD	Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name: **Total Senior/Key Person** (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Research Assistant						(b) (4), (b) (6)
1	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)
						Total Salary, Wages and Fringe Benefits (A+B)	

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 4

ORGANIZATIONAL DUNS*: 1446765660000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: The Henry M. Jackson Fdn. for the Adv'mt. of Mil. Med., Inc.

Start Date*: 03-01-2023 **End Date*:** 02-29-2024 **Budget Period:** 4

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**

Additional Equipment: File Name:

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	3,500.00
2. Foreign Travel Costs	18,500.00
Total Travel Cost	**22,000.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget (C-E) (Funds Requested)

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 4

ORGANIZATIONAL DUNS*: 1446765660000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: The Henry M. Jackson Fdn. for the Adv'mt. of Mil. Med., Inc.

Start Date*: 03-01-2023 **End Date*:** 02-29-2024 **Budget Period:** 4

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	41,439.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
8 . AKTA Service Contract	4,500.00
Total Other Direct Costs	**45,939.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**74,999.99**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . USU Indirect Cost Rate FY20	30.45	74,999.99	22,837.50
2 . HJF Companywide G&A FY20	16 9	97,837.48	16,534.53
		Total Indirect Costs	**39,372.03**

Cognizant Federal Agency (Agency Name, POC Name, and POC Phone Number): USAMRAA, Jennifer C. Jackson, 301-619-2054

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**114,372.02**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	114,372.02

L. Budget Justification*	File Name. Budget_Justification_Broder_SE_Asia_(1).pdf (Only attach one file.)

RESEARCH & RELATED Budget (F-K) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date: 2019-06-28T16:02:40 000-04:00

OMB Number: 4040-0001
Expiration Date: 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 5

ORGANIZATIONAL DUNS*: 1446765660000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: The Henry M. Jackson Fdn. for the Adv'mt. of Mil. Med., Inc.

Start Date*: 03-01-2024 **End Date*:** 02-28-2025 **Budget Period:** 5

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1.		Christopher		Broder	PhD	Co-Investigator		[redacted]					(b) (4), (b) (6)
2.		Eric		Laing	PhD	Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name: **Total Senior/Key Person** (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Research Assistant	[redacted]					(b) (4), (b) (6)
1	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)
						Total Salary, Wages and Fringe Benefits (A+B)	

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date: 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 5

ORGANIZATIONAL DUNS*: 1446765660000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: The Henry M. Jackson Fdn. for the Adv'mt. of Mil. Med., Inc.

Start Date*: 03-01-2024 **End Date*:** 02-28-2025 **Budget Period:** 5

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**
Additional Equipment: File Name:	

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	3,500.00
2. Foreign Travel Costs	18,500.00
Total Travel Cost	**22,000.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget (C-E) (Funds Requested)

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 5

ORGANIZATIONAL DUNS*: 1446765660000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: The Henry M. Jackson Fdn. for the Adv'mt. of Mil. Med., Inc.

Start Date*: 03-01-2024 **End Date*:** 02-28-2025 **Budget Period:** 5

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	41,439.00
2. Publication Costs	
3. Consultant Services	
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
8 . AKTA Service Contract	4,500.00
Total Other Direct Costs	**45,939.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**74,999.99**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . USU Indirect Cost Rate FY20	30.45	74,999.99	22,837.50
2 . HJF Companywide G&A FY20	16 9	97,837.48	16,534.53
		Total Indirect Costs	**39,372.03**

Cognizant Federal Agency (Agency Name, POC Name, and POC Phone Number): USAMRAA, Jennifer C. Jackson, 301-619-2054

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**114,372.02**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	114,372.02

L. Budget Justification*	File Name. Budget_Justification_Broder_SE_Asia_(1).pdf (Only attach one file.)

RESEARCH & RELATED Budget (F-K) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date: 2019-06-28T16:02:40 000-04:00

HENRY M JACKSON FOUNDATION BUDGET JUSTIFICATION

The Henry M Jackson Foundation for the Advancement of Military Medicine Inc (HJF) in partnership with the Uniformed Services University of the Health Sciences (USUHS) will manage this proposal, if awarded.

A. Key Personnel

Christopher Broder, Ph.D., Principal Investigator [redacted] (b) (4), (b) (6) for Years 1-5). Dr. Broder will be responsible for the overall coordination of this project. He will provide necessary instruction to the Co-Investigator and assist with collaboration with the prime. Dr. Broder is a government employee and no salary support is requested.

Eric Laing, Ph.D., Co-Investigator [redacted] (b) (4), (b) (6) for Years 1-5). Dr. Laing will be responsible for conducting training on site, and for the Luminex training modules to be conducted at partner institutes. He will coordinate efforts in Bethesda, MD and Southeast Asian regional partners and provide the necessary concepts and practice of viral glycoprotein antigen preparation for uses in and validation of Luminex and other serological assays such as ELISA. Dr Laing will co-supervise serological work performed and participate in data analysis. Dr. Laing is a government employee and no salary support is requested.

B. Other Personnel

TBD, Research Assistant I [redacted] (b) (4), (b) (6) for Years 1-5). This individual will provide partial laboratory support for this project. They will be responsible for producing protein antigens, ordering beads, supplies, preparing shipments and other laboratory support as instructed by the senior staff. This person will be an employee of the Henry M. Jackson Foundation and salary support is requested.

C. Equipment

No equipment over $5,000 will be purchased.

D. Travel

Domestic Travel. Domestic travel will be used for Co-Investigator to attend annual NIH meetings as well as to attend conferences and meetings to learn new techniques, disseminate research data and professional advancement. Depending on the location, 1-2 lab members will attend an annual conference such as The American Society of Virology. The government GSA rates will be used for all domestic travel. This will be for all years.

Year 1	Year 2	Year 3	Year 4	Year 5
$3,500	$3,500	$3,500	$3,500	$3,500

Foreign Travel. Foreign travel support for will be used to travel to partner institutes in Southeast Asia to provide the serological assay training and data interpretation/analysis. We anticipate 1-2 members of the lab to provide training, and oversight of serological screening. The government GSA rates will be used for all international travel. This will be for all years.

Year 1	Year 2	Year 3	Year 4	Year 5
$18,500	$18,500	$18,500	$18,500	$18,500

F. Other Direct Costs

Materials and Supplies. Based on current prices, the following supplies will be needed to support this project: 20 protein production, magnetic beads, cell culture materials, affinity matrices and control IgG materials. There is a fluctuation in between years due to using stored samples versus gathering other samples.

Year 1	Year 2	Year 3	Year 4	Year 5
$41,439	$41,439	$41,439	$41,439	$41,439

Service agreement
We request support of $4,500 for a maintenance agreement for the ÄKTA full service contract. This ÄKTA pure protein purification system is critical to meeting the specific aims of this research. This is for all years.

H. HJF FY20 Fringe Benefit and In Direct Cost Rates

The HJF indirect cost is calculated based on the value-added cost base overhead rates. The IDC rate applied is 30.45% USU on-site overhead rate for all allowable direct costs; an additional 16.90% HJF Companywide G&A rate is applied on the total direct cost less subaward plus the USU on-site overhead rate.

The HJF fringe benefit rate is 30.75% for Tier 1 employees and 4.87% for Tier 2 employees. The HJF employees on this project are all Tier 1 employees.

The above fringe benefits and indirect cost provisional billing rates for FY 2020 were approved by the U.S. Army Medical Research Acquisition Activity on May 7, 2019.

RESEARCH & RELATED BUDGET - Cumulative Budget

	Totals ($)	
Section A, Senior/Key Person		0.00
Section B, Other Personnel		35,304.95
Total Number Other Personnel	5	
Total Salary, Wages and Fringe Benefits (A+B)		35,304.95
Section C, Equipment		0 00
Section D, Travel		110,000 00
1. Domestic	17,500.00	
2. Foreign	92,500 00	
Section E, Participant/Trainee Support Costs		0 00
1. Tuition/Fees/Health Insurance	0.00	
2. Stipends	0.00	
3 Travel	0.00	
4. Subsistence	0.00	
5. Other	0.00	
6. Number of Participants/Trainees	0	
Section F, Other Direct Costs		229,695.00
1. Materials and Supplies	207,195.00	
2. Publication Costs	0.00	
3. Consultant Services	0.00	
4. ADP/Computer Services	0 00	
5. Subawards/Consortium/Contractual Costs	0 00	
6. Equipment or Facility Rental/User Fees	0.00	
7. Alterations and Renovations	0.00	
8. Other 1	22,500 00	
9. Other 2	0.00	
10. Other 3	0 00	
Section G, Direct Costs (A thru F)		374,999 95
Section H, Indirect Costs		196,860 15
Section I, Total Direct and Indirect Costs (G + H)		571,860.10
Section J, Fee		0 00
Section K, Total Costs and Fee (I + J)		571,860 10

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA AI-19-028 Received Date 2019-06-28T16:02 40.000-04:00

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 1

ORGANIZATIONAL DUNS*: 6081952770000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: The University of North Carolina at Chapel Hill

Start Date*: 03-01-2020 **End Date*:** 02-28-2021 **Budget Period:** 1

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	Ralph		Baric		Co-Investigator							(b) (4), (b) (6)
2 .	Dr.	Amy		Sims		Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name: **Total Senior/Key Person** (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Research Assistant						(b) (4), (b) (6)
1	Lab Technician						
2	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)
						Total Salary, Wages and Fringe Benefits (A+B)	

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date: 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 1

ORGANIZATIONAL DUNS*: 6081952770000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: The University of North Carolina at Chapel Hill

Start Date*: 03-01-2020 **End Date*:** 02-28-2021 **Budget Period:** 1

C. Equipment Description		
List items and dollar amount for each item exceeding $5,000		
Equipment Item		**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file		
	Total Equipment	**0.00**
Additional Equipment: File Name:		

D. Travel		Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)		1,000.00
2. Foreign Travel Costs		
	Total Travel Cost	**1,000.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 1

ORGANIZATIONAL DUNS*: 6081952770000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: The University of North Carolina at Chapel Hill

Start Date*: 03-01-2020 **End Date*:** 02-28-2021 **Budget Period:** 1

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	30,585 00
2. Publication Costs	500.00
3. Consultant Services	
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
8 . Animal Housing	1,000.00
Total Other Direct Costs	**32,085.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**125,000.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . UNC Indirect Cost Rate	55.5	125,000.00	69,375.00
		Total Indirect Costs	**69,375.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**194,375.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	194,375.00

L. Budget Justification*	File Name:
	UNC Budget Justification_FINAL.pdf
	(Only attach one file.)

RESEARCH & RELATED Budget (F K) (Funds Requested)

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 2

ORGANIZATIONAL DUNS*: 6081952770000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: The University of North Carolina at Chapel Hill

Start Date*: 03-01-2021 **End Date*:** 02-28-2022 **Budget Period:** 2

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1	Dr.	Ralph		Baric		Co-Investigator		[redacted]					(b) (4), (b) (6)
2	Dr.	Amy		Sims		Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name: **Total Senior/Key Person** (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Research Assistant	[redacted]					(b) (4), (b) (6)
1	Lab Technician						
2	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)

Total Salary, Wages and Fringe Benefits (A+B)

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date: 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 2

ORGANIZATIONAL DUNS*: 6081952770000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: The University of North Carolina at Chapel Hill

Start Date*: 03-01-2021 **End Date*:** 02-28-2022 **Budget Period:** 2

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**
Additional Equipment: File Name:	

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	1,000.00
2. Foreign Travel Costs	
Total Travel Cost	**1,000.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 2

ORGANIZATIONAL DUNS*: 6081952770000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: The University of North Carolina at Chapel Hill

Start Date*: 03-01-2021 **End Date*:** 02-28-2022 **Budget Period:** 2

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	30,585 00
2. Publication Costs	500.00
3. Consultant Services	
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
8 . Animal Housing	1,000.00
Total Other Direct Costs	**32,085.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**125,000.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . UNC Indirect Cost Rate	55.5	125,000.00	69,375.00
		Total Indirect Costs	**69,375.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**194,375.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	194,375.00

L. Budget Justification*	File Name:
	UNC Budget Justification_FINAL.pdf
	(Only attach one file.)

RESEARCH & RELATED Budget (F K) (Funds Requested)

OMB Number: 4040-0001
Expiration Date: 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 3

ORGANIZATIONAL DUNS*: 6081952770000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: The University of North Carolina at Chapel Hill

Start Date*: 03-01-2022 **End Date*:** 02-28-2023 **Budget Period:** 3

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1	Dr.	Ralph		Baric		Co-Investigator							(b) (4), (b) (6)
2	Dr.	Amy		Sims		Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name: **Total Senior/Key Person** (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Research Assistant						(b) (4), (b) (6)
1	Lab Technician						
2	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)

Total Salary, Wages and Fringe Benefits (A+B)

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date: 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 3

ORGANIZATIONAL DUNS*: 6081952770000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: The University of North Carolina at Chapel Hill

Start Date*: 03-01-2022 **End Date*:** 02-28-2023 **Budget Period:** 3

C. Equipment Description		
List items and dollar amount for each item exceeding $5,000		
Equipment Item		**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file		
	Total Equipment	**0.00**
Additional Equipment: File Name:		

D. Travel		Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)		1,000.00
2. Foreign Travel Costs		
	Total Travel Cost	**1,000.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 3

ORGANIZATIONAL DUNS*: 6081952770000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: The University of North Carolina at Chapel Hill

Start Date*: 03-01-2022 **End Date*:** 02-28-2023 **Budget Period:** 3

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	30,585 00
2. Publication Costs	500.00
3. Consultant Services	
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
8 . Animal Housing	1,000.00
Total Other Direct Costs	**32,085.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**125,000.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . UNC Indirect Cost Rate	55.5	125,000.00	69,375.00
		Total Indirect Costs	**69,375.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**194,375.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	194,375.00

L. Budget Justification*	File Name:
	UNC Budget Justification_FINAL.pdf
	(Only attach one file.)

RESEARCH & RELATED Budget (F K) (Funds Requested)

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 4

ORGANIZATIONAL DUNS*: 6081952770000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: The University of North Carolina at Chapel Hill

Start Date*: 03-01-2023 **End Date*:** 02-29-2024 **Budget Period:** 4

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	Ralph		Baric		Co-Investigator							(b) (4), (b) (6)
2 .	Dr.	Amy		Sims		Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name: **Total Senior/Key Person** (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Research Assistant						(b) (4), (b) (6)
1	Lab Technician						
2	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)
						Total Salary, Wages and Fringe Benefits (A+B)	

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date: 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 4

ORGANIZATIONAL DUNS*: 6081952770000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: The University of North Carolina at Chapel Hill

Start Date*: 03-01-2023 **End Date*:** 02-29-2024 **Budget Period:** 4

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**
Additional Equipment: File Name:	

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	1,000.00
2. Foreign Travel Costs	
Total Travel Cost	**1,000.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget (C-E) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA AI-19-028 . Received Date: 2019-06-28T16:02.40 000-04.00

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 4

ORGANIZATIONAL DUNS*: 6081952770000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: The University of North Carolina at Chapel Hill

Start Date*: 03-01-2023 **End Date*:** 02-29-2024 **Budget Period:** 4

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	30,585 00
2. Publication Costs	500.00
3. Consultant Services	
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
8 . Animal Housing	1,000.00
Total Other Direct Costs	**32,085.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**125,000.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . UNC Indirect Cost Rate	55.5	125,000.00	69,375.00
		Total Indirect Costs	**69,375.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**194,375.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	194,375.00

L. Budget Justification*	File Name:
	UNC Budget Justification_FINAL.pdf
	(Only attach one file.)

RESEARCH & RELATED Budget (F K) (Funds Requested)

OMB Number 4040-0001
Expiration Date 10/31/2019

RESEARCH & RELATED BUDGET - SECTION A & B, Budget Period 5

ORGANIZATIONAL DUNS*: 6081952770000

Budget Type*: ○ Project ● Subaward/Consortium

Enter name of Organization: The University of North Carolina at Chapel Hill

Start Date*: 03-01-2024 **End Date*:** 02-28-2025 **Budget Period:** 5

A. Senior/Key Person

	Prefix	First Name*	Middle Name	Last Name*	Suffix	Project Role*	Base Salary ($)	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits ($)*	Funds Requested ($)*
1 .	Dr.	Ralph		Baric		Co-Investigator							(b) (4), (b) (6)
2 .	Dr.	Amy		Sims		Co-Investigator							

Total Funds Requested for all Senior Key Persons in the attached file

Additional Senior Key Persons: File Name: **Total Senior/Key Person** (b) (4), (b) (6)

B. Other Personnel

Number of Personnel*	Project Role*	Calendar Months	Academic Months	Summer Months	Requested Salary ($)*	Fringe Benefits*	Funds Requested ($)*
	Post Doctoral Associates						
	Graduate Students						
	Undergraduate Students						
	Secretarial/Clerical						
1	Research Assistant						(b) (4), (b) (6)
1	Lab Technician						
2	**Total Number Other Personnel**					**Total Other Personnel**	(b) (4), (b) (6)

Total Salary, Wages and Fringe Benefits (A+B)

RESEARCH & RELATED Budget (A-B) (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 . Received Date: 2019-06-28T16:02:40.000-04:00

RESEARCH & RELATED BUDGET - SECTION C, D, & E, Budget Period 5

ORGANIZATIONAL DUNS*: 6081952770000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: The University of North Carolina at Chapel Hill

Start Date*: 03-01-2024 **End Date*:** 02-28-2025 **Budget Period:** 5

C. Equipment Description	
List items and dollar amount for each item exceeding $5,000	
Equipment Item	**Funds Requested ($)***
Total funds requested for all equipment listed in the attached file	
Total Equipment	**0.00**
Additional Equipment: File Name:	

D. Travel	Funds Requested ($)*
1. Domestic Travel Costs (Incl. Canada, Mexico, and U.S. Possessions)	1,000.00
2. Foreign Travel Costs	
Total Travel Cost	**1,000.00**

E. Participant/Trainee Support Costs		Funds Requested ($)*
1. Tuition/Fees/Health Insurance		
2. Stipends		
3. Travel		
4. Subsistence		
5. Other:		
Number of Participants/Trainees	**Total Participant Trainee Support Costs**	**0.00**

RESEARCH & RELATED Budget {C-E} (Funds Requested)

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA AI-19-028 . Received Date: 2019-06-28T16:02.40 000-04.00

RESEARCH & RELATED BUDGET - SECTIONS F-K, Budget Period 5

ORGANIZATIONAL DUNS*: 6081952770000
Budget Type*: ○ Project ● Subaward/Consortium
Organization: The University of North Carolina at Chapel Hill

Start Date*: 03-01-2024 **End Date*:** 02-28-2025 **Budget Period:** 5

F. Other Direct Costs	Funds Requested ($)*
1. Materials and Supplies	30,585 00
2. Publication Costs	500.00
3. Consultant Services	
4. ADP/Computer Services	
5 Subawards/Consortium/Contractual Costs	
6. Equipment or Facility Rental/User Fees	
7. Alterations and Renovations	
8 . Animal Housing	1,000.00
Total Other Direct Costs	**32,085.00**

G. Direct Costs	Funds Requested ($)*
Total Direct Costs (A thru F)	**125,000.00**

H. Indirect Costs

Indirect Cost Type	Indirect Cost Rate (%)	Indirect Cost Base ($)	Funds Requested ($)*
1 . UNC Indirect Cost Rate	55.5	125,000.00	69,375.00
		Total Indirect Costs	**69,375.00**

Cognizant Federal Agency
(Agency Name, POC Name, and POC Phone Number)

I. Total Direct and Indirect Costs	Funds Requested ($)*
Total Direct and Indirect Institutional Costs (G + H)	**194,375.00**

J. Fee	Funds Requested ($)*

K. Total Costs and Fee	Funds Requested ($)*
	194,375.00

L. Budget Justification*	File Name:
	UNC Budget Justification_FINAL.pdf
	(Only attach one file.)

RESEARCH & RELATED Budget (F K) (Funds Requested)

UNIVERSITY OF NORTH CAROLINA AT CHAPEL HILL BUDGET JUSTIFICATION, SUBAWARD

A. Senior/Key Personnel

Ralph Baric, PhD Co-Investigator will commit [redacted] (b) (4), (b) (6) to this project. Dr. Baric is a known expert in coronavirus cross species transmission and pathogenesis and has studied this group of viruses for over 30 years. His group developed the first reverse genetic systems for epidemic and zoonotic SARS-like and coronaviruses and they have studied the ability of these viruses to replicate efficiently in various primary human airway epithelial cell cultures as well as other key primary cell types. His group has also studied the sensitivity of these viruses to be controlled by existing vaccines and therapeutics both in vitro and in vivo. Dr. Baric will lead the studies at the University of North Carolina at Chapel Hill. He will design research strategies, interpret findings and review research outcomes with Dr. Sims and Mr. Yount. At a regular basis, Dr. Baric will report the results of the teams research to Dr. Daszak, and together, they will use this information to identify additional research priorities and design downstream studies. Drs. Daszak and Baric have published together in the past and participated on research project applicat ons. He will work closely with Drs. Sims and Tse and Mr. Yount to prepare timely reports, share research and discuss future research directions with the group.

Amy Sims, PhD Co-Investigator will commit [redacted] (b) (4), (b) (6) to this project. Dr. Sims has over 22 years of research studying coronavirus molecular biology, replication and pathogenesis. She has published over 50 papers including seminal papers on characterizing host response patterns of primary human lung airway epithelial cells and other cell types after infection with SARS-CoV, MERS-CoV, influenza and various SARS-like bat coronaviruses. She is not only well versed in the preparation, cultivation and maintenance of primary human lung cells but also proficient at studying virus infection outcomes, in the presence and absence of antiviral therapeutics. She is also expert in coronavirus reverse genetics. In consultation with Dr. Baric, Dr. Sims will design experiments, perform infections and characterize epidemic and bat SARS-like coronavirus replication in human cells. She will compile data and share these results with the research team. Dr. Sims will also interface and work closely with Mr. Yount, who will assist in these studies, including infections, cell preparations and characterizing virus growth efficiency in these cultures. Dr. Sims has over 15 years of experience working in a BSL3 laboratory and oversees the management of these facilities. She has select agent clearance.

B. Other Personnel

Dr. Herman Tse, Research Associate will comm t [redacted] (b) (4), (b) (6) to this project. He is well trained in molecular biology, synthetic genome design, whole genome sequencing, virus reverse genetics using flaviviruses and coronaviruses as models, virus recovery and characterization in cell in culture. He is completed his training for BSL3 research over the next month and has select agent paperwork under review. He will work closely with Drs. Baric and Sims to design experiments, sequence novel virus isolates, and design and recovery recombinant viruses from molecular clones. He will report his findings to Dr. Baric and prepare reports and presentations regarding his research productivity during the course of the program.

Mr. Boyd Yount, Laboratory Technician will commit [redacted] (b) (4), (b) (6) to this project. Mr. Yount has published over 50 papers on coronaviruses and developed the first reverse genetic platforms for SARS-CoV, MERS-CoV and various SARS-like bat coronaviruses. He has also designed and recovered recombinant clones for flaviviruses, alphaviruses and influenza viruses. He will work closely with Drs. Baric, Sims and Daszak to design and recover select bat SARS-like, MERS-like and other coronaviruses or flaviviruses for downstream studies in the Baric laboratory including characterizing virus phenotypes in primary cells as well as cells expressing various human and animal receptors. He will prepare virus stocks. Mr. Yount w ll work closely with Drs. Baric and Sims to design and implement experiments in the BSL3 laboratory, prepare reports and research outcomes during the course of the program. Mr. Yount has over 15 years of experience in a BSL3 setting and is well versed in all the techniques used in this proposal. He has select agent clearance.

Fringe Benefits

Benefits are for faculty, staff and postdoctoral research associates are calculated as follows: Faculty and Staff – 24.519% Social Security and retirement and $6,104 for health insurance.

C. Supplies ($30,585)
Materials and Supplies. A variety of culture media and serum ($5,000), primary cell procurement ($4000), recombinant DNA supplies, antibodies and enzymes ($4000), synthetic DNAs ($5000) and an assortment of miscellaneous supplies/disposables such as gloves, chemicals, plasticware, etc.($3000) and chemicals ($1585) are needed during the course of the program to recover recombinant viruses and maintain cells in culture, and perform virus growth. Funds are also requested for collaborative cross and standard laboratory mice ($5000) used to develop improved animal models of human disease. In addition, personnel protective equipment (PPE), portal breathing apparati (PAPR), globes and protective clothing are used in the BSL3 setting ($3,000).

D. Travel ($1,000)
Domestic
Travel to EcoHealth Alliance and foreign locations will be covered by funding available through the core grant to EcoHealth Alliance. Dr. Baric requests $1,000 to travel and present research findings at a national or international meeting.

International
No international travel is requested.

E. Other Direct Costs ($1,500)
Other Costs.
Funds are requested for animal housing for the mice costs ($1,000) as well as for publication costs ($500).

F. Indirect Costs
In an agreement with DHHS dated 11/23/2016 the indirect cost rate for The University of North Carolina is 55.5% of modified total direct costs.

RESEARCH & RELATED BUDGET - Cumulative Budget

	Totals ($)	
Section A, Senior/Key Person		248,790.00
Section B, Other Personnel		210,785.00
Total Number Other Personnel	10	
Total Salary, Wages and Fringe Benefits (A+B)		459,575.00
Section C, Equipment		0 00
Section D, Travel		5,000 00
1. Domestic	5,000.00	
2. Foreign	0 00	
Section E, Participant/Trainee Support Costs		0 00
1. Tuition/Fees/Health Insurance	0.00	
2. Stipends	0.00	
3 Travel	0.00	
4. Subsistence	0.00	
5. Other	0.00	
6. Number of Participants/Trainees	0	
Section F, Other Direct Costs		160,425.00
1. Materials and Supplies	152,925.00	
2. Publication Costs	2,500.00	
3. Consultant Services	0.00	
4. ADP/Computer Services	0.00	
5. Subawards/Consortium/Contractual Costs	0 00	
6. Equipment or Facility Rental/User Fees	0.00	
7. Alterations and Renovations	0.00	
8. Other 1	5,000 00	
9. Other 2	0.00	
10. Other 3	0 00	
Section G, Direct Costs (A thru F)		625,000 00
Section H, Indirect Costs		346,875 00
Section I, Total Direct and Indirect Costs (G + H)		971,875 00
Section J, Fee		0 00
Section K, Total Costs and Fee (I + J)		971,875 00

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Total Direct Costs less Consortium F&A

NIH policy (NOT-OD-05-004) allows applicants to exclude consortium/contractual F&A costs when determining if an application falls at or beneath any applicable direct cost limit. When a direct cost limit is specified in an FOA, the following table can be used to determine if your application falls within that limit.

Category	Budget Period 1	Budget Period 2	Budget Period 3	Budget Period 4	Budget Period 5	TOTALS
Total Direct Costs less Consortium F&A	1,050,579	1,050,579	1,050,579	1,050,579	1,050,579	5,252,894

PHS 398 Cover Page Supplement

OMB Number: 0925-0001

Expiration Date: 03/31/2020

1. Vertebrate Animals Section

Are vertebrate animals euthanized? ● Yes ○ No

If "Yes" to euthanasia

Is the method consistent with American Veterinary Medical Association (AVMA) guidelines?

● Yes ○ No

If "No" to AVMA guidelines, describe method and provide scientific justification

2. *Program Income Section

*Is program income anticipated during the periods for which the grant support is requested?

○ Yes ● No

If you checked "yes" above (indicating that program income is anticipated), then use the format below to reflect the amount and source(s) Otherwise, leave this section blank.

*Budget Period	*Anticipated Amount ($)	*Source(s)

PHS 398 Cover Page Supplement

3. Human Embryonic Stem Cells Section

*Does the proposed project involve human embryonic stem cells? ○ Yes ● No

If the proposed project involves human embryonic stem cells, list below the registration number of the specific cell line(s) from the following list http://grants nih.gov/stem cells/registry/current htm. Or, if a specific stem cell line cannot be referenced at this time, check the box indicating that one from the registry will be used:

❑ Specific stem cell line cannot be referenced at this time One from the registry will be used.

Cell Line(s) (Example: 0004):

4. Inventions and Patents Section (Renewal applications)

*Inventions and Patents: ○ Yes ● No

If the answer is "Yes" then please answer the following.

*Previously Reported: ○ Yes ○ No

5. Change of Investigator/Change of Institution Section

❑ Change of Project Director/Principal Investigator

Name of former Project Director/Principal Investigator

Prefix:

*First Name

Middle Name:

*Last Name:

Suffix:

❑ Change of Grantee Institution

*Name of former institution:

Tracking Number: GRANT12891702

Funding Opportunity Number: RFA-AI-19-028 , Received Date: 2019-06-28T16:02 40 000-04 00

PHS 398 Research Plan

OMB Number: 0925-0001
Expiration Date: 03/31/2020

Introduction	
1. Introduction to Application (for Resubmission and Revision applications)	
Research Plan Section	
2. Specific Aims	EIDRC_SE_Asia_Specific_aims_v6_FINAL_FINAL.pdf
3. Research Strategy*	EIDRC_SEA_Research_Strategy_FINAL.pdf
4. Progress Report Publication List	
Other Research Plan Section	
5. Vertebrate Animals	Vertebrate_Animals_Section_FINAL.pdf
6. Select Agent Research	EIDRC_Agent_and_Biohazards_FINAL.pdf
7. Multiple PD/PI Leadership Plan	
8. Consortium/Contractual Arrangements	EIDRC_Contractual_Arrangments_FINAL.pdf
9. Letters of Support	EIDRC_LOS_FINAL.pdf
10. Resource Sharing Plan(s)	EIDRC_Resource_Sharing_Document_FINAL.pdf
11. Authentication of Key Biological and/or Chemical Resources	EID_SEARCH_Authentication_of_Key_Reagents.pdf
Appendix	
12. Appendix	

Tracking Number: GRANT12891702
Funding Opportunity Number: RFA-AI-19-028 Received Date: 2019-06-28T16:02:40.000-04:00

Southeast Asia is one of the world's highest-risk EID hotspots, and the origin of the SARS pandemic, repeated outbreaks of novel influenza strains and the spillover of dangerous viral pathogens such as Nipah virus. It is a wildlife 'megadiversity' region, where a rapidly expanding human population is increasing contact with wildlife, and increasing the risk of zoonotic disease outbreaks. The overarching goal of this proposal is to launch the **E**merging **I**nfectious **D**iseases - **S**outh **E**ast **A**sia **R**esearch **C**ollaboration **H**ub **(EID-SEARCH)** to analyze the diversity of key viral pathogens in wildlife, the frequency and causes of their spillover, and to identify viral etiologies of undiagnosed 'cryptic' outbreaks in people. EID-SEARCH includes leaders in the field of emerging viral pathogens at key US institutions, and in Thailand, Singapore, and the 3 major Malaysian administrative regions, whose collaborative networks span >50 clinics, laboratories, and research institutes across almost all SE Asian countries. This hub, and the network, will act as an early warning system for outbreaks - a way to exchange information, reagents, samples and technology, and a collaborative power-house for translational research. The long-term collaboration among the key personnel, and multidisciplinary skillsets from epidemiology, clinical management, lab analysis, through wildlife biology and data analysis **will act as significant assets when deployed to help counter outbreaks in the region.** The research goals of this EIDRC follow three specific aims:

Specific Aim 1: Identify, characterize and rank spillover risk of high zoonotic potential viruses from wildlife. We will: 1) analyze some of the tens of thousands of archived wildlife samples at our disposal, conduct geographically- and taxonomically-targeted field surveillance in wild mammals (bats, rodents, primates), and use serological & PCR assays to identify known high-profile zoonotic pathogens, or close relatives with potential to infect people; 2) biologically characterize novel viruses that our analyses suggest have high spillover and pandemic potential; and 3) conduct *in vitro* receptor binding assays and cell culture experiments, and *in vivo* animal model infections using humanized mice and the collaborative cross mouse to assess their potential to infect people and cause disease.

Specific Aim 2: Identify evidence and analyze risk factors for viral spillover in high-risk communities using novel serological assays. Assessing the spillover of rare or novel zoonotic agents will require targeted surveillance of high-risk communities and approaches that can deal with the low statistical probability of identifying rare events. To achieve this, we will 1) conduct targeted cross-sectional serological surveys of human communities with extremely high geographic and cultural, occupational and behavioral exposure to wildlife-origin viruses; 2) design and deploy novel serological assays to identify baseline spillover of known or novel CoVs, PMVs and FVs in these populations; and 3) analyze and test hypotheses on the occupational, cultural and other risk factors for spillover (e.g. hunting wildlife).

Specific Aim 3: Identify and characterize viral etiology of 'cryptic' outbreaks in clinical cohorts. Our prior work provides substantial evidence of spillover leading to undiagnosed illness in people in the region. To test if these represent 'cryptic' outbreaks of novel viruses, we will conduct syndromic surveillance at regional clinics for the communities sampled in SA2. We will: 1) enroll and collect biological samples, and detailed survey data on risk factors, from patients presenting with influenza-like illness, severe respiratory illness, encephalitis, and other specific symptoms; 2) conduct molecular and follow-up serological diagnostic assays to test causal links between their syndromes and known and novel viral agents identified in SA1. Where viruses are identified, we will attempt to isolate and characterize them, then use the survey data, ecological and phylogenetic analyses to identify likely reservoir hosts/spillover pathways and inform intervention programs.

This research will advance our understanding of the risk of novel viral emergence in a uniquely important region. **It will strengthen in-country research capacity** by linking local infectious disease scientists **with an international collaborative network that has proven capacity to conduct this work and produce significant findings.** These include: testing of tens of thousands of samples from wildlife, humans and livestock in the region; discovery of hundreds of novel viruses from zoonotic viral families in wildlife; outbreak investigations in rural communities across SE Asia; discovery of the bat-origin of SARSr-CoVs; discovery of a novel bat-origin SADS-CoV killing >25,000 pigs in S. China; and development of novel serological and molecular assays for high-impact viruses, and state-of-the-art *in vitro* and *in vivo* assays to characterize viral pathogenic potential. This body of collaborative research provides proof-of-concept that EID-SEARCH has the background, collaborative network, experience, and skillset to act as a **unique early warning system for novel EIDs of any etiology threatening to emerge in this hottest of the EID hotspots.**

II. Research Strategy:

1. Significance: Southeast Asia is a critical hotspot for emerging diseases due to its high biodiversity of wildlife and their viruses, and the presence of key ecological and socioeconomic drivers of emergence **(Fig. 1)** (*1*). These include dense human populations living in networks of rural and urban communities, with strong cultural and occupational connection to wildlife and livestock farming and trading, and intimate connection to global travel networks (*2*). The region is undergoing rapid environmental and demographic change, both of which increase the risk of disease emergence and spread. Pathogens that emerge in this region often spread and sometimes enter the USA (e.g. prior influenza pandemics, SARS) and threaten global health security.

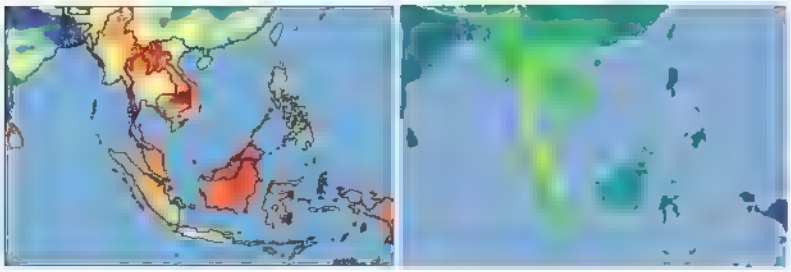


Fig. 1: Southeast Asia, and in particular, parts of Thailand and Malaysia are hotspots of risk for disease emergence **(left)**, and predicted high diversity of 'missing' or as-yet undiscovered viruses, yellow = highest diversity **(left)**. From (*1-3*).

Not surprisingly novel viruses, including near-neighbors of known agents, have emerged in the region leading to often unusual clinical presentations **(Table 1)**.This adds to a significant background burden of repeated Dengue virus outbreaks in the region (*20*), and over 30 known *Flavivirus* species circulating throughout S. and SE Asia (*21*). The events in **Table 1** are dominated by three viral families: coronaviruses (CoVs), paramyxoviruses (PMVs - particularly henipaviruses) and filoviruses (FVs), which are initial examples of our team's research focus and capabilities. These viral groups have led to globally important emerging zoonoses (*4, 5, 22-31*), causing tens of thousands of deaths, and costing billions of dollars (*32-34*). Furthermore, near-neighbors of known pathogens in these families have been reported throughout the region, including by members of our consortium: henipaviruses in bats in Thailand, Cambodia, Philippines, Laos, Indonesia, China, Malaysia, Bangladesh and India (*35-41*); a novel henipavirus, Mòjiāng virus, in wild rats in Yunnan (*14*); serological evidence of FVs in bats in Bangladesh (*42*) and Singapore (*43*); Nipah- and Ebola-like viruses in *Hipposideros*, *Cynopterus* and *Rhinolophus* species in Malaysia (Hughes *et al.*, in prep.); evidence of novel FVs in bats in China (*44-46*), including Měnglà virus that appears capable of infecting human cells (*47*); novel PMVs in bats and rodents consumed as bushmeat in Vietnam (*48*); a lineage C β-CoV in bats in China using the same cell receptor as MERS-CoV to infect human cells *in vitro* (*49*); MERSr-CoVs in bat guano harvested as fertilizer in Thailand (*50*), and directly in bats (Wacharapluesadee *et al.*, in prep.); 172

Viral agent	Site, date	Impact	Novelty of event	Ref.
Nipah virus	Malaysia, Singapore 1998-9	~246 human cases, ~40% fatal	2nd emergence of a zoonotic henipavirus, 1st large outbreak	(*4-6*)
Melaka & Kampar virus	Malaysia 2006	SARI in family group, individual	1st disease due to bat-origin reoviruses, also Singapore, Vietnam etc.	(*7-10*)
Reston filovirus	Philippines 2008	Seropositive people killed pigs,	No prior FVs in pigs	(*11*)
Thrombocytopenia Syndrome virus	E. Asia 2009	100s of deaths in people	Novel tick-borne zoonosis with large caseload	(*12*)
Reston filovirus	Shanghai 2011	PCR positive pigs	Further evidence of pig RESTV infection	(*13*)
Mòjiāng virus	Yunnan 2012	Death of 3 mineworkers	1st evidence of rodent origin henipavirus in people	(*14*)
Nipah-like virus	Philippines 2015	Killed horses	No prior horse infection for NiV, known for HeV	(*15*)
SARSr-CoV & HKU10-CoV	S China 2015	Seropositive people	1st evidence human infection HKU10 & SARSr-CoV	(*16*)
SADS-CoV	China 2017	>25,000 pig deaths seronegative people	Novel emergence of bat-origin CoV	(*17*)
Nipah virus	Kerala 2018, 2019	Killed 17/19 people 2018, 1 infected 2019	1st outbreak of NiV outside Bangladesh, W. Bengal focus	(*18, 19*)

Table 1: Recent emergence events in SE Asia indicating potential for novel pathways of emergence, or unusual presentations for known or related viruses.

novel β-CoVs (52 novel SARSr-CoVs) and a new β-CoV clade ("lineage E") in bats in S. China that occur throughout the region (*24, 49, 51, 52*); 9 novel wildlife-origin CoVs and 27 PMVs in Thailand, and 9 novel CoVs in Malaysia reported by us from USAID-PREDICT funding (*51, 53*). These discoveries underscore the clear and present danger of zoonotic events in the region. The wide diversity of potentially pathogenic viral strains also has significant potential use in broadly active vaccine, immunotherapeutic and drug development (*49*).

Most high-impact zoonotic viruses originate in wildlife reservoirs, sometimes spilling over first into livestock 'amplifier' hosts, or directly into localized human populations with high levels of animal contact **(Fig. 2)**. Efforts to prevent emerging zoonoses have targeted these high-risk populations in regions prone to disease emergence (*31, 54*). However, these regions tend to be in the developing world, where nations often lack the resources to investigate novel zoonotic events, or wildlife reservoirs of zoonoses, and prioritize more immediate public health concerns such as Dengue virus or NTDs (*20*). Zoonotic disease surveillance and control is also hampered by inadequate information on basic disease ecology (e.g. range of wildlife reservoirs, risk factors for spillover) and pathogen biology (viral diversity, pathogenesis), and by logistical challenges sharing novel diagnostics, animal models, samples and reagents at sites where outbreaks begin (*55*). Countermeasure and vaccine development is challenged by the small number of isolates available, and the presence of closely-related strains, some with evidence of transmission to people but with unknown pathogenicity. For example, using NIH and other funding, we found serological evidence of exposure to African henipaviruses in 3-4% of a sample of people in Cameroon, with a significant risk factor being butchering of bats; and serological responses to bat SARSr-CoVs in 6/209 (2.87%) and bat HKU10-CoV in 2/412 (0.5%) people living close to a bat cave in Yunnan, all novel viruses with unknown clinical impact (*16, 56*). We discovered two novel bat-borne reoviruses, Melaka and Pulau viruses, and showed that 14/109 (13%) of people living in close proximity to bat roosts on Tioman Island, Malaysia were exposed to these viruses (*7*) as well as 12/856 (1.4%) of a random sample screened in Singapore (*8*). Previous studies in the Philippines found famers and butchers who had contact with sick pigs tested positive for Reston ebolavirus antibodies but had not experienced illness (*11*), and it was our team that discovered Philippine bats as natural reservoir hosts for Reston virus (*57*). In preliminary screening in Malaysia with funding from DTRA we found serological evidence of exposure to henipaviruses (Hendra, Nipah and Cedar) in 14 bats and 6 human samples, and Ebola (Zaire and Sudan)-related viruses in 11 bats, 2 non-human primates (NHP) and 3 human samples (Hughes, in prep.).

Even when spillover leads to outbreaks of illness and mortality, they are often unreported, undiagnosed or misdiagnosed. We initiated targeted syndromic surveillance of encephalitis patients in Bangladesh clinics and showed that Nipah virus (NiV) causes repeated annual outbreaks with an overall mortality rate of ~70% (*58*). NiV has been reported in people in West Bengal, India, which borders Bangladesh (*28*), in bats in Central North India (*59*), and now in people in Kerala, South India in 2018 and 2019, raising the specter of future spillover at other sites in the region (*18, 60*).

Fig. 2: Our Early Warning Approach: Most zoonotic viruses emerge from wildlife hosts, sometimes via livestock **(lower panel)**, to cause small scale outbreaks (green) or larger chains (red) of human-to-human transmission **(middle)**. In some cases, these spread more widely via air travel **(upper)**. Our EIDRC proposal targets each stage: **SA1** examines the diversity and spillover potential of viral threats in targeted SE Asian wildlife; **SA2** seeks evidence of their spillover into focused high-risk human populations; **SA3** identifies their capacity to cause illness and to spread more widely. Figure from (*54*)

Under a current NIAID R01, we have shown that we can use analytical approaches to target surveillance of wildlife and people and identify likely sites of spillover. We used phylogenetic analysis of bat hosts and their CoVs to identify a key cave complex in SW Yunnan Province that harbors all the genetic elements of SARS-CoV (*61*), as well as a series of SARSr-CoVs that can infect human cells *in vitro*, cause SARS-like clinical signs in humanized mice, and evade vaccine treatment and therapeutics (*24, 49, 51, 52, 62-64*). We conducted risk factor surveys and biological sampling of human populations living close to this cave and found serological evidence of spillover in people highly exposed to wildlife (*16*). **This work provides proof-of-**

concept for an early warning approach that we will expand in this EIDRC to target other viral groups in one of the world's most high-risk EID hotspots.

The overall premise of this EIDRC proposal is that there is substantial evidence that: 1) diverse CoVs, henipaviruses and FVs related to known human pathogens are circulating in wildlife reservoirs in Southeast Asia; **2)** these viruses likely spillover regularly to people, are often unreported or misdiagnosed, and their clinical manifestations and potential to cause pandemics are unknown and underestimated; and **3)** our strategy for targeted surveillance and detection of spillover and illness in at-risk human populations can be used as an 'early warning system' to conduct public health interventions and disrupt disease emergence. To scale-up this approach, we propose to launch **EID-SEARCH** (the **E**merging **I**nfectious **D**iseases - **S**outh **E**ast **A**sia **R**esearch **C**ollaboration **H**ub), to better understand, and respond to, the risk of zoonotic viral emergence in Southeast Asia. We will initially focus on the diversity of known and novel CoVs, henipaviruses, and FVs in wildlife reservoirs. We will use this work to build our center's interactive network throughout the region, bridge barriers, provide early focal point for basic and translational studies, develop sample handling and storage routines, communication networks, cohort management, infrastructure development, and cross-training in surveillance and novel diagnostic platforms. We will develop and transfer technology to test these viruses' capacity to infect human cells and mouse models, develop new specific and sensitive serological and molecular diagnostic tools, conduct surveillance of human communities with high risk of exposure to wildlife, and clinical cohorts to identify evidence of spillover of viruses causing previously 'cryptic' clinical syndromes in people. We will test the capacity of novel viruses to infect human cells and/or mouse models, and thus asses potential for spillover and spread which will feed into our risk models. Our group also has extensive experience in other viruses, including vector-borne flaviviruses, and alphaviruses, and will use this experience to provide robust long-term surveillance, diagnostics, and basic science opportunities. While the current proposal focuses its basic and applied research agendas on this group of viral EID, we note that the EID-SEARCH is poised to rapidly respond to any outbreak. **Thus, FVs, henipaviruses and CoVs are examples of sentinel surveillance systems in place that illustrate EID-SEARCH's capacity to identify and initiate a rapid response targeting any novel microbial pathogen that emerges in this region.**

2. Innovation: Previous work by our consortium has developed strategies to target surveillance in wildlife and people to better anticipate and identify early spillover events and pre-empt outbreaks of emerging viruses. In the EID-SEARCH we scale up this approach in a central research "hub" made up of leading laboratories, clinics and surveillance sites in three critically high-risk EID hotspot countries in SE Asia. EID-SEARCH's reach is expanded through its regional network of collaborators that covers nearly all of the greater SE Asia region. The innovation of the EID-SEARCH is in: **1)** Its multidisciplinary approach that combines modeling to target geographic and taxonomic sampling targets with on-the-ground zoonotic disease surveillance in human and wildlife populations; **2)** the biological characterization approach that identifies how likely viruses are to be able to infect people, and enables evaluation of existing countermeasure technologies; an approach that is grounded in our successful work on SARSr-CoVs; and **3)** the strategic sampling of both high-risk communities with extensive animal contact at the front-lines of viral spillover *and* syndromic clinical cohorts that present with signs of novel viral emergence, to identify risk of viral spillover in an early warning system approach **(Fig. 2). In Aim 1, we will target viruses in archived and newly collected wildlife samples, and characterize their risk of spillover to people**. We will use spatial and phylogeographic analyses to identify the geography and species of wildlife to test samples from, and to further characterize viruses we have recently discovered. We will use *in silico* methods (novel ecological-phylogenetic risk ranking and mapping of receptor binding domains), cell culture, and animal models to assess their potential for spillover into high-risk human populations. **In Aim 2, we will conduct targeted cross-sectional serological surveys of human communities with high levels of animal contact to find evidence of viral spillover, and identify occupational and other risk factors for zoonotic virus transmission.** We will use serological tests targeting viruses identified in Aim 1 to identify the baseline spillover of known or novel CoVs, henipaviruses and FVs in these populations. Serological findings will be analyzed together with subject metadata (including a simple animal-contact survey, location data, viral sequence/isolates etc.) to identify zoonotic risk factors and routes of exposure from specific wildlife or vector species. **In Aim 3, we will use syndromic surveillance of clinical human cohorts to identify evidence of viral etiology for otherwise 'cryptic' outbreaks.** We will enroll and

collect biological samples from patients in local clinics and hospitals who present with syndromes previously linked to known viral agents and live within communities at high risk for disease emergence. We will conduct molecular and follow-up serological diagnostic assays to identify likely viral etiology of syndromes that may represent otherwise cryptic events. Where viruses are identified, we will attempt to isolate or molecularly re-derive them, and use survey data, ecological and phylogenetic analysis to identify likely reservoir hosts and inform intervention programs. Our US partner BSL-4 laboratory, NEIDL, will attempt isolation and characterization of viruses requiring BSL-4 of containment (e.g. novel filoviruses, close relatives of Hev/NiV).

3. Approach: 3.1. Research team: The EID-SEARCH builds on long-term collaboration among world leaders in emerging virus research with proven experience collaborating internationally on field, lab and human surveillance research **(Fig. 3)**. Over the past two decades, our consortium partners have conducted high profile research on EIDs within the region and globally, including identifying the wildlife reservoirs for NiV and Hendra virus (HeV), MERS- and SARS-CoVs (*24, 27, 59, 61, 65-67*), discovering SADS-CoV (*17*), and developing an array of serological, molecular, *in vitro* and *in vivo* approaches to characterizing high-risk CoVs, henipaviruses, and FVs (*62-64, 68-81*). Our team has substantial experience conducting human surveillance in the community and during outbreaks (**Sections 2.2.a., 2.2.b., 2.2.c, 3.2.a, 3.2.b)**, including: USAID-PREDICT, and DTRA-funded viral surveillance of indigenous communities in Peninsular Malaysia and syndromic surveillance of hospital patients in Sabah (Co-I Hughes); collection of >2,000 serum samples from healthy blood donors and sanitation workers, febrile and influenza like illness (ILI), and diarrheal stool samples from children under 5 years of age across Borneo Malaysia (Co-I Kamruddin); collaboration on the MONKEYBAR project with the London School of Hygiene and Tropical Medicine to analyze risk and prevalence of the zoonotic malaria *Plasmodium knowlesi* through case control and cross-sectional studies in Sabah villagers (n=~800, 10,000 resp.) and clinical observational studies to determine the etiology of central nervous system infections and acute undifferentiated febrile illness in Sabah. (Co-Is William, Rajahram, Yeo); and community-based surveillance of hundreds of bat-exposed villagers in Thailand (Co-Is Wacharapluesedee, Hemachudha). As a proof-of-concept of how our team can rapidly scale up resources for diagnostics and surveillance in the face of a new EID, in 2016, we discovered a novel bat-origin HKU-2 CoV (*82, 83*) killing >20,000 pigs in S. China, designed PCR and serological assays, surveyed pig farmers for evidence of exposure, and conducted experimental infections, pathogenesis and molecular studies, **all in the span of 3 months** (*17, 84*).

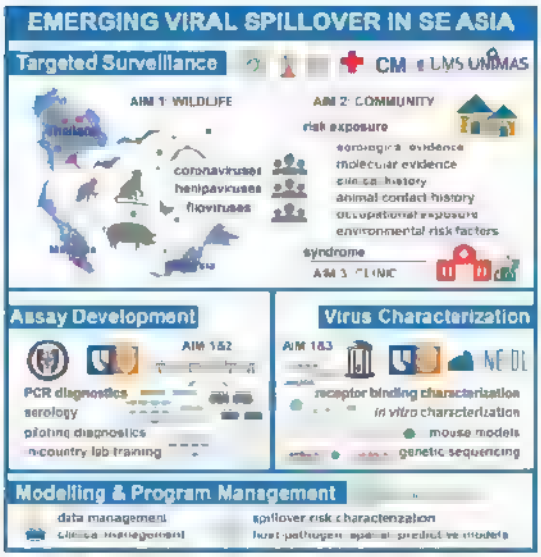


Fig. 3: EID-SEARCH scope, core institutions, and roles.

The administration of this center **(Section 4.1.)** will be centralized at EcoHealth Alliance (EHA) led by PI Daszak, who has >20 years' experience managing international research collaborations on emerging zoonoses, and has collaborated with all partners in the EIDRC consortium for 5-20 yrs on NIAID- and USAID-funded research. He will oversee all activities in this EIDRC, supported by Deputy lead, Dr. Olival – who has managed human and wildlife disease surveillance projects in SE Asia for >10 years, and a **Core Executive Committee (Section 4.1.a)**. Co-Is Olival and Zambrana are leaders infectious disease analytics, and head the modeling and analytics work for USAID-PREDICT. Co-Is Wang, Baric, Broder, Anderson, and Laing have developed a unique array of *in vitro* cell culture, serological and molecular reagents to identify and characterize emerging viruses in people and animals (henipaviruses and other PMVs, CoVs, FVs and many others). Co-Is Wacharapluesedee, Hemachudha, and Hughes and collaborators have coordinated clinical and community surveillance of people, and of wildlife and livestock within Thailand and Malaysia for the past 15 years, in collaboration with Ministries of Health, Agriculture and Environment. Finally, this consortium has extensive external funding from NIH, DoD, USAID, DHS and other USG agencies supporting laboratory, analytical and field studies directly related to the current proposal, and will bring substantial leverage to our EIDRC.

3.2. Geographical focus: The three core (hub) countries for this proposed EIDRC are Thailand, Malaysia and Singapore, three contiguous EID hotspot countries that stretch through one of the most significant foci of EID origins globally. Our proposed work includes sampling wildlife and people in Thailand, Peninsular Malaysia, Sarawak and Sabah, and thus contains overlapping wildlife biogeography with India, Bangladesh, Myanmar, SW China, Laos, Cambodia, Vietnam, Philippines, and Indonesia. It encompasses diverse cultural and socioeconomic backgrounds which have correspondingly diverse and intensive interactions with wildlife reservoirs and the global travel network. We have already begun sampling of wildlife hunters, livestock workers, wildlife farmers and market workers, rural villagers living close to high risk wildlife species, people otherwise highly exposed to animals in these countries, and clinical cohorts, as part of current/prior NIH, DTRA, and USAID funding Our core member's extensive network of collaborators in clinics, research institutes and public health laboratories in almost every other Southeast Asian country positions the EID-SEARCH within a much larger catchment area for emerging zoonoses and will allow us to rapidly scale up to include additional sites in response to an outbreak or shift in research priorities. We will conduct regular meetings with key research, public health and community leaders, including >50 leading laboratories/institutions in 10 countries **(Section 4.2)** to maintain these collaborative relationships with the core members of our consortium (**Fig. 4**). We will use these, and our annual meetings, to share information on novel research and diagnostic approaches, pathogens that are of key pandemic potential, regions or populations at high risk of spillover, and information from the greater network on likely outbreaks of novel disease. This platform will coordinate sample sharing and diagnostic platforms and help build a rapid response to outbreaks across the region.

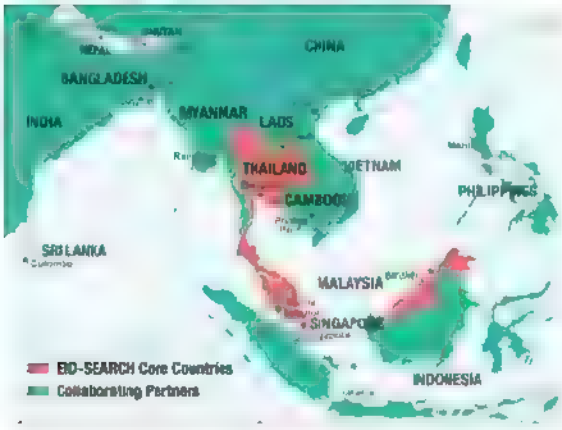


Fig.4 : Map of Southeast Asia indicating three hub countries for this proposed EIDRC (**Red**: Thailand, Singapore, Malaysia) and countries in which Key Personnel have existing collaborating partners via other funded work (**Green**), indicating that EID-SEARCH provides access to key collaborators and sites throughout the region.

3.3. Capacity for linkage with other NIAID studies, and scaling up to respond to outbreaks: EID-SEARCH US-based partners include senior scientists with significant experience on NIAID-funded projects, extensive collaborations with other NIAID-funded scientists, and previous experience working with NIAID leadership through workshops, review of programs (e.g. PI Daszak's role in NIAID CEIRS external review), and work on study sections. These contacts ensure that the EID-SEARCH senior leadership will be ready and able to rapidly set up data, sample and reagent/assay sharing protocols with NIAID researchers, the other EIDRCs, the EIDRC CC and other NIAID research centers. EID-SEARCH in-country partners include senior medical doctors and infectious disease specialists at national and regional hospitals in each country and administrative state in this proposal. On news of potential outbreaks, **EID-SEARCH will rapidly mobilize its core staff and their extensive collaborative network across almost all SE Asian countries (Fig. 4) (Sections 4.1.a, 4.2. 4.3).** The core analytical approach can be used to rapidly identify sampling sites and targets to harvest vectors, vector borne arboviruses, birds and mammalian species that harbor most other viral threats. Through existing projects such as the USAID PREDICT Project and DTRA-funded biosurveillance projects, EHA is currently partnered with hospitals and researchers across South and Western Asia, West and Central Africa, and Latin America. Our partners already have capacity to conduct human and wildlife sampling and testing for novel viral agents, so expanding in geography or scale is readily achievable given sufficient resources.

Aim 1: Identify, characterize and rank spillover risk of high zoonotic potential viruses from wildlife.

1.1 Rationale/Innovation: The vast majority of emerging zoonotic pathogens are linked directly or indirectly to wildlife host, particularly from important mammalian groups like bats, rodents and NHPs (*3*). Our previous work on wildlife origin viruses demonstrates that zoonotic viral emergence tends to occur in specific regions with high diversity of wildlife that harbor viruses of zoonotic potential, and human populations that have close contact to these wildlife **(Fig. 1)** (*2, 3*). In Aim 1 **(see Fig. 9 for overview)**, we will strategically conduct EID

surveillance by applying risk analytics to prioritize the regions, wildlife species, and human populations that have a particularly high risk of viral spillover. We will target high-risk zoonotic host reservoirs (bats, rodents and NHPs) in these regions and apply novel predictive models to estimate viral diversity and host range to identify wildlife species that have been ignored or under-sampled by previous zoonotic disease surveillance efforts. We will strategically collect specimens from these species and screen them, together with some of the tens of thousands of recently collected samples we have archived, for known and novel agents. We will begin screening using conserved PCR assays to identify known and novel viruses in high risk RNA viral families, *Coronaviridae*, *Paramyxoviridae*, and *Filoviridae*. We will expand to other groups of pathogens, including arboviruses, pending available resources and priorities established with the EIDRC coordinating center (EIDRC-CC) and other regional EIDRCs. Using risk ranking algorithms and a series of ecological and virologica risk factors, we will triage the wildlife viruses we discover for further genomic characterization and viral isolation. On this subset of viruses, we will then use *in vitro* and *in vivo* approaches (viral rescue, cell lines, gene edited humanized transgenic mice and the collaborative cross genetic reference mouse population) previously developed and widely used by our team to predict capacity of novel viruses to infect people and spillover (*63, 85-88*). These high-risk viruses and their close relatives will be targets for human community serosurveys and clinical sampling in Aims 2 and 3, respectively.

1.2 Preliminary data: 1.2.a. Geographic targeting: EHA has led the field in analyzing where the highest risk of zoonotic spillover is across the globe, identifying SE Asia as a major EID hotspot (*1, 2*). These hotspots are sites where high wildlife biodiversity, human population density and rapid ecologic change collide **(Fig 1)**. Using host and ICTV viral data for all known mammalian viruses, and generalized additive models to correct for sampling bias, we are able to predict the relative number of yet-to-be-described viruses that a species harbors (*3*). This demonstrates substantial undiscovered viral diversity in mammals across Southeast Asia, and particularly in regions of Thailand, Singapore and Malaysia **(Fig. 1)**. Separately, we found that factors driving spillover (host diversity, climate) differ from those driving spread in human populations (population density, bushmeat hunting, livestock production) (*89*). We therefore analyze capacity for viral spread as a separate risk factor, using our unique demographic and air travel and flight data modeling software (*90, 91*). In the current proposed work, we will use all the above approaches to target wildlife sampling (archival and new field collections) in Aim 1, to inform sites for human sampling in Aim 2, and to assess risk of spread in Aim 3.

1.2.b. Reservoir host species targeting: Our analysis of all known mammalian host-viral associations demonstrates that bats, rodents and NHPs represent the three most important reservoirs for zoonoses, responsible for the highest proportion of known and predicted viral diversity of zoonotic potential (*3*). Thus, the bulk of our proposed wildlife sampling and testing will consist of these three taxa with a focus on bats, because this group is the known or hypothesized reservoir for the majority of high-impact zoonotic CoVs, PMVs and FVs (*50, 92-94*). Bats have the highest proportion of predicted zoonotic viruses in any mammalian group (*2*), and are exceedingly diverse in Southeast Asia (~500 species). To further prioritize taxonomic sampling targets within these diverse geographic hotspots, we used a novel Bayesian phylogeographic algorithm to identify host genera and species that are the most important centers of evolutionary diversity for a given viral group, e.g. bat genera for β-CoVs **(Fig. 5)** (*51*). This approach will be extended to other mammal taxa and viral families of interest, allowing us to identify the reservoir hosts of specific zoonotic viral groups, where viral diversity is likely highest

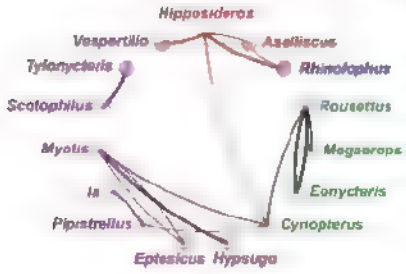


Fig 5: Preliminary analysis of sequence data collected under prior NIH funding, identifying SE Asian bat genera with the highest β-CoV evolutionary diversity. We will apply this Bayesian discrete phylogeographic model to identify taxonomic and geographic centers of viral diversification and sharing for relevant PMV, CoV, FV and other virus clades. Line thickness proportional to probability of virus sharing between two genera. Inter-family switches in red.

Finally, we have designed a strategy to estimate sampling gaps, using a viral 'mark-recapture' approach we previously published (*95, 96*) **(Fig. 6)**. Using prior data for bat, rodent and NHP viral discovery vs. sampling rates, we can identify the likely total viral diversity for specific host groups in a region, and use this to estimate sample sizes to discovering the majority of unknown viruses within a specific family or genus. **In the current**

proposal, we will use these analyses to estimate geographic and species-specific sampling targets **to more effectively identify new strains to support experimental infection studies and risk assessment.**

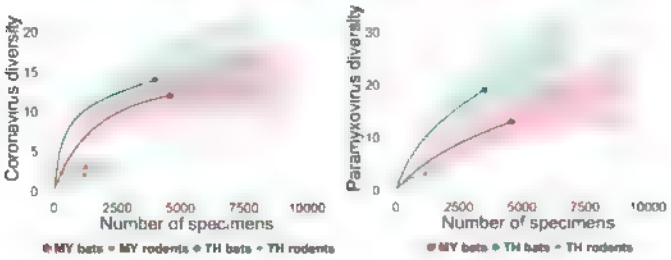


Fig. 6: Estimated CoV **(left)** and PMV **(right)** diversity in bats and rodents from Thailand and Malaysia, using data from PCR screening and RdRp sequences from >10,000 specimens in bats and 4,500 in rodents. Bats have 4X more viral species than rodents, controlling for sampling effort. We estimate that additional collection of 5k-9k bat specimens and testing of our archived bat and rodent specimens alone will identify >80% of remaining CoV and PMV viral species in these key reservoirs, yielding >800 unique viral strains.

1.2.c. Sample testing to identify known and novel viruses: We have conducted extensive wildlife surveillance for novel viruses across Southeast Asia in prior NIAID funded work and as part of the USAID PREDICT project. Under the 10-year PREDICT program globally, we identified 912 novel and 210 known viruses, more than the total number of viruses previously recognized in mammals by the ICTV (*97*). This work included collecting nearly 300,000 individual mammal samples from 14 EHA-led PREDICT countries, and PCR-screening of more than 60,000 individual specimens (*53*). In southern China alone, we identified 178 β-CoVs, of which 172 were novel, discovered a new β-CoV clade, "lineage E" (41), diverse HKU3r-CoVs (179 sequences) within a 'sister' clade to the SARS-CoV lineage, and a new bat-origin SADS-CoV, responsible for killing >25,000 pigs in Guangdong Province (*17*). We have collected 28,957 samples from bats, rodents and NHPs in Thailand and 47,178 in Malaysia, **but have only tested a minority of these using PCR.** We have identified 100 novel viruses in Thailand and 77 in Malaysia. **Furthermore, we have only sequenced a small segment of one gene for all novel viruses found. We have archived duplicate samples which are now available for use in this project**, including fecal, oral, urogenital, serum samples, and biopsies from bats, rodents, and NHPs. In the current proposed work, <u>we will attempt to sequence, isolate and characterize those viruses that our analyses below suggest are most likely to be able to infect humans.</u>

1.2.d. <u>In vitro</u> & <u>in vivo</u> *characterization of viral potential for human infection:* Using Coronaviridae as an example, we have conducted *in vitro* and *in vivo* experiments to characterize the pathogenic potential of novel SARSr-CoVs from bats. We isolated three SARSr-CoVs from bat feces: WIV1, WIV16 and Rs4874, with Spike (S) protein sequences that diverged from SARS-CoV by 3-7% (*24, 61, 98*). We conducted full-length genome sequencing of 12 other novel SARSr-CoVs, some highly similar to outbreak SARS-CoV in the most variable genes (*61*). Using our reverse genetics system we constructed chimeric viruses and rederived full length recombinant SARSr-CoV from in silco sequence. All 3 SARSr-CoV full length isolates and the two chimeric viruses replicated efficiently in Vero E6 cells and in HeLa cells expressing hACE2, civet and bat ACE2, but not in those without ACE2 (*24, 61, 98*). We used the SARS-CoV reverse genetics system (*72*) to generate a chimeric virus with a mouse-adapted SARS-CoV backbone expressing SHC014 S protein with 10% sequence divergence from SARS-CoV S. This and the other full length and chimera viruses replicated in primary human airway epithelium, using the human ACE2 receptor to enter into cells (*62*). Thus, **SARSr-CoVs with diverse variants of SL-CoV S protein without deletions in their RBD can use human ACE2 as receptor for cell entry.** The Baric lab has a well-established hACE2 and DPP4 transgenic mouse model that **we used to assess the capacity of novel SARSr-CoVs and MERS-CoV to infect humans and cause disease** (*85, 99*). Infection of bat SARSr-SHC014 or WIV1 caused SARS-like clinical signs in the transgenic hACE2 mouse model **that weren't reduced by immune-therapeutic monoclonals that attenuate SARS-CoV pathogenicity, nor after challenge following vaccination against SARS-CoV** (*62*) **(Fig. 7)**. We repeated this virus characterization approach with chimeras using HKU3r-CoV S proteins that are ~25% divergent from SARS-CoV S, **and found that they are unable to use the ACE2 receptor**. Additionally, we were unable to culture HKU3r-CoVs in Vero E6, or human cell lines.

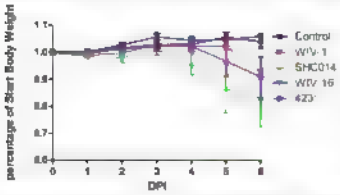


Fig. 7: Body weight change in hACE2 transgenic mice after SARSr-CoV infection, demonstrating that bat-origin SARSr-CoVs cause similar clinical signs to outbreak SARS-CoV strain (4231) (*62, 63*).

A similar approach to the above pipeline for CoVs will be applied to novel henipaviruses we discover during our research. The broad mammalian tropism of HeV and NiV (*68*) is likely mediated by their usage of highly conserved ephrin ligands for cell entry (*19, 100*). A third isolated henipavirus Cedar virus does not cause pathogenesis in animal models. **Co-Is Broder and Laing** have developed a reverse genetics system and rescued a recombinant CedV to test ephrin receptor usage/tropism and pathogenicity during henipavirus infections (*77*). CedV is unable to use the Ephrin-B3 receptor (*77, 101*) which is found in spinal cord and may underlie NiV encephalitis (*102*) and that pathogenesis also involves virulence factors V and W proteins. The putative henipaviruses, Ghana virus and Mòjiāng virus, predict V and W protein expression, with GhV able to bind to ephrin-B2, but not -B2 (*103*), and the receptor for MoJV remains unknown (*104*) but is likely ephrin-B2 (*105*). Our group has also used similar methods to test the hypothesis that novel Filoviruses discovered in wildlife are able to infect people. NiV, EBOV and MERS-CoV all infect primary microvascular endothelial cells, which are available at Co-I Baric's lab for EID-SEARCH collaborators (*71, 106*) Primary human lung endothelial cells are highly susceptible to Ebolavirus infection (*107*), and Huh7 cells can be used to isolate virus from clinical samples (*108*) offering advantages for reverse genetic recovery of novel FVs (*109*). The three filovirus genera, *Ebolavirus*, *Marburgvirus* and *Cuevavirus*, use Niemann–Pick type C1 (NPC1) protein as cell entry receptor (*110*). For novel filoviruses, cell culture would be carried out under BSL-4, however they can readily be characterized following identification of their encoded GP sequences which can be pseudotyped into recombinant GP-bearing vesicular stomatitis virus (VSV) pseudovirions (*111*). These pseudovirions can be safely used to characterize the tropism and entry filoviruses mediated by GP without a need for BSL4 containment. **Co-Is Wang and Anderson** used cells originating from various mammalian species to determine spillover and/or zoonotic potential of MLAV, a newly discovered Asian filovirus (*47*). Despite the low amino acid sequence identity (22–39%) of the glycoprotein with other filoviruses, MLAV is capable of using NPC1 as entry receptor. Cells from humans, monkeys, dogs, hamsters and bats were able to be infected with a MLAV pseudovirus, implying a broad species cell tropism with a high risk of interspecies spillover transmission.

Mouse models. For novel viruses across all families, we will use the UNC collaborative cross mouse that captures 90% of the diversity within all mouse groups to assess the most suitable model for further experiments (*112*). We have used this model for CoV, FV (Ebola), Flaviviruses, and alphaviruses infections. Clinical signs such as weight loss, hemorrhage, encephalitis, and, acute or chronic arthritis were recapitulated in these mice following SARS, EBOV, West Nile virus and Chikungunya infections, respectively (*86-88, 113-116*). Note that CC OR3015 shows hemorrhagic disease phenotypes after EBOV infection **(Fig. 8)**. *Bat Models.* Duke-NUS has developed two models for bat *in vivo* studies: a colony of *Eonycteris spelaea* (cave dwelling small fruit bat) and a bat mouse model, which contains the bat immune system in an immunodeficient mouse (*117*). In a proof of concept study, **Co-Is Wang and Anderson** infected *E. spelaea* bats with MERS-CoV to demonstrate their susceptibility and suitability for infection with a bat borne virus under BSL3 containment. These bats and the bat mouse model will serve to complement and expand studies from the UNC collaborative cross mouse, pending further funding from EIDRC CC. Recombinant viruses, transgenic mouse models and experimental recombinant protein constructs described above will be made available to the EID-SEARCH consortium and other EIDRCs following standard procedures **(see Resource Sharing Plan)**.

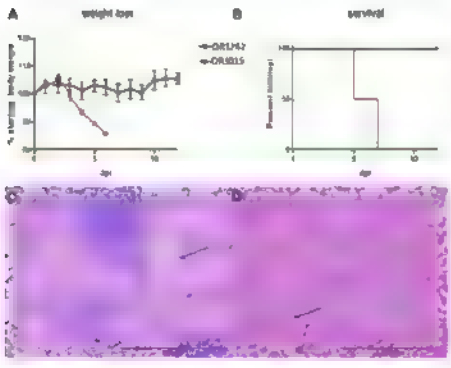


Fig. 8: EBOV Infection in Collaborative Cross Mouse. **Panel A/B**: Wt EBOV in two different CC lines demonstrate different disease patterns. **Panel C/D:** Hemorrhagic phenotypes on d. 6 (arrow) in spleen and liver, resp. From (*86*).

1.3. General Approach: We will conduct analyses to geographically- and taxonomically-target testing of samples from wild mammals that are most likely to harbor known high-profile zoonotic pathogens, or close relatives with potential to infect people. This includes selecting from tens of thousands of samples collected on recent projects and stored in freezers in our laboratories, and new sampling of wildlife in high risk locales. We will use viral family level PCR assays to identify and partially characterize viruses, then follow up sequencing of relevant receptor binding proteins to assess homology and predict binding affinity, then attempt to isolate and

biologically characterize viruses that phylogenetic and other data suggest have high spillover and pandemic potential. We will follow this with *in vitro* binding assays and cell culture experiments, and *in vivo* animal model infections to assess their potential to infect people and cause disease **(Fig. 9)**. EHA will lead the study design, targeted sampling, and data analysis; Co-Is Hughes and Wacharapluesadee will lead field sampling and in-country testing; Duke-NUS, UNC, USUS will lead the serological and PCR diagnostic development and the *in vitro* and *in vivo* analyses, as well as cross-training and tech transfer to the hub labs in Thailand and Malaysia. This will include via support of one Malaysian Ph.D student, Mei-Ho Lee (CM Ltd.) who has worked with the EID-SEARCH collaborators for 9 years. The focus of her study will be infection potential of novel CoVs and PMVs already found in bats in Malaysia under preliminary data for this proposal.

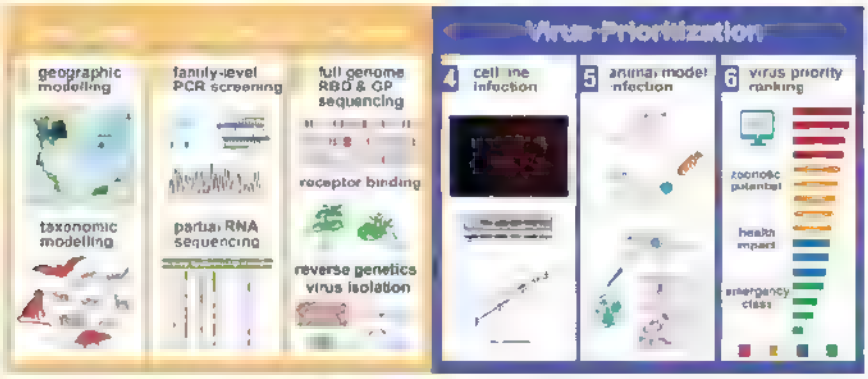


Fig. 9: Aim 1 will use analytical tools to target selection of archived and newly collected samples, conduct PCR and sequencing of novel viruses, recover by reverse genetics, and assess zoonotic potential using *in vitro* and *in vitro* models and analyses.

1.4 Wildlife samples: 1.4.a. Geographic and taxonomic targeting for newly collected wildlife samples: We will prioritize sites within each country that rank highest for both the risk of zoonotic disease emergence (*2*) and the predicted number of 'missing' zoonotic viruses (*3*). Our preliminary analysis **(Fig. 1)** suggests priority areas include: the Kra Isthmus (S. Thailand) and adjacent forests in N. Peninsular Malaysia, NW Thailand (near the Myanmar-Laos border), and lowland rainforests of Sarawak and Sabah. In each of these 'hottest of the hotspots' regions, we will identify 2-4 distinct sampling sites based on the geographic distribution of key hosts we prioritize for additional wildlife sampling. We will priority rank bat, rodent, and NHP species using host trait-based models (*3*). We will also identify species predicted to be centers of evolutionary diversity for CoVs, PMVs, and FVs using ancestral host reconstruction of available sequence data and Bayesian discrete phylogeographic models (*118-120*). We will leverage our strong collaborations with wildlife experts in Malaysia and Thailand, including many of whom are based at our core partner institutions, to ground-truth geographic and taxonomic model outputs with local expert knowledge to ensure the sampling plan is realistic based on current species distributions, population size estimates, seasonality, and accessibility to sites. Most zoonotic viruses are naturally carried by multiple wildlife host species, and there are strong, predictable relations between host phylogeny and viral taxonomy (*3*). We will use a combined network analysis and phylogeographic model to rapidly predict and prioritize new (unsampled) hosts for important, novel viruses we discover during our research. We have shown this relatively simple model (using just wildlife species range overlap and phylogenetic similarity between host species) is both generalizable to estimate host range for all mammalian and avian viruses *and* robust – accurately predicting hosts 98% of the time when cross-validated using data from known viruses (*121*).

1.4.b. Sample size justifications for testing new and archived wildlife specimens: We calculate initial sample sizes targets using our preliminary data on average PCR prevalence from screening tens of thousands of bat, rodent and NHP specimens for CoV and PMVs based on previous studies in Malaysia and Thailand. We will refine these sample size targets, in real-time, over the course of our project using viral discovery curve analyses **(Fig. 6)** to either scale-up or scale-back new sampling and testing of archived specimens for each species depending on viral capture rates. We will only collect additional specimens projected from each prioritized taxa to achieve statistically robust sample sizes and to complement our archived specimens. For example, *Rousettus* spp. bats, known FV reservoirs, were not adequately sampled under PREDICT research in Thailand. Preliminary analysis indicates that, for all viral target families, we will require ~14,000 new samples to identify 80% of remaining viral species diversity in our study region, ~5,000 samples from Thailand and ~9,000 samples from Malaysia **(Fig. 10)**. Viral strain diversity from a sampling effort this size is expected to number in the hundreds of strains. For example, given ~6% prevalence of CoVs in bat species previously sampled under the PREDICT project, a target of 14,000 individuals would yield ~800 PCR positive individuals,

representing, an estimated ~600 novel sequences/strains. Similarly, for PMVs, which have an average PCR detection prevalence of ~1.5%, sampling of 14,000 individuals would yield ~200 positives and an estimated 150 unique strains. Filovirus estimates are not feasible yet due to the small number of positive samples in prior studies, but will be estimated as the project begins. From each mammal, we will collect serum, whole blood, throat swabs, urine and fecal samples or rectal swab using our previously-validated nondestructive methods. We will sample sites at different time-points throughout each year, and sample an equal number of males and females to account for seasonal or sex-specific differences viral shedding **(See Vertebrate Animals)** (*122, 123*). Dead or animals euthanized due to injury will be necropsied.

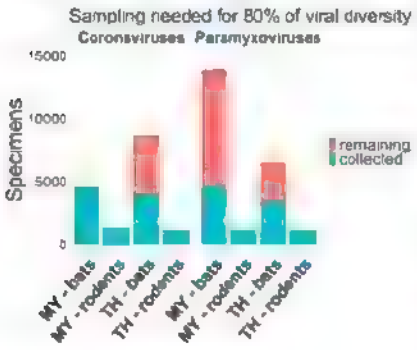


Fig. 10: Stacked bar plot showing number of currently-archived specimens **(blue)** and new specimens required **(orange)** to discover 80% of predicted number of CoVs and PMV species from high-risk bat and rodent taxa in Malaysia and Thailand.

1.4.c. Sample collection, testing, viral isolation: Wildlife will be captured and sampled using previously published techniques, by personnel wearing appropriate personal protective equipment (Tyvek suits or dedicated long external clothing, double nitrile gloves, leather gloves, an N95 or p100 respirator, and safety glasses) (*53, 93, 95, 96, 122, 124*). All samples will be placed in a vapor phase liquid nitrogen dry shipper immediately upon collection, and then transferred to a -80C freezer once back in the lab, until testing. Viral RNA will be extracted from bat fecal pellets/anal swabs. RNA will be aliquoted, and stored at -80C. PCR screening will be performed with pan-coronavirus (*125, 126*), filovirus (*127*) and paramyxovirus primers (*128*), in addition to virus specific primers where additional sensitivity is warranted in key viral reservoirs, i.e. Nipah virus or MERS virus specific primers (*129, 130*). PCR products will be gel purified and sequenced. We will attempt isolation on samples that contain viruses of interest (determined in **Aim 1.5 below**), using Vero cells and primary cell culture from the wildlife taxonomic order (bat, rodent and NHP cell lines) Over 70 bat cell lines are maintained at Duke-NUS from five different bat species. These include primary lung, brain, bone marrow, heart, kidney, intestine, liver, lymph node, muscle, spleen, PBMC and ovary/testes from *Eonycteris spelaea, Cynopterus bracyhotis, Rhinolophus Lepidus, Myotis muricola* and *Pteropus alecto* bats. In addition we have 8 immortalized cell lines, including those derived from lungs, therefore suitable for the isolation of respiratory viruses.

1.4.d. Moving beyond RNA viruses: To detect pathogens from other families, such as non-RNA viruses, we will combine conserved PCR assays with NGS. We will perform either unbiased NGS, or use a pan-viral enrichment library to sequence full-length genomes (*131*). We will conduct this work via EID-CC research projects or as part of outbreak detection/investigation in the region from DNA viruses or other agents.

1.4.e. Sequencing Spike Glycoproteins: Based on earlier studies, our working hypothesis is that zoonotic CoVs, FVs and henipaviruses encode receptor binding glycoproteins that elicit efficient infection of primary or continuous human cell lines (e.g., lung, liver, etc.) (*16, 61, 62*). Characterization these for SARSr-CoVs suggest that viruses up to 10%, but not 25%, different in the spike glycoprotein use human and bat ACE2 receptors for docking and entry. Uneven sampling gaps (e.g., no strains were found with 10-25% spike variation) prevent a thorough understanding of the transition point where the most divergent strains lose human ACE2 receptor usage. Our viral discovery curves **(Fig. 6)** suggest further sampling will reveal a rich diversity of as-yet-undiscovered SARSr-CoVs and strains of other viruses that fill in the phylogenetic tree between currently-described viruses. In this aim we will use phylogenetic and viral discovery analysis to specifically target bat species and regions that are under-sampled to allow sufficient power to identify and characterize missing strain diversity for potential zoonoses. We will sequence the S proteins of novel SARSr-CoVs to prioritize viruses for experimental work in Aim 3 to test this hypothesis. Likewise, we will test the hypothesis that phylogenetic related zoonotic receptor binding protein genes of MERS-related, Ebola-related and NiV/HeV-related viruses will also program efficient entry via human and ortholog receptors. For all novel virus strains, we will sequence the complete entry spike genes by amplifying overlapping fragments using degenerate primers as shown previously (*24, 61*). ***Reverse Genetics:*** Full-length genomes of selected CoVs, FVs or henipaviruses (representative across subclades) will be sequenced using NEBNext Ultra II DNA Library

Prep Kit for Illumina and sequenced on a MiSeq sequencer. PCR or Minion sequencing will be performed to fill gaps in the genome. The full length spike gene sequences, including the amount of variation in the receptor binding residues that bind the appropriate human receptor will be used to select strains for Aim 3 experiments. We will sequence full length genomes of high risk strains that are antigenically distinct and escape SARS or MERS-CoV cross neutralization, synthetically reconstruct a small subset (1-2) and evaluate growth in Vero, BHK and Huh7 cells (*63, 132*). From full length sequences, synthetic clones will be ordered to recover recombinant viruses using reverse genetics as described by our groups (*62, 63, 77, 109, 133, 134*). Recombinant virus growth will be accessed in Vero, BHK, Huh7 and select bat cells and recovered viruses used for downstream studies. Virus strain prioritization is described below.

1.5. Assessing risk for spillover. 1.5.a. Capacity to infect human cells: We will use a series of cell cultures to assess the capacity of target viruses to enter human cells. For CoVs, FVs and henipaviruses, we will use primary human ciliated airway epithelial cells (HAE) and lung endothelial cell cultures derived from the lungs of de-identified transplant recipients. HAE are highly differentiated and grown on an air-liquid interface for several weeks prior to use (*62, 63, 132*). We will prepare HAE and lung endothelial cultures from three different patient codes in triplicate in collaboration with the tissue procurement facility at the Cystic Fibrosis Center at UNC. Cultures will be inoculated with chimeric bat SARSr-CoVs or novel FVs or henipaviruses to assess efficient replication. At 72 hpi, cultures will be fixed for immunofluorescent staining using antisera to the SARS-CoV conserved nucleocapsid protein (N) or to structural genes of the other viruses (*64, 71*). SARSr-CoVs that differ significantly in S protein sequence (11-24%) from epidemic SARS-CoV yet replicate *in vitro*, will also be evaluated for sensitivity to neutralization in Vero cells by PRNT50 assays using broadly SARS-CoV cross reactive human mAbs S227.14, S230.15, S215.17, and S109.8 (*63, 135*) or monoclonal antibodies targeting the Ebola or Marburg E glycoprotein (Available through BEI), or NiV/HeV glycoproteins (*136*). As controls or if antisera is not available, the S genes of novel SARSr-CoV or spike entry genes of other novel viruses under investigation will be inserted into VEE 3526 replicon vectors (VRP3526-S), packaged and used to vaccinate mice (*137*). Polyclonal sera against test bat-SARS virus or other spike genes will be harvested and tested for ability to cross neutralize SARS-CoV, GD03, WIV-1, SHC014, WIV-16, other novel SARSr-CoV and HKU3-SRBD by PRNT50 assay (*63, 138, 139*). Using PRNT50 titers with sera (n=4 each) among these viruses, antigenic cartography (*140*) will allow comparison of antigenic vs. phylogenetic distance, identifying the transition at which SARSr-CoV strains escape SARS-CoV based vaccines, informing immunotherapeutic and vaccine design strategies (*141-143*). Similar approaches will be applied to novel MERS-related viruses, other CoV, FVs or henipaviruses. While most wildlife-origin viruses with unknown transmission potential or pathogenicity in people uncategorized, we use BSL-3 for isolation as standard, and cell culture for potentially BSL-4 pathogens will be undertaken at collaborating institute NEIDL. To facilitate this, duplicate samples in culture medium from animals PCR +ve for FVs and very close relatives of NiV or HeV will be shipped to NEIDL **(See letter of support)** for culture, characterization and sharing with other approved agencies including NIH Rocky Mountain Laboratories where PI Daszak and Co-Is Baric have ongoing collaborations. Similarly, some duplicate samples of animals PCR +ve for CoVs will be shipped to UNC for further characterization by Co-I Baric. Where feasible and appropriate, training opportunities at NEIDL and UNC for in-country staff will be given, thereby enriching hands-on collaboration across sites.

1.5.b. Host ACE2, DPPR, Niemann-Pick C1 (NPC1) and EphrinB2/EphrinB3 receptors: We will sequence relevant host receptors for select mammalian wildlife species we find positive for strains of high-priority CoV clades, and all new henipaviruses and FVs. Of particular interest is homology across 18 bat and human orthologue ACE2 contact interface residues that engage the SARS RBD as a potential indicator of SARSr-CoV cross species transmission potential and growth in human cells (*70*). Likewise, variation in the NPC1 receptor has been shown to alter EBOV ability to infect in humans and bats, so this can be structurally mapped for prediction and downselection of strains (*144*). Signatures of positive selection in bat NPC1 were concentrated at the virus-receptor interface, with the strongest signal at the same residue that controls EBOV infection in *Eidolon helvum* cells. Thus NPC1 is a genetic determinant of FV susceptibility in bats, and some NPC1 variations likely reflect host adaptations to reduce FV replication and virulence (*145*). NiV and HeV use ephrin B2 or ephrin B3 as a receptor, and variation affects its ability to use human vs bat receptor molecules (*103, 146*).

1.5.c. Host-virus evolution and predicting receptor binding: We will use Bayesian and Maximum Likelihood phylogenetic analyses of RNA-dependent RNA polymerase (RdRp) sequences from PCR screening, receptor binding glycoproteins, and/or full genome sequence data (when available) to reconstruct the evolutionary history of the novel bat SARSr-CoVs, bat MERSr-CoV, FVs and henipaviruses that we identify. We will run co-phylogenetic analyses to map out instances of host-switching (*147, 148*) and ancestral state reconstruction analyses **(Fig. 4)** to identify the most important species for shaping evolutionary diversity for these viruses (*51, 149*), allowing for more targeted future surveillance and spillover mitigation interventions. For receptor binding glycoprotein sequence data from characterized viruses, we will apply codon usage analyses and codon adaptation indices, as used recently on henipaviruses (*150*), to assess the relative contributions of natural selection and mutation pressure in shaping host adaptation and host range.

1.5.d. Viral strain prioritization: Of the expected 100-200 novel SARSr-CoV strains, and approximately 600 total CoV strains, we will down-select to prioritize for further characterization based on S genes that are: i) different from SHC014, WIV1, SARS-CoV with diversity ranges of 10-25%; ii) have virus S RBD that could use human/bat receptors; iii) have recombinant chimeric spikes indicative of gene flow between clade I and II strains; iv) have bat ACE2 or DPP4 receptors that might select for spike RBDs that can use human receptors for entry (15/18 conserved residues in human/bat ACE2 molecules that bind SARSs-CoV S RBD domains are likely more efficient receptors than 3/18 conserved sites). Using structural models based on the SARS S glycoprotein, the extent and location of antigenic variation will be annotated onto the structure, further resolving the locations of highly evolving and conserved structural motifs/epitopes that function in protective immunity (*135, 151-153*). For novel henipaviruses, we will examine the receptor-binding proteins (e.g. envelope attachment (G) proteins) for sequence and structural homology with particular attention to conversation of amino acids that mediate ephrin receptor binding. We will prioritize strains that are predicted to interact with ephrin-B2 and expression V/W proteins to determine whether these viruses represent zoonotic threats. Using the recombinant Cedar virus (rCedV) platform, we will be able to rescue rCedV that express heterotypic G proteins to explore receptor utilization and tissue dissemination in animal models. We will assess ability to infect human cells using a continuous lung epithelial cell line, Calu3, which our group has previously used to generate data on NiV and HeV growth curves and a variety of host expression changes after infection (*154*). We will also use primary human airway cultures and microvascular endothelial cells to assess human infection for FVs, henipaviruses and MERSr- and SARSr-CoVs (*155*) (*156*) . There is some evidence for NiV and HeV replication in mouse lung, low level titers in young animals, 10 fold higher titers in aged mice (*157, 158*). Thus it is likely these models could be improved in the collaborative cross mouse resource at UNC. We have identified CC lines that are highly vulnerable to wildtype SARS and others that develop hemorrhagic disease following mouse adapted Ebola infections (*86-88*).

1.5.e. Animal models: We will use <u>transgenic mouse models</u> and the <u>UNC Collaborative Cross model</u> to assess spillover potential of viruses. For work on CoVs, we will follow the protocols in the <u>transgenic mouse model</u> used by the Baric lab previously. Briefly, in the BSL3 lab, 10- to 20-week old hACE2 or hDPP4 transgenic mice will be intranasally inoculated with 5 x 10^4 PFU of full length wildtype rbat CoV, or chimeric SARSr-CoV or MERSr-CoV encoding different bat CoV spike proteins respectively, then monitored daily for weight loss, morbidity, and clinical signs of disease. Mice will be euthanized at 2, 4, and 6 dpi (endpoint of 14 dpi), organs harvested and virus quantified by plaque assay or genome (mRNA1) RT-PCR. After 7 days in formalin, tissues for histopathology will be removed from the BSL3 and stained with H&E, and for immunohistochemistry using polyclonal antibodies against the N protein. We will conduct limited evaluation of existing countermeasures using therapeutic monoclonal antibodies *in vitro*. Existing SARSr-CoV or MERS-CoV mAbs (*159, 160*) will be diluted in DMEM starting at 1:20, and serial dilutions mixed with an equal volume of 50 PFU of chimeric bat SARSr-CoVs encoding different spike proteins and RFP indicator genes, then incubated on Vero E6 cells at 37°C for 1 h. Antibody neutralization titers will be evaluated by plaque quantification at 4-5dpi. In select instances, hACE2 transgenic mice will be injected with SARS-CoV mAbs, and infected with chimeric bat SARSr-CoVs. Clinical signs and morbidity will be assessed and tissue pathology examined and compared with mice without treatment of mAbs to determine the therapeutic effect on SARSr-CoV infection, and protection of SARSr-CoV by wildtype SARS-S based vaccines assessed as described (*132, 161*). We will sequence full length genomes of high risk strains that are antigenically distinct and escape SARS or MERS-

CoV cross neutralization, synthetically reconstruct a small subset (1-2), recover full length viruses and evaluate the ability of nucleoside analogues to inhibit growth in HAE cultures and/or *in vivo* (*63, 132*). For the Collaborative Cross model, we will infect six to eight mice from 6-8 Collaborative Cross mouse lines (10 weeks of age) with six test viruses/yr, intransasally or by subcutaneous infection with 1 x 10e4 virus. Animals will be followed for weight loss, morbidity, mortality and other clinical disease symptoms (e.g., hunching, hindleg paralysis). One half the animals will be sacrificed at day 3 and day 7 pi. to evaluate virus growth in various organs, and organ pathology. In highly vulnerable lines, additional experiments will be performed using more animals, evaluating virus growth, clinical disease symptoms, respiratory pathology, tropism and organ pathology through day 28 pi. We anticipate that some CC lines will prove highly vulnerable to select wildtype viruses, because of host susceptibility combinations that promote severe disease outcomes.

1.6. Potential problems/alternative approaches: Challenges with logistics or obtaining permission for wildlife sampling in sites we select. We have a >20-year track record of successful field work in Malaysia, and >10 years in Thailand, and have strong established partnerships with local wildlife authorities and communities to ensure access. We have existing permissions in place which will be renewed at the start of this project. Due to the abundance of wildlife habitats in the region, if access to a site is withdrawn, we will rapidly identify a suitable, complementary site with similar bat species composition and abundance. Finally, we have already collected tens of thousands of wildlife samples from the region and will focus on these while waiting for permission. **We may not identify novel viruses in our sample wildlife species due to seasonality of viral shedding or other factors.** We have calculated sample sizes based on realistic detection rates from our extensive preliminary data, and are confident that we will detect and identify large numbers of potentially zoonotic pathogens, particularly for CoVs and PMVs. We acknowledge that FV strain diversity may be harder to capture, given relatively low seroprevalence in bat populations – suggesting lower levels of viral circulation (*42, 43*). However, our team was the first and only group to sequence FV RNA from Asian wildlife species (*46, 47, 57*), and we are confident that with our targeted sampling and testing strategy offers the best chance globally to identify additional strains of Ebola and related viruses. The sampling regions we have selected are subtropical, and our previous data, and even published studies in temperate regions (*162*), do not suggest a strong pattern of seasonality in CoV shedding, and where seasonal patterns do occur, i.e. for henipaviruses in Thailand (*163*), or can be predicted from wildlife serology data, we will be sure to conduct sampling at different timepoints throughout the year to account for this.

Aim 2: Identify evidence and analyze risk factors for viral spillover in high-risk communities using novel serological assays.

2.1 Rationale/Innovation: Rapid response requires early detection. Assessing the spillover of rare or novel zoonotic agents will require targeted surveillance of high-risk communities that interface frequently with wildlife that harbor high risk emerging viral strains. To enhance the low statistical probability of identifying these rare events, In Aim 2 we will target rural human communities inhabiting regions identified in Aim 1 as having high viral diversity in wildlife, that also engage in practices that increase the risk of spillover (e.g. hunting and butchering wildlife). We will initially identify 4 subsites in each of Thailand, Peninsular Malaysia, Sarawak, and Sabah for sampling. We will design and deploy human risk factor questionnaires, and specific and sensitive serological assays to identify the baseline frequency, and causes of, spillover of known and related novel viral pathogens in these populations. **We will use the results to test a key hypothesis: that hunting wildlife increases the risk of exposure to novel viruses, compared to the rest of the community.** The alternative hypothesis is that seroprevalence in the general community is not statistically different to those who hunt and butcher wildlife, because exposure to wildlife pathogens is largely through inhabiting a biodiverse landscape where wildlife make indirect contact with people (e.g. via fomites). For participants who report symptoms related to 1) severe/acute respiratory illness (SARI/ARI); 2) Influenza-like illness (ILI); 3) fever of unknown origin (FUO); 4) encephalitis; 5) hemorrhagic fever; or 6) unusual presentation of high fever with severe diarrhea; all within the last 10 days, an additional sample type will be collected, two nasal or oropharyngeal swabs. Samples will be marked for additional PCR-based assays to identify presence of known and novel CoVs, henipaviruses and FVs, and for isolation and biological characterization of potential pathogens, using the approach laid out in Aim 1.

2.2 Preliminary data on high-zoonotic risk human community surveillance: 2.2.a Biological sample collection in SE Asia: Our long-term collaboration in the region has included qualitative and quantitative survey data, and collecting large archives of banked human sera and other biological samples from high zoonotic-risk populations. For example, under the USAID-PREDICT project, EHA has collected 1,400 and 678 specimens in Malaysia and Thailand respectively from people living in zoonotic disease interfaces, all of which will be available for retrospective serological testing by EID-SEARCH which we have ensured is compliant with our existing IRB. Our core group has collected and tested many thousand additional specimens from other important community cohorts **(Table 2)**, and some of these will continue under EID-SEARCH **(Section 2.4)**.

Country, site	Lead	# enrolled, focus	Findings
Peninsular Malaysia	Hughes	9,800+ samples, Orang Asli indigenous pop., for PCR/serol.	25+ novel CoVs, influenza, Nipah ab+ve, FV ab+ve
Malaysia Sabah	Kamruddin	1,283 for serology	40% JE, 5% ZIKV ab+ve
Malaysia Sabah	William	10,800 for zoonotic malaria study	High burden of macaque-origin malaria
Malaysia Sabah	Hughes	150 bat cave workers	Ongoing
Malaysia Sarawak	Siang	500 Bidayuh and Iban people	8% PCR prevalence HPV in women
Malaysia PREDICT	Hughes	1,400 high zoonotic-risk communities for viral PCR, serology	Ongoing. Multiple known and novel CoVs, PMVs, others.
Thailand	Wacharapluesadee	100s of bat guano harvesters/villagers	Novel HKU1-CoV assoc. clinical findings
Thailand PREDICT	Wacharapluesadee	678 high zoonotic-risk communities for viral PCR, serology	Ongoing Multiple known and novel CoVs, PMVs, others.
Singapore	Wang	856, for Melaka virus	7-11% MELV ab+ve

Table 2: Biological sample collection from healthy populations conducted by members of **EID-SEARCH** in our hub countries.

Of particular interest is the access to indigenous communities in Peninsular Malaysia (Orang Asli) and Sarawak (Bidayuh, Iban people), and the bat guano harvesters in Thailand. These communities hunt, butcher and eat wildlife daily, and work in supremely high-risk zoonotic interfaces (e.g. bat caves). One of our indigenous community sites is experiencing an ongoing outbreak of unknown etiology that we are investigating currently **(Section 3.2.a)**.

2.2.b Human Contact Risk Factors: EHA is the lead organization across all 27 USAID-PREDICT project countries for collecting data on, and analyzing the human aspects of, zoonotic spillover risk (*164, 165*). We conducted exploratory studies using standardized one-on-one semi-structured interviews and site observation data with people living in hotspot areas or engaged in high-zoonotic spillover risk activities, using these data to assess local social and cultural norms underlying wildlife contact (*165*). We then developed a risk factor survey to accompany human biological sampling to evaluate the type and frequency of animal contact, wildlife exposure in daily life, occupational risk in markets and long the wildlife value chain, and unusual illnesses reported over the past 12 months. We conducted cross-sectional studies in high risk populations in 27 countries, and study participants provided biological samples (oral/oropharyngeal swab, nasal/nasopharyngeal swab, urine sample/urogenital swab, fecal sample/rectal swab, whole blood, serum, plasma). For example, survey and biological samples were collected from: 1,585 participants from 7 sites in Yunnan, Guangxi, and Guangdong provinces, China; 1,400 participants from 4 sites in Malaysia; and 678 participants from 4 sites in Thailand. Samples were tested with novel serological assays and results analyzed against risk factors from survey data (*16*). In China, CoV-seropositive individuals were mostly farmers/peasants (8/9), living in Yunnan province (7/9), 41-60 yrs old (7/9), with domestic contact with rodents (6/9), that are male (6/9). Although these results are preliminary and don't provide detailed information on routes of exposure, they identify key subpopulations to target that would likely increase the opportunity for identifying evidence of spillover for other CoVs, PMVs and FVs. Data from PREDICT surveys have been used to help identify target populations in Aim 2, identify strategies to better target at-risk people, and conduct focused **human risk factor surveys and serosurveys to produce statistically significant findings for henipaviruses, CoVs and FVs.** In Aim 2, we will use combined biological sampling and risk factor surveillance in targeted populations within the community to 1) test the hypothesis that occupational (i.e. wildlife hunting) risk factors correlate with seropositivity to henipaviruses, FVs and CoVs; 2) assess possible health effects of infection in people; and 3) where recent

illness is reported, obtain biological samples for PCR testing and potential viral isolation and characterization. Obtaining this information could be a significant step in understanding the likelihood of recent 'hidden' spillover events and their public health impacts, as well as the risk of future emergence of viral disease.

2.2.c. Risk factors for illness: Our preliminary data in Thailand, Malaysia and other SE Asian countries revealed that frequent contact with wild (e.g. bats, rodents, NHPs) and domestic animals (e g. poultry, swine) among local communities was associated with a high percentage of self-reported severe/acute respiratory illness (SARI/ARI) and Influenza-like illness (ILI) symptoms **(Section 3.2.b)**. In addition, people involved in crop production, hunting and butchering of wildlife reported statistically significantly higher SARI and ILI symptoms (Li *et al.*, in prep.). **These preliminary data suggest a target population and sites for current proposal with the correct targets for serological surveillance and risk factor surveys in Aim 2 to produce statistically significant findings**. Coupled with better serological tools from our team **(Section 2.2.d)**, we will be able to identify the likely routes of exposure to known or novel coronaviruses, henipaviruses, and FVs in the study region, as well as build data on the illnesses they cause in people.

2.2.d. Serological platform development: Most emerging viruses produced a short-lived viremia in people so that large samples sizes are required to provide enough PCR-positive individuals to analyze infection patterns. For Aim 2, we will focus on serological sampling in the community, because antibodies are typically long-lived and can be used to assess prior virus exposure or infection with much smaller samples sizes (*123*). Most serological assays target a single protein, and for emerging viruses, it's often unclear which viral antigen will be immunodominant during human infection, and therefore which to target in developing serological assays. Co-Is Wang, Anderson (Duke-NUS) and Broder, Laing (USUS) have developed a series of approaches to deal with this problem, and which will be used in testing human biological samples in Aims 2 and 3. Henipaviruses, FV and CoVs express envelope receptor-binding proteins that are the target of protective antibody responses. Co-I Broder has led efforts to express and purify henipavirus native-like virus surface proteins for immunoassay application (*166, 167*), developing monoclonal antibodies (*168, 169*) and as subunit vaccines (*170, 171*), has developed a novel, multiplex microsphere immunoassay (MMIA) allowing serum samples to be simultaneously tested for antibodies reactive with henipaviruses, FVs and CoVs. This MMIA uses a Luminex-based multiplex platform and custom designed virus receptor-binding proteins expressed in a mammalian cell-culture system and purified as native-like oligomeric proteins. These oligomeric antigens retain post-translational modifications and quaternary structures, allowing capture of conformational-dependent antibodies raised during a natural infection, which represent the majority of the protective humoral response. The known diversity of henipaviruses includes five presently described viruses, NiV, HeV, CedV, GhV and MojV and this assay has been expanded to include all described species **(Fig. 11)**. In the past, our collaborators have used NiV and HeV G protein antigens in a MMIA assay to identify a serological footprint of NiV-related African henipaviruses and exposure to virus(es) antigenically-related to NiV in livestock sampled in Bangladesh (*78, 79*). To strengthen serological data interpretation, the G protein from each virus is integrated into the MMIA so that virus-specific vs. henipavirus cross-reactive antibodies can be detected and address specificity of past virus exposure. Extensive cross-reactivity exists among ebolaviruses and between ebolaviruses and marburgviruses (*172-174*). We are validating the MMIA pan-FV assay for specificity, and as part of this, in collaboration with Duke-NUS, we have found serological evidence of past exposure to a filovirus(es) most antigenically-related to ebolaviruses (e.g. Ebola virus, Bundibugyo virus), but unreactive with Reston virus GP in three under-sampled fruit bat species, suggesting that novel FVs circulate within bat hosts in SE Asia (*43*). **This platform has now been set up for use in Malaysia and Thailand and will be available for use in this proposed work.** Co-Is Hughes, Broder, Laing have conducted initial screening of human, wildlife and livestock samples at high-risk interfaces in Malaysia, finding serological evidence of past exposure to viruses antigenically-related to NiV and EBOV in humans, bats and non-human primates (NHPs).

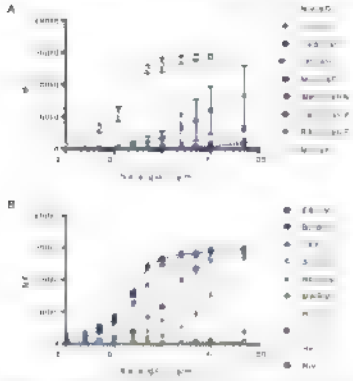


Fig. 11: Validation of multiplex microsphere immunoassay (MMIA) specificity and identification of immunologically cross-reactive viruses for A) NiV B) EBOV.

Co-Is Wang and Anderson (Duke-NUS) have developed a phage-display method to screen antibodies for all known and related bat-borne viruses, including henipaviruses, FVs and CoVs and have set up a similar Luminex-based assay. Additionally the Duke-NUS team has demonstrated capacity for rapid and cost-effective development of LIPS serological assays against novel viral agents **(Sections 2.6.a, 3.2.a)**. These will be used for verification and expanded surveillance. For molecular investigation (Aim 2 & 3), we will combine targeted PCR with a discovery-driven enrichment NGS strategy to not only survey currently known viruses, but also to discover potential novel viruses. Both the phage-display serological and enrichment platforms can be rapidly updated to include new viruses identified.

2.3 General Approach/Innovation: Our human sampling approach uses two approaches in Aims 1 & 2 (Fig. 12). In Aim 2 we will conduct community-based surveillance using a brief, focused questionnaire to identify the prevalence and frequency of risk-factors for viral spillover in tandem with collection of high quality biological samples to determine the seroprevalence of spillover viruses in at-risk human populations. We will use generalized linear models to analyze correlation between biological results and risk-factors for viral spillover. **In Aim 3**, we will conduct clinic-based syndromic surveillance and biological sampling at clinics/hospitals that are the catchment healthcare facilities for the communities sampled in Aim 2. Both community-based and clinic-based syndromic surveillance programs are cross sectional case-control studies designed with the sample sizes necessary to statistically quantify (with a power of 80%) risk factors and health impacts for viral spillover, linked to serological status and PCR prevalence in symptomatic patients. All human sampling conducted under Aims 2 and 3 will adhere to strict criteria for inclusion and recruitment and protection of human subjects from research risk **(see Human Subjects and Clinical Trials Information)**.

Fig. 12: Human sampling approach. Aim 2 **(left)** focuses on serology in high-risk communities to identify evidence of population exposure to novel zoonotic viruses. Aim 3 **(right)** sets up clinical cohorts at hospitals serving these high-risk communities to conduct syndromic surveillance and identify the etiology of new viral syndromes

2.4 Target population & sample sizes: We will target populations in the same geographic regions as those identified in Aim 1 that harbor wildlife with high potential zoonotic viral diversity, that are EID hotspots, and that are well-connected through regional travel and trade hubs to the global travel network **(Fig 13)**. Within each geographic region we will identify populations at four sub-sites, building on our preliminary data **(Table 2)**. We will target specific communities based on our analysis of previously collected behavioral questionnaire data, and other publicly available data (e.g. wildlife hunting licenses sold in a region, number of guano caves accessed for fertilizer etc.) to identify key at-risk populations and occupations with high exposure to wildlife. We will conduct concurrent sampling trips at visits to sub-sites during which members of the community will be enrolled and wildlife surveillance activities conducted. Individuals living or working around wildlife habitats (e.g. bat caves/roosts), who hunt wildlife, work with wildlife or livestock, or slaughtering wildlife will be considered for enrollment. Participants will complete a consent form and questionnaire in addition to having biological samples collected. During these community trips after data collection the field research staff will conduct community meetings to help inform the public health risk of zoonoses. **Target populations:** *Thailand (Co-I Wacharapluesadee):* 100 subjects of healthy high-risk community from 2 study sites, Chonburi (NiV, other PMVs and CoVs found by PCR in bats in our previous work), and Ratchaburi (bat guano harvester villages where we found a MERSr-CoV in bat guano (*50, 175*) and serological evidence of α-CoVs, HKU1-CoV in people (*175*). *Peninsular Malaysia (Co-I Hughes, CM Ltd.):* We will expand our sampling of the Orang Asli indigenous communities to include sub-sites in communities in Districts we have already sampled and

additional Districts in the States of Kelantan Perak, Pahang, and Kelantan all close to bat caves. Samples will be stored and tested at NPHL. *Sarawak (Co-I Tan, Fac. Med. Hlth. Sci. UNIMAS):* We will expand our sampling of the Bidayuh and Iban indigenous people to include the Dayak and Orang Ulu ("people of the interior") because this group has a more intimate connection to remote wildlife-rich areas than the other two, albeit all are hunters. Human sampling will be led by UniMAS in collaboration with CM Ltd / EHA. *Sabah:* We will conduct sampling at the Madai bat and bird cave that has 200 permanent residents who harvest bird's nests for soup, and >1,000 during the harvesting season and at Gomantong cave – one of the largest bat and cave swiftlet nesting sites in the world. *Sabah: (Co-I Hughes):* We will conduct sampling at the Madai bat and bird cave that has 200 permanent residents who harvest bird's nests for soup, and >1,000 during the harvesting season and at Gomantong cave – one of the largest bat and cave swiftlet nesting sites in the world. Protocols follow those for Peninsular Malaysia *Singapore: (Co-I Wang, Duke-NUS):* Active human surveillance will be not be conducted in Singapore, but archived human specimens e.g. from our Melaka virus serosurvey (*8*), will be made available to conduct retrospective serosurveys for specific pathogens that are identified as high interest to the EIDRC, NIH, and EID-CC.

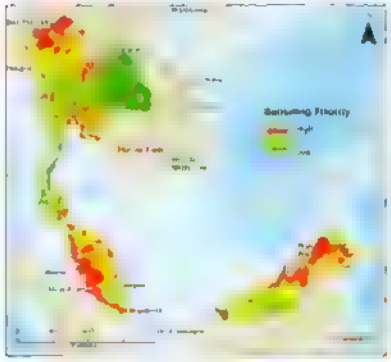


Fig. 13: Targeting high-risk sites for human zoonotic disease surveillance in Thailand and Malaysia. This map plots areas with high numbers of expected viruses in wildlife (*3*), greater spillover probability based on EID risk factors (*2*), and higher levels of connectivity (measured by road density data) that may facilitate person-person spread.

Sample sizes: From our previous work we conservatively anticipate that 10-30% of the community population will have had exposure to wildlife allowing us to capture highly exposed and non-exposure individuals at each site. Individuals living or working around wildlife habitats (e.g. bat caves/roosts) who hunt wildlife, work with wildlife or livestock farming, transportation, selling, or slaughtering wildlife in the surveyed areas will be targeted so that they make up ≥30% of the sampled population in each community. We will stratify sampling to ensure appropriate representation of sex, demographic, and socio-economic factors at each community site. In each of our regions, we will conduct sampling at four sub-sites in populations with high prevalence of high occupational and environmental risk of exposure to wildlife populations, sampling 175 persons at each sub-site. We will target populations with, on average, 30% or higher prevalence of occupational or environmental exposures to wildlife based on data from previous studies. This design will give us >80% power to detect 5 percentage point differences in seroprevalence against any of our viral groups between baseline and high-risk subgroups. We conservatively assume 5% base seroprevalence, as well as assuming high spatio-temporal variance amongst sub-sites, with baseline varying 0-25% amongst sub-sties and the fraction of the population at risk varying from 20-40%. (Power calculation conducted by 500 simulations of a generalized linear mixed model (GLMM)). For community-based surveillance, we will enroll 700 individuals per study region, allowing us to make county/province-level comparisons of differing effects; the total sample will be 3,500 participants over 5 years.

2.5 Data & sample collection: Following enrollment, biological specimens (5mL will be drawn for whole blood and serum collection, samples will be aliquoted, at least one max 500 µL of whole blood and two 500 µL serum samples) will be collected by locally certified healthcare professional proficient in phlebotomy techniques and a short questionnaire will be administered by trained project staff that speak appropriate local language to all participants. Through the serological findings and the survey we will investigate the details of five risk factors related to high risk wildlife exposure, to maximize the power of the analyses, based on continuing analysis of our previous work, and will focus on: 1) occupation and occupational exposures; 2) observed or reported interactions with priority wildlife, especially bats, in/around house; 3) proximity of residence or work place to environments of increased risks, e.g. nearby bat roosts; 4) working or regular visitor to animal markets; 5) self-reported ILI/SARI clinica diagnosis or symptoms in the past 12mo and lifetime. For participants who report the symptoms relating to 1) severe/acute respiratory illness (SARI/ARI); 2) Influenza-like illness (ILI) 3) fever of unknown origin (FUO); 4) encephalitis; or 5) hemorrhagic fever within the last 10 days, an additional samp e type will be collected, nasal or oropharyngeal swab (2x). Blood of participants whose serum tests positive for emerging viral pathogens will be taken and Peripheral Blood Mononuclear Cells (PBMCs) frozen for future use.

These will be used for future harvesting of polyclonal and monoclonal antibodies as potential therapeutics/ diagnostics **(see Letter of Support NEIDL)**.

2.6: Laboratory analysis: 2.6.a Serological testing: We will screen all human specimens for henipaviruses, FVs and CoVs using our novel, multiplex microsphere immunoassay (MMIA) **(Section 2.2.d)**. We will use ELISA and serum neutralization tests (SNT) as confirmatory, where feasible and appropriate for the biocontainment level given sensitivity and specificity variation, and the need for live virus for SNTs **(See Select Agent Research)**. Serologic evidence of local spillover will be used to prioritize zoonotic strains for recombinant virus recovery from full length sequences. Preliminary data suggest ELISA will be effective for some viral groups. We previously developed a SARSr-CoV specific ELISA for serosurveillance using the purified NP of a bat SARSr-CoV (Rp3). The specificity of this assay was evaluated using polyclonal antibodies against HKU1, OC43, 229E, NL63, MERS-CoV and EBOV and no significant cross-activity detected (*16*). **This suggests that if we can expand our NP serology tests to cover other bat CoVs, and that doing so may identify many more seropositive individuals.** For CoVs, we will therefore use two serological testing approaches: 1) testing human sera collected from both community- and clinic- based sampling for a panel of bat CoVs that will include SARS-CoV, MERS-CoV, SADS-CoV and a range of bat SARSr-CoVs (*16*); 2) testing for antibodies to common human CoVs (HCoV NL63, OC43 – **Section 2.8**). We will test panels of NP and G recombinant proteins to assess if this approach will act as a comparison to MMIA for FVs and PMVs.

2.6.b RT-PCR testing. Specimens from individuals in the community who reported being symptomatic within the last 10 days **(Section 2.5)** will be screened using RT-PCR initially for CoVs, PMVs, and FVs following published protocols **(Section 1.4.c)**. Positive samples will be subjected to full genome sequencing and RT-PCR amplification of the glycoprotein genes. Samples from the clinic-based syndromic surveillance will also be tested using RT-PCR for Influenza A & B, HCoV NL63, OC43, HKU1, SARS-CoV & 229E, NiV, HeV, Ebola (WHO PCR protocol) based on the symptom as rule-outs.

2.6.c Biological characterization of viruses identified: Novel viruses identified in humans will be recovered by cultivation or viruses re-derived from full length genome sequences using reverse genetic approaches. Viruses will be characterized for growth in primary human cell lines and in mouse models, including the Collaborative Cross Mice or humanized mice expressing human receptors from related strains. The approaches are discussed in more detail under Aim 1.

2.7 Epidemiological analysis: We will conduct a cross sectional case-control study to identify risk factors for Henipavirus, FVs, and CoVs spillover. "Cases" are defined as participants whose samples tested positive for Henipavirus, FVs, or CoVs by serological tests. "Controls" will be selected from the pool of participants admitted to the studies and whose samples tested negative for Henipavirus, FVs, or CoVs. We will use nearest neighbor matching to pair cases demographically (e.g. age, sex, location) with controls at a 1-to-3 ratio or greater. We will use generalized linear models and least absolute shrinkage and selection operator (LASSO) regression analyses (*176*) to analyze correlation between biological results, serological/PCR status, and risk factors related to high risk wildlife exposure including: 1) occupation and occupational exposures; 2) observed or reported interactions with priority wildlife, especially bats, in/around house; 3) home or work proximity to environments of increased risks, e.g. nearby bat roosts; 4) working or regular visitor to animal markets; 5) self-reported ILI/SARI clinical diagnosis or symptoms lifetime and past 12mo. Additionally, we will use this procedure to determine how clinical presentation differs between Henipavirus, FVs, or CoVs in exposed and unexposed participants, as well as in the time course of illness, severity of symptoms, and type of symptoms.

2.8 Potential problems/alternative approaches: Rarity of spillover events means it may be difficult to identify sufficient seropositives to statistically analyze human risk profiles. First, we will be targeting our community-based surveillance to subpopulations with high-levels of wildlife exposure, at sites selected for diverse and prevalent viruses to increase likelihood of finding positive individuals. Second, our serology testing will include a multi-plex panel of assays for a large diversity of viruses, increasing likelihood of positives. For example, in previous work our overall bat CoV PCR prevalence in the community was, 11.8%; β-CoV, 3.4%; α-CoV, 9.1%). Thus, using this broad serological panel to screen individuals prone to contact with species of higher zoonotic risk increases the potential for detecting spillover with enough power for statistical analyses,

and will shed light on behaviors that predispose to spillover. Third, we will include common human CoVs, PMVs, and influenza viruses in our panel, so that even if low prevalence of wildlife viruses is found, we will be able to conduct a valuable cross-sectional study of the seroprevalence of more common human viruses. Finally, we will be able to assess relative measures of human-wildlife contact from our survey work. We will analyze intensity of contact with high-risk taxa against other risk factors to provide useful proxy information for spillover risk. **Serological testing may be difficult to interpret in the presence of known and novel viruses.** We will use the three-tiered serological testing system outline in **2.6.a** to try to identify exposure to these 'novel' viruses. However, we know exposure to a range of related viruses generates antisera that are cross-reactive with known, related virus antigens - a serious challenge to serological surveillance and diagnostics. Our collaborations have already demonstrated that SE Asia bat sera samples screened with our pan-filovirus MMIA have been exposed to an Ebola-like virus, that is antigenically-distinct from known Asiatic filoviruses, Reston virus and Měnglà virus (*43*). Using these three serological platforms we will address inherent challenges of indirect virus surveillance through antibody capture by testing multiple binding assay platforms and antigens, using positive control samples to establish serological profiles against known viruses that will aid in our interpretations of cross-reactive antisera responses likely representative of 'novel' viruses.

Aim 3: Identify and characterize viral etiology of 'cryptic' outbreaks in clinical cohorts.

3.1 Rationale/Innovation: Our previous research **(Table 1)** and other data suggests that there are substantial numbers of outbreaks or clinical cases for which the etiologic agent is not diagnosed, e.g. (*177, 178*). To investigate this in SE. Asia, we have assembled a multi-disciplinary team that includes senior infectious disease doctors and clinicians and will work directly with local clinics and regional hospitals to identify the 'cryptic' outbreaks or cases that occur in the region. **In Aim 2, we will conduct serology in high zoonotic-risk communities to find evidence of prior exposure in people,** i.e. evidence of viral spillover into the community. In Aim 3 we identify members of these communities presenting at clinic with undiagnosed illness that may have high-impact zoonotic viral etiology. **Therefore, in Aim 3 we focus on PCR to identify the putative viruses that are replicating in these actively-infected patients (Fig. 12).** We will enroll, and collect high quality biological samples from patients who live in rural communities linked to Aim 2 and who present at regional clinics or hospitals with symptoms typical of high impact zoonotic viruses. We will collect detailed survey data to assess their contact type and frequency with wildlife and livestock and conduct molecular and serological diagnostic assays to test causal links between their syndromes and the known and novel viral agents identified in Aim 1. We will conduct molecular viral discovery assays on patients who present with symptoms indicative of a high-risk zoonotic virus. If novel pathogens are identified by PCR, we will attempt to isolate, obtain full genome sequence and/or biologically characterize the wildtype or molecularly re-derived pathogen, using the *in vitro* and *in vivo* strategy laid out in Aim 1.

3.2 Preliminary data clinical surveillance: 3.2.a. Clinical surveys and outbreak investigations: Our longterm collaboration in the region has included the following activities investigating clinical syndromes: *Peninsular Malaysia*: **At the time of writing, an outbreak of suspected undiagnosed viral illness in the indigenous Batek Orang Asli ("people of the forest") community living at Gua Musang ("civet cat cave") district, in Kelantan, Malaysia, close to Taman Negara – a National Park containing the oldest known rainforest**. This community is one where we have conducted prior routine surveillance and biological sampling, demonstrating proof-of-concept that our two-pronged high-risk community/clinic approach will work. Dozens of people are affected and the outbreak is currently being investigated by our group in collaboration with the Malaysian NPHL. The Orang Asli continue to practice traditional subsistence hunting of wild animals (bats, rodents, primates). These communities are remotely located, in heavily forested areas, with limited access to medical services. This outbreak, and others that will continue to emerge just like it, underscore the critical need for our EIDRC - to improve the technological tools, training, and human capacity for rapid EID surveillance, diagnosis, and response at the frontlines of disease emergence in SE Asia. **Investigating this outbreak is a key priority if EID-SEARCH is funded.** *Sabah:* Co-I Kamruddin (BMHRC) is leading an asymptomatic leptospirosis study on sanitation workers, an ILI study in a Kota Kinabalu clinic and diarrheal study in children under 5 yrs. Co-Is William, Tan and others have conducted clinical observational studies to determine the etiology of central nervous system infections and acute undifferentiated febrile illness in Sabah.

Co-Is William and consultant Yeo have collaborated with Co-I Wang to enroll 90 adult and over 100 pediatric participants with central nervous system infections, negative tests for malaria and dengue from 3 district hospitals in Sabah to determine the various etiologies. While a proportion tested positive for rickettsial agents, the majority had no clear diagnosis. Co-Is William, Rajahram, and Yeo have conducted clinical studies of over 200 inpatients with acute febrile illness with negative tests for malaria and dengue from 3 district hospitals in Sabah to determine the various etiologies. While a high proportion tested positive for rickettsial agents, the majority had no clear diagnosis. *Sarawak:* Co-I Siang (UNIMAS) is conducting a survey of high-risk female Kelabit indigenous people and has found 8% with HPV52 as the dominant strain. He is working on clinical cohorts of hand, foot and mouth disease and will recruit patients from that study in the current proposed work. Finally, Co-Is Siang, Kamruddin are conducting a long-term study of rotavirus and other viral etiologies of acute gastroenteritis in Kuching, Sarawak that will include swine herders and farmers. The Baric lab is a global leader in norovirus VLP diagnostic reagents to detect serologic evidence of norovirus gastroenteritis, as well as RT-PCR detection of novel noroviruses in humans, and has identified novel bat noroviruses, suggesting further opportunities for expansion of this work (*142, 179-181*). This work is particularly relevant in Malaysia because pig farms are shunned by the government and local villagers to they are placed far away from town centers, deep in the forest, and it is this scenario that led to the emergence of Nipah virus in 1998-9 (*6, 22*). *Thailand:* Co-Is Hemachudha, Wacharapluesedee (TRC-EID, Chulalongkorn Univ. Hosp.) work in coordination with the Thailand Ministry of Health to investigate outbreak etiology, including the first case of imported MERS-CoV in Thailand, **for which we produced sequence confirmation within 24 hours from acquiring the specimen.** Three imported MERS cases have been detected in Thailand since 2015, and all cases were confirmed at the TRC-EID. We worked during the Zika outbreak to identify > 500 PCR-positive Zika patients with sequence confirmation. We have also worked on returning and suspected Ebola travelers, syndromic surveillance for SARI, encephalitis, Hand Foot and Mouth disease in children and viral diarrhea. Consultant Hickey (US CDC, Thailand), screened specimens collected between 1998 and 2002 from a large cohort of children from Kamphaeng Phet Province to examine Dengue virus and JE epidemiology (*182, 183*). Among the 784/2,574 convalescent sera henipavirus-specific antibodies were detected in 13 serum samples (1.7% seroprevalence), suggesting prior exposure to endemic henipaviruses or a related PMV in rural Thailand. *Singapore:* Duke-NUS has worked with the Ministry of Health to investigate Zika cases (*184*), and other EIDs. With EHA and others, Duke-NUS has developed novel CoV assays for clinical surveillance, and for expedited analysis during outbreaks. Our pipeline of novel virus detection, reservoir host identification, serological assay development, and serological testing is as rapid as several months, with the development of novel serological assays from sequence data in 7 days (*17*). **For example, with the discovery of SADS-CoV, we identified and fully sequenced a new virus, screened archived wildlife specimens to identify the natural reservoir host species (*Rhinolophus* spp. bats), developed LIPS serological assays, and tested human and swine samples to assess seroprevelance in less than 3 months (*17*).**

3.2.b Analysis of self-reported illness: We have developed a standardized approach for analyzing data from study participants on self-reported symptoms related to target illnesses: fever with cough and shortness of breath or difficulty breathing (severe acute respiratory illness - SARI); fever with muscle aches (fevers of unknown origin (FUO); and, cough or sore throat (influenza-like illness - ILI). For all of our prior human clinical surveillance in 20+ countries, including in Malaysia and Thailand, we used a least absolute shrinkage and selection operator (LASSO) regression to identify associations between participants who reported ILI and/or SARI symptoms and demographics, occupation, and contact with animals in the last year. Results have clear biological relevance. For example, in Yunnan, China, factors strongly associated with prior disease involve animal hunting and consumption **(Fig. 14).** We will expand this approach for all clinical syndromes in Aim 3, and use targeted questions to assess patient's exposure to wildlife in terms that are relevant to each specific country.

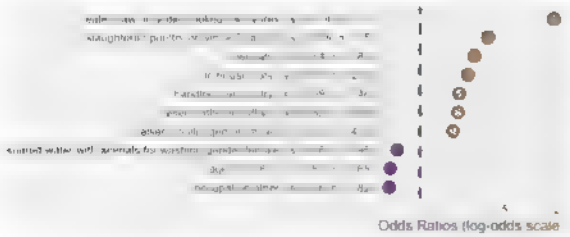


Fig. 14: Factors associated with self-reported ILI & SARI in prior 12 months (s = bootstrap support; n = #+ve out of 1,585 respondents). **Orange circles** = odds ratios > 1 (+ve association); **purple** = odds ratios <1 (-ve association).

3.3 General Approach: Our previous research suggests that there are substantial numbers of outbreak cases for which the etiologic agent has not been identified. To capture these, we will expand on our current syndromic surveillance to enroll, and collect high quality biological samples from patients who present at regional clinics and live in rural communities linked to Aim 2. Case definitions and enrollment criteria include: 1) severe/acute respiratory illness (SARI/ARI); 2) Influenza-like illness (ILI); 3) fever of unknown origin (FUO); 4) encephalitis; 5) hemorrhagic fever; or 6) high fever/diarrhea with unusual presentation. We will collect survey data to assess contact with wildlife, and occupational and environmental exposures, conduct molecular and serological assays to test causal links between their syndromes and the known and novel viral agents identified in Aim 1. If novel pathogens are identified by PCR, we will attempt to isolate and biologically characterize the pathogen, using the collaborative cross to identify an appropriate animal model to conduct preliminary pathogenesis work. We will then use behavioral survey data, ecological and phylogeographic analyses to assess the likely reservoir hosts to inform intervention programs.

3.4 Clinical cohorts. 3.4.a Cohort selection: We will initiate active clinic-based syndromic surveillance at 2 town-level level clinics and 2 provincial-level hospitals in each Thailand, Peninsular Malaysia, Sabah and Sarawak. These serve as the catchment healthcare facilities for people in our community-based surveillance of Aim 2 and are inclusive of wildlife sampling sites in Aim 1. Patients ≥ 12 years old presenting at the health facility who meet the syndromic and clinical case definitions above will be recruited into the study after completing a consent form. We will aim to enroll 300 participants per hospital, with that we will have a 95% probability of detecting live virus in patients in each hospital assuming a population prevalence of 1%. This sampling effort will total of 4,800 individuals for clinical syndromic surveillance. We assume up to 40% loss from follow-up, therefore yielding 2880 participants that will be available for follow-up blood sampling **(Section 3.4.b)**. While enrollment is limited by the number of patients that come to the healthcare facility presenting with relevant clinical symptoms, in our work in the PREDICT project we enrolled an average of 100 participants per year, so we are confident this is an achievable enrollment target. Study data will be pooled across country regions, as clinical patients are limited by the number of individuals presenting at hospitals. "Cases" will be determined as participants whose samples tested positive for either CoVs, henipavirus, or FVs, PCR tests. "Controls" will be selected from the pool of participants admitted to the studies and whose samples tested negative. We will use nearest neighbor matching to pair cases demographically (e.g. age, sex, location) with controls at a 1-to-3 ratio or greater. Sites: *Thailand:* We will work with two primary hospital, Phanat Nikhom Hosp., Chonburi district (Key Pers. Dr. P. Hemachudha) & Photharam Hosp., Ratchaburi Province, and a large tertiary hospital, King Chulalongkorn Memorial Hospital, Bangkok Thailand (Co-I Dr. T. Hemachudha). *Peninsular Malaysia:* **Focusing immediately on the current outbreak in Orang Asli, we will work closely with the Malaysian Ministry of Health to support their investigation, and with 6 Orang Asli clinics which focus solely on this indigenous community.** Co-I Sellaran (Lintang Clinic, Kuala Kangsar) refers patients to Sungai Siput Hospital and Gen. Hospital, Ipoh. Key Pers. I Lotfi (Pos Betau clinic, Kuala Lipis) will continue collaboration with Co-I Hughes in the communities at that site. *Sarawak:* Key Pers. Diyana (Director, Bario Clinic) refers patients to Miri Hospital (Co-I Utap) and serves people from the Kelabit, and nomadic tribes in the region, as well as populations within a number of large towns. *Sabah:* We will continue our collaboration with Queen Elizabeth Hospital, QEH (Key Pers. Lee, Rajahram) and Hospital University Malaysia Sabah, HUMS (Co-I Lasimbang, Director). Both clinics include our targeted sites for **Aim 2** in their catchment, and both have ongoing collaboration with the Borneo Medical Health Ctr (Co-I Kamruddin, Director). *Singapore:* Currently, there are no plans to conduct clinic surveillance based on budget constraints. However, in the event that that is an evolving need for clinic surveillance, enrollment, and sampling, we have close working relationships with all hospitals in the country, and the central infectious disease reference lab (key clinicians at which are aware of our proposal). This would allow us to rapidly on-board a hospital based site.

3.4.b Clinic enrollment and follow-up: We will recruit inpatients and outpatients to participate in the study after initial screening to determine if they meet our clinical case definitions. Once consented and enrolled, biological samples will be collected by trained and locally certified hospital staff and a questionnaire administered by trained hospital or research staff that speak appropriate local language. Every effort will be made to take samples concurrently when collecting samples for normative diagnostics. For both inpatients and outpatients, samples will be collected no more than 10 days of reported onset of illness to increase the chance

of PCR detection of viruses (*185*). Where possible, we will follow up 35 days after enrollment to collect an additional two 500 µL serum samples conduct a standardized questionnaire supplement to collect additional data on the course of symptoms in the interim period. This gives adequate time for development of IgG, which occurs <28 days after onset of symptoms for SARS patients (*186-188*). Serum samples will be used to screen panels of high risk human and local zoonotic Filovirus, Henipavirus and Coronavirus strains as described in Aim 2. These samples may prove valuable to collaborators in that the PBMC could be used in production of therapeutic antibodies.

3.4.c Sampling and clinical interview: Biological specimens whole blood (5mL will be drawn for whole blood and serum collection, samples will be aliquoted, at least one max. 500 µL whole blood; two 500 µL serum samples) and two nasal or oropharyngeal swabs will be collected from all participants, and a questionnaire will be administered. We will investigate five risk factors, to maximize the power of the analyses, all related to high risk wildlife exposure, based on continuing analysis of our previous work, and will include: 1) occupation and occupational exposures; 2) observed or reported interactions with priority wildlife, especially bats, in/around house; 3) proximity of residence or work place to environments of increased risks, e.g. nearby bat roosts; 4) working or regular visitor to animal markets; 5) self-reported ILI/SARI clinical diagnosis or symptoms in the past 12mo and lifetime. With additional consent considerations for participants enrolled from clinical settings, we will review clinical records to collect data on medical history, clinical syndromes, and patient etiology. Blood will be taken for future harvesting of Peripheral Blood Mononuclear Cells (PBMCs), as per **Section 2.5**.

3.5 Sample testing: The standard syndromic diagnostic PCR assays for common pathogens will be conducted and the results will be shared with the hospital with 48 hours. Specimens will be further tested for 3 viral families; CoV, PMV and filovirus by consensus PCR **(Section 1.4.c)**. Necropsy samples from deceased patients will be further characterized by NGS if previous PCRs are negative and unable to identify the cause of infection. Co-Is Wang, Anderson will conduct a VirScan serological assay using paired serum samples at Duke-NUS that identifies antibodies with a four-fold rise in titer in the convalescent sample compared with the acute sample, thereby indicating a possible etiological agent. A PCR test with the specific primer from each virus antibody positive case will be further tested from acute specimens to confirm infection

3.6 Viral risk characterization and potential for pandemic spread: We will use statistical models built from collated biological, ecological, and genetic data to assess the likelihood of pathogenicity for the range of diverse viruses we will characterize. The aim is to quickly identify and assess which viruses pose the most significant risk to human health and thus prioritize additional resources to more fully characterize, better understand pathogenicity, and invest in our animal model pipeline and ultimately therapeutic development for those pathogens. We will combine two independent but related statistical models to predict pathogen spillover risk and pathogenicity. First, we will expand a simple generalized additive modeling approach (*3*) to assess spillover risk probability to a new virus that is currently not known to infect people, when we have only limited genetic data from initial PCR screening and sequencing. Additional data from receptor binding protein homology and cell line infection experiments will be incorporated into the model framework as available. Second, given high likelihood to spillover and infect humans, or direct evidence of human infection from our clinical surveillance, we will then assess the likelihood of pathogenicity based on traits for phylogenetically related nearest neighbor viruses as a first approximation and incorporating more detailed data from genomic characterization and animal model experiments (Aim 1). Epidemiological trait data for ~300 viral species known to infect people (e.g. case fatality rate, global estimates of number of human cases per year or decade, R_0, infectious period, and primary symptoms) have been collated by recent studies and will be used as predictor variables (*189*). Thirdly, we will apply tools already developed, and being refined by EHA under DTRA and DHS supported research, to predict pandemic spread for viruses using global flight models, as well as additional datasets on human movement and connectivity across Southeast Asia (*90, 91*) **(Fig. 15)**.

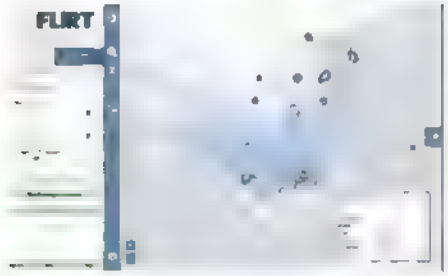


Fig. 15: Probability feed from EHA's Flight Risk Tracker tool (FLIRT). This image is of the likely pathways of spread and establishment for a Nipah-like virus emerging from Sabah, based on human movement and airline flight data (*90, 91*).

3.7 Potential problems/alternative approaches: Patients visiting clinics may have cleared virus, but not yet developed IgG antibodies, reducing seropositive cases. Our 35 day follow-up sampling should account for this because the maximum lag time between SARS infection and IgG development is ~28 days and Ebola virus infection and IgG approximately 20 days (*185-188, 190*). We also expect that patients in rural communities will only visit clinics when symptoms have progressed, likely coinciding with late illness and onset of IgG. We will also have data from our community study that can be analyzed in conjunction with, or in the absence of, clinical data from the hospital data to identify PCR- or seropositives. Finally, the risk of limited detection is outweighed by the potential public health importance of discovering active spillover of new henipaviruses, FVs or CoVs infection.

4. Administrative Plan

4.1. Project management: **4.1.a. Administrative core:** The EID-SEARCH organizational partner roles are laid out by Specific Aim above **(see Fig. 3)**. EcoHealth Alliance (EHA) will lead the administrative core of the EID-SEARCH, including: coordination and management of all human and animal research; communication with consortium partners, NIH, other EIDRCs, and the EIDRC-CC; data management and quality assurance; modeling and analysis; and compliance with all US, international, and institutional rules and regulations. The administration will be led by PI Daszak, who has >20 years' experience managing international research collaborations on emerging zoonoses, and has collaborated with all partners in the EIDRC consortium for 5-20 yrs on NIAID- and USAID-funded research **(Fig. 16)**. He also has direct experience as one of two external reviewers of one of the CEIRS partners for NIAID (Program officer Diane Post). PI Daszak will be assisted by Deputy Lead, co-I Olival, who has overseen zoonotic disease research in Southeast Asia for >10 years and working directly with our partners in Thailand and Malaysia for 15 years. Senior program manager (Chmura) and full-time program assistant (Hamel) will provide administrative support. The EID-SEARCH data management, epidemiological analysis, and modeling activities will be led by co-Is Olival and Zambrana who have led all modeling and analytics on USAID USAID PREDICT for the last 10 years. They will overse a programmer/data scientist (Mendelsohn), evolutionary biologist/bioinformatician (Latinne), and human epidemiologists (Dawson, Li, Martinez). Our human epidemiology team will work directly with country teams in Malaysia and Thailand to manage human surveillance, IRB applications and approvals, and ensure compliance with all human subjects work. EHA's senior veterinarian (Field) and wildlife field biologist (Phelps) have extensive experience working that bats, rodents, and primates in SE Asia and will coordinate all training and field research in Malaysia and Thailand and ensure compliance with IACUCs.

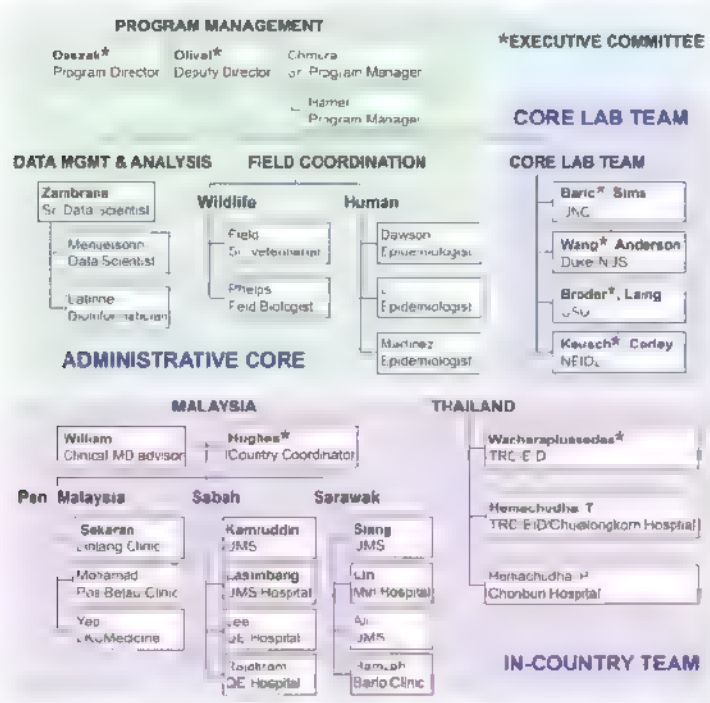


Fig. 16: Administration and program management for the **EID-SEARCH**

The EID-SEARCH core laboratory team includes global experts in virology, molecular pathogenesis, and the development of assays, reagents, and therapeutics for high consequence viral zoonoses (Co-Is Wang, Anderson at Duke-NUS; Baric, Sims at UNC; Broder, Laing at USU; Keusch, Corley at NEIDL). The core laboratory team will work with in-country diagnostic labs in Thailand (Wacharapluesedee, Hemachudha at the TRC-EID, Chulalongkorn University) and Malaysia (Hughes, Lee, CM Ltd.). Wacharapluesedee and Hughes will additionally serve as country coordinators for the EID-SEARCH, liaising directly with EHA on weekly conference calls, and working with in-country partners to ensure the smooth operation and coordination of clinical and community surveillance and wildlife research in Thailand and Malaysia, respectively. **A Core Executive Committee** comprising PI Daszak, Deputy Lead and Co-I Olival, and leads from each core partner and country: Co-Is Hughes, Wacharapleusadee, Baric, Wang, Broder, Keusch (or alternates), will conduct

regular conference calls and in-person meetings to facilitate rapid decision making within the EID-SEARCH. **This committee will also convene to manage EID-SEARCH response to outbreaks.**

4.1.b Project Management in Thailand and Malaysia: Wacharapluesedee and Hughes have collaborated directly with EHA for >15 years, including acting as country coordinators on the USAID PREDICT project for the last 10 years (project end date Sept. 2019). They maintain strong ties with Ministries of Health (MOH), Agriculture and Environment, multiple universities and research institutions, clinics, and hospitals, in their respective countries and across the region. The EID-SEARCH will use these connections to disseminate results, obtain permissions to conduct sampling, and also rapidly respond to and assist with outbreaks as they happen. Peninsular Malaysia, Sarawak, and Sabah are the three main Malaysian administrative regions, and effectively operate as three separate countries, with different regulations and government structures. We therefore provide specific details on the management of EID-SEARCH activities in each:

Coordination among Peninsular Malaysia, Sabah and Sarawak will be led by co-I Hughes (Conservation Medicine Ltd), and follow a successful model we implemented under USAID-PREDICT. **On Peninsular Malaysia** this project will be administered through the Zoonosis Technical Working Committee (ZTWC) established under the PREDICT project with a binding MOU among EHA, CM Ltd. and ZTWC, and including officers from MOH, Dept. of Veterinary Services, and PERHILITAN (the Govt. wildlife agency). EHA will communicate weekly with Co-I Hughes to coordinate and monitor implementation of research and reporting to ZTWC. Co-I Hughes will coordinate activities at all other Peninsular Malaysia institutions: NPHL, the National reference laboratory for diagnostic confirmation of pathogens, will manage molecular and serological screening (BioPlex) of Orang Asli samples, and serological screening of syndromic samples from Sabah and Sarawak; the PERHILITAN molecular zoonosis laboratory will store and conduct molecular and serological screening on wildlife samples; and Universiti Putra Malaysia (UPM) Faculty of Veterinary Medicine will conduct molecular and serological screening (BioPlex) of livestock samples, should these be required. **For Sabah & Sarawak**, work will be administered through the Sabah Zoonotic Diseases Committee (SZDC), a working technical committee comprising appointed and authorized officers from Sabah State Health Dept., Department of Veterinary Services, Sabah Wildlife Dept. (SWD), Universiti Malaysia Sabah (UMS) and EHA, all of which are also committed through a signed MOU. Co-I Hughes will oversee work at all other partners in Sabah, including: the Kota Kinabalu Public Health Lab (KKPHL) for molecular screening of syndromic samples from Sabah and Sarawak; the SWD Wildlife Health and Genetic and Forensics Lab for molecular screening of Sabah wildlife samples; The Borneo Medical Health Research Center (BMHRC) for screening some Sabah wildlife and livestock samples, if required, and human syndromic samples from Sabah and Sarawak. **In Thailand** all human community and wildlife research and testing will be coordinated by co-I Wacharapluesedee from the TRC-EID center. Clinical surveillance will be overseen by senior clinical physician and co-I T. Hemachudha.

4.1.c. Approval and release of results: In our experience, it is critical when working in resource-poor countries, on potentially important pathogens, to strictly adhere to protocols for release of results. EID-SEARCH will liaise with existing points of contact in the Ministries of Health, Environment, and Agriculture in each our administrative areas to approve and release project findings publicly. Results from human screening will be shared with participants when they become available, as per our IRB agreements ensuring no violations to anonymize data requirements (**see Protection of Human Subjects**).

4.2. Flexibility to extend the EID-SEARCH to new sites as needed: The EID-SEARCH consortium partners maintain extensive working relationships with leaders in EID outbreak control, clinical investigations and research at over 50 clinics, research institutes and public health laboratories across Southeast Asia. Due to space constraints, we haven't listed each of these, nor have we solicited >50 Letters of Support for this project. However, each core EID-SEARCH partner has contacted their networks and obtained permission for inclusion in the broader goals of the EIDRC. As examples of these contacts, our core partner, the Thai Red Cross Emerging Infectious Disease Health Science Centre (TRC-EID) at Chulalongkorn University, also serves as the WHO Collaborating Centre for Research and Training on Viral Zoonoses and has ongoing research collaborations across WHO SEARO countries including Bangladesh, Bhutan, Democratic People's Republic of Korea, India, Indonesia, Maldives, Myanmar, Nepal, Sri Lanka, (Thailand), Timor-Leste; and has recently served as a training hub for scientists from Malaysia, Myanmar, Laos, the Philippines, and China to learn methods of wildlife sampling and diagnostic screening. Our Thai clinicians (Co-I T. Hemachudha and KP P.

Hemachudha) provide regular case consultations and clinical trainings for doctors across SEARO countries, including with Yangoon General Hospital and the National Health Lab in Myanmar, 2018. To maximize leverage of this broad network, EHA has budgeted for annual meetings in SE Asia, in addition to regular smaller network meetings, with our core team and key public health experts from network labs in each of the 10 SE Asian countries. Additionally, we will set up a listserv and an internal communication network to facilitate collaboration and information exchange, including on the first reports of new disease outbreaks. Our annual and smaller network meetings will critically allow face-to-face meetings of the EID-SEARCH that will foster greater sharing of information on novel research and diagnostic approaches, pathogens that are of key pandemic potential, regions or populations at high risk of spillover, and information from the greater network on likely outbreaks of novel disease. This platform will coordinate sample sharing and diagnostic platforms and help build a rapid response to outbreaks in the region, guided by the PI, Deputy and the Executive Committee.

4.3. Outbreak response: EHA collaboration with expert networks around the world allows us to mobilize and enhance effective One Health response to disease emergencies (*191*), ranging from real-time situation updates and risk analyses to on-the-ground investigations (*192-194*). We will adopt management tools from Emergency Operating Center (EOCs) (*195*) and Incident Management Systems (IMS) (*196*), to shift resources where necessary to help respond to novel zoonotic outbreak events and other public health emergencies. EHA has extensive experience working with governments in low and middle income countries (LMIC) applying these principles of epidemic preparedness during outbreak responses we've been involved with under the USAID-PREDICT project. For example, at the request of the government of Bangladesh, we provided technical field and laboratory support for Nipah virus and avian influenza outbreak investigations, assisting with wildlife sampling as part of the outbreak response alongside human and domestic animal sampling. In India, we provided technical assistance in response to the Nipah virus outbreak in Kerala in 2018. Last month in Indonesia were assisted the Ministry of Health's Center for Health Laboratory in Makassar to provide technical assistance in a mysterious outbreak in a small village in South Sulawesi that killed 4 villagers and infected 72. Our network partners include the key government and govt. approved laboratories that would be directly involved in public health emergency response in their respective countries. The serological and PCR platforms that EID-SEARCH develops will be made available to the main government outbreak investigation teams for clinical work and research during the outbreak. EID-SEARCH will also offer assistance training and conducting animal sampling during an outbreak, epidemiological analysis and modeling to help identify likely reservoirs or likely pathways to spread. Technical and material support for lab, field and analytical activities during an outbreak will be provided by EHA, UNC, USU, Duke-NUS, and NEIDL, as well as in-country partners. Any clinical samples, viral isolates and sequence data will be shared among partners to promote the rapid development of new diagnostic assays, reagents, and therapeutics that can be deployed to the region or other regions as part of the larger NIH EIDRC network.

Finally, while the initial pathogen focus of our group is on CoVs, PMVs and FVs, our broad collaborative group has multidisciplinary expertise on a number of virus-host systems. For example: PI Daszak was PI on a subaward from PI Laura Kramer's U01 on Poxviruses and Flaviviruses, managing a multidisciplinary research project on West Nile virus ecology. He was also co-I on a 5-year NSF-funded project to understand West Nile virus dynamics and risk in the USA (*197-201*); Co-I Baric is a global leader in Norovirus research leading to the development of vaccines and therapeutics (*202-205*); Co-I Wang has conducted significant work on bat immunology, therapeutic, and reagent development, as well as being involved in a range of outbreak investigations, viral discovery programs and other research on a wide diversity of viral groups (*206-215*). Additionally, the serological and PCR-based diagnostic platforms being developed by Co-Is Wang and Broder are adaptable to other viral targets. The modeling tools developed by Co-Is Olival and Zambrana-Torrelio can be used to predict the emergence and spread of diverse viral targets, including influenza, antimicrobial resistance, and vector-borne diseases (*216-221*). Our clinicians working in Thailand and Malaysia have a wide range of infectious disease investigations to adapt to any outbreak situation.

4.4. Communications: EHA will coordinate communication among all co-Is and key personnel, including:

- Multiple meetings per week with PI, Deputy Lead, Senior Program Manager (on project and task status)
- Weekly web/phone meetings between Program Manager and subawardee admin. staff
- Monthly web/phone conferences between EHA PIs and all subawardee PIs.

- Monthly web conferences between key personnel (research presentations/coordination)
- In-person Annual meetings with partner leads, key personnel at EHA and two in-person partner meetings annually between subawardees.
- Annual in-person meeting among all key personnel

4.5. Problem identification and resolution: Regular planning, monitoring, and evaluation meetings will be the primary mechanisms for problem identification. Minor problems (e.g. delays in sample availability or test results) will be dealt with internally through appropriate action and resolution monitored by PI Daszak and co-I Olival, and our Senior Program Manager. In the event of significant problems, such as prolonged poor productivity, inadequate scientific collaboration, or major disputes regarding research direction or resource allocation, EHA will assist with resolving the problem through negotiation with relevant co-Is and consultation with the Executive Committee. Should a resolution not be forthcoming, consultation with the EIDRC-CC, additional external technical advisors, and NIH staff may be warranted.

4.6. Adaptive management and risk mitigation: Maintaining a timeline and meeting milestones will require strict and continuous oversight of all project phases, frequent and regularly scheduled communication, and the ability to make decisions and implement strategies. To maintain our timeline on all projects, including the EID-SEARCH, we use an adaptive management approach to continually evaluate these trade-offs, to make decisions about when iteration is appropriate and when it is necessary to move forward with current information. Our ethos is that regular, scheduled communication among all staff, partners and collaborators will go a long way towards mitigating risks, especially if the process is collaborative and transparent.

5. Data Management Plan

EHA will house the Data Management and Analysis (DMA) team for EID-SEARCH, led by Co-PIs Olival and Zambrana-Torrelio and include Key Personnel Latinne and Mendelsohn. EHA has served as the data and analysis hub for numerous multi-institutional, multi-sectoral, international disease research groups, including acting as Modeling and Analytics lead for the PREDICT project (*122*), the Western Asia Bat Research Network (*222*) and EHA's Rift Valley Fever Consortium. We will leverage our experience and infrastructure from those projects to benefit the EID-SEARCH. **5.1. Project Database:** We will create a dedicated, centralized EID-SEARCH database to ingest, store, link, and provide for analysis all data associated with the proposed study and other expanded projects associated with the research network. The database will be SQL-based and use encrypted, secure cloud hosting services and enable export to archival and platform-independent formats. It will ensure data and metadata compatibility between project components, track data versioning and annotations. The system will be designed to work with both with both paper- and tablet-based field data entry and with the Lockbox laboratory information management systems **(Section 5.2)** in place in individual partner labs. The database will use existing metadata standards, including NCBI standards for genetic and molecular data and Ecological Metadata Language (EML) for field and wildlife data, as well as other standards and formats designated by the EIRDC CC. This will enable rapid publication and deposition of data. Granular security and privacy controls will be applied so that specific expansion projects undertaken in the network may be managed while maintaining data confidentiality as needed.

5.2. Biological Specimen Management: Project laboratories will use the Lockbox Laboratory Information Management System (LIMS), to manage the security, traceability, and quality of biological specimens. The LIMS will support sample barcoding at creation, tracking through transport, storage/inventory, and use via portable scanners. Lockbox supports CLIA and ISO 17025 as well as direct export to NCBI formats such as Sequence Read Archive. We will use the Lockbox LIMS application programming interface (API) to link to the central project database and associated samples with field and ecological data. We note that the project focuses on highly pathogenic viruses, including select agents; Lockbox LIMS supports sample tracking and movement compliant with US Select Agent Regulations and US Department of Commerce Pathogen Import and Export Control Regulations, and includes all necessary encryption, security, and backup protocols.

5.3. Training: Members of the DMA team will team will develop documentation and provide training for field and laboratory teams at all partner institutions in data management, metadata standards and data hygiene best practices. The DMA team will act as trainers and consultants for partner institutions in experimental

design, power analysis, data analysis, and computational and reproducibility issues, and visit each partner institution and/or field team base for training workshops and analysis consultations.

5.4. Data Identification and Privacy: For human clinical data and questionnaires, data will be identified by a unique identification code assigned to each individual and only this, de-identified code will be accessible in the project database, and destroyed at the end of the project - as per details provided in the Clinical Management Plan and Protection of Human Subjects forms.

5.5. Computing Resources: EHA operates a cluster of high-performance servers for data analysis activities, as well as infrastructure to launch cloud-based computing environments (**see EHA Facilities**). Our servers host all necessary software for statistical and bioninformatics work that is available to the DMA and partners anywhere in the world. We use a mixture of cloud services (AWS, Azure, Backblaze, GitHub) to provide redundancy, backup, version control, and rapid post-disaster recovery, and will be available to all project partners for analysis and training.

5.6. Data and Code Sharing: See details provided in the **Resource Sharing Plan.**

6. Clinical Management Plan

6.1. Clinical site selection: Our consortium partners have been conducting lab and human surveillance research, including during outbreaks, for >20 years and have developed strong relationships with local clinical facilities and processes in SE Asia and in LMIC globally. The plan for selection of clinical sites will begin in the same geographic regions as those identified in Aim 1 with high zoonotic viral diversity. Clinical sites will additionally serve as the catchment healthcare facilities for people in our community-based surveillance of Aim 2. We have already developed successful working relationships with the major healthcare facilities in Thailand and Malaysia and will use these established partners to rapidly gain appropriate permits and begin data collection quickly. Focusing on these EID hotspots in select biogeographic areas (see **Fig 13**) also reduces the number of additional sites needed to meet our goals within our geographic range. The capacity and capability requirements for clinical sites are fairly minimal, and include ability to enroll patients that meet the clinical case definitions of interest, collect and temporarily store biological samples, and follow standards for data management and subject protection with locked filing cabinets to store all paper records and an encrypted computer. We will be enrolling inpatient and outpatient participants within 10 days of the presentation of symptoms to increase the chance of PCR detection of viruses so we will not wait for advanced normative diagnostic tests, that are likely unavailable in the more remote sites, to be completed. We will work with clinical sites to determine the best process for project staff, in most cases supporting the time of currently hired staff at each site. We will recruit and train hospital staff in project-specific procedures including enrollment of patients, sample types to be collected, storage of samples, administration of the questionnaire, and data management plans. During the development and onboarding of new clinical sites we will assess the physical needs of the site and what supplies will be required for collection of data.

6.2. Standardized approach, oversight, and implementation: Management and oversite for all study sites will be undertaken by the local country coordinator with support from our Core Administrative team at EHA. Our research team has over 10 years of experience building capacity on human subjects' research and has developed training resources and materials for standardized implementation of community and clinical research and SOPs for screening, enrollment, and retention of participants. The country coordinator will conduct regular site visits to the clinical sites and annual visits to observe, monitor and evaluate the research process, and conduct follow-up training if required. Through our work with clinical sites under the USAID-PREDICT project we have developed culturally appropriate screening measures for clinal sites that do not disrupt the flow or quality of medical treatment received by the patient. This was done by working collectively with clinical staff to evaluate current procedures and patient flow at the site to determine the most efficient while minimal invasive inclusion of our study into the daily working of the clinal site. Most efficiently this was done by adding minimal basic screening questions to the current clinal intake forms, which allows the clinal research officer to quickly scan charts or logs for potential patients to enroll avoiding potential enrollees from being overlooked if staff are too busy or not on duty. Patients will be enrolled following established clinical criteria (**see Section 6.3**), samples collected and brief surveys conducted to assess the participants contact with wildlife through: 1) occupational exposures; 2) animal contact; and 3) the environment. With permission

from each clinic, and consent from participants, we will review clinical records to collect data on medical history, clinical syndromes, and patient etiology. Additionally, we will be following up with clinical participants to determine how clinical presentation differs between CoV, henipavirus, or FV in exposed and unexposed participants, as well as in the time course of illness, severity of symptoms, and type of symptoms. The country coordinator will be continually monitoring the project database to ensure we hit target sample sizes. While patient's enrollment is limited by the number of individuals presenting at hospitals, in previous research we enrolled an average of 105 patients per year, ranging from 77-244.

6.3. Clinical cohort setup, recruitment, enrollment: We will recruit inpatients and outpatients from clinical sites to participate in the study after initial screening to determine if they meet the clinical case definitions for 1) severe/acute respiratory illness (SARI/ARI); 2) Influenza-like illness (ILI); 3) fever of unknown origin (FUO); 4) encephalitis; 5) hemorrhagic fever, of unknown etiology or severe diarrhea with unusual presentation for symptoms to increase the chance of PCR detection of viruses. Once enrolled, biological samples will be collected by trained hospital staff. When possible, samples will be taken concurrently with samples being collected for normative diagnostics. We will collect 5mL of blood for whole blood and serum collection, samples will be aliquoted, at least one max. 500 µL whole blood; two 500 µL serum samples and two nasal or oropharyngeal swabs will be collected. Controls who test positive for CoVs, FVs, or Henipaviruses will be selected from the pool of participants admitted to the studies and whose samples tested negative for coronaviruses, henipavirus, or filoviruses. We will follow up 35 days after enrollment to collect an additional 5mL blood draw for collection of two 500 µL serum samples and a standardized questionnaire supplement to collect additional data on the course of symptoms in the interim period. Following up 35 days post initial collection gives adequate time for 1) development of IgG and IgM, which occurs <28 days after onset of symptoms to evaluate the immunological progression of disease and 2) further the risk assessment of the participants to monitor contact with wildlife, people, and to assess the likely reservoir hosts to collect information to inform potential intervention programs.

6.4. Utilization of collected data: Sampling of wildlife and the enrollment of community surveillance participants and a clinical cohort of participants give us the ability to assess the viruses that are circulating in each of the three populations in a similar geographic region. We will use phylogenetic analysis to compare the relationship between wildlife viruses found and viruses fond in human participants. Additionally, the questionnaire data will allow us to assess relative measures of human-wildlife contact that we will analyze the intensity of contact with species known to be at a higher risk for spillover against other risk to provide useful proxy information for spillover risk. The clinical cohort will be split into cases and controls. "Cases" are defined as participants whose samples tested positive for either CoV, henipavirus, or FV via PCR tests. "Controls" will be selected from the pool of participants admitted to the studies and whose samples tested negative. We will use nearest neighbor matching to pair cases demographically (e.g. age, sex, location) with controls at a 1-to-3 ratio or greater. In clinical study, we will use this procedure to determine how clinical presentation differs between virus-exposed and -unexposed participants, as well as in the time course of illness, severity of symptoms, and type of symptoms. We will model the outcomes to analyze correlation between biological results and risk factors related to high risk wildlife exposure. With this collective data set we aim to quantify and detect novel viruses likely to spillover regularly to people, are often unreported or misdiagnosed as their clinical manifestations, and are unknown to detect cryptic outbreaks causing previously 'hidden' clinical syndromes in people. Our strategy for targeted surveillance and detection of spillover and illness in at-risk human populations can be used as an 'early warning system' to conduct public health interventions and disrupt disease emergence.

6.5. Development of reagents of value to the community. Members of the EID-SEARCH consortium have substantial experience producing reagents, assays, and other products that are used widely by the clinical and research community, and some of which are on a pathway to commercialization. These include: PIs Daszak and Co-I Olival have produced software for analyzing the spread of novel viral agents through air travel networks; Co-I Baric has collaborated with a Norovirus surveillance collaboration with surveillance cohort at CDC and has developed therapeutics that have reached phase 2 and 3 clinical trials, He is currently working with Takeda Sanofi Pasteur on a Dengue therapeutic and with NIH on a tetravalent vaccine, Co-I Broder

developed a Hendra virus subunit vaccine that was commercially produced by Zoetis for horses and is labeled for human use under compassionate circumstances during outbreak situations.

6.6. Potential expansion: Expansion of the research project to other clinical sites or research areas could happen as new information is gathered, either through our research, the EID-SEARCH information network, or an outbreak being identified in the region by other organizations. If expansion is required we would rapidly shift research activities towards the clinical or community sites where the outbreak is active, using the same process we used to set up initial research locations. First, by working with local stakeholders to create a working relationship and on-boarding new clinical research staff through advanced trainings of project aims, SOPs on data collection and storage, and ethical guidelines. The network of infectious disease researchers in the community and hospital settings would allow for an accelerated response to any potential infectious disease outbreaks as staff are well trained on ethical guidelines for working with human subjects, data and specimen collection, storage, and transpiration, project staff would be on the front lines ready for the call to action. Ideally, our testing for viruses in priority viral families may lead to the discovery cryptic outbreaks before it spreads in the general public. Biological results coupled with survey data on key risk factors will provided necessary information for granular understand of disease spread.

7. Statistical Analysis Plan:

7.1. Framework: Statistical analyses across the project will be conducted under a common Bayesian framework. These models provide a unified, probabilistic approach best-suited for estimating effect sizes in heterogenous populations of human clinical and wildlife subjects in observational studies. Within this Bayesian framework, we will use generalized linear mixed models to estimate population prevalences and seroprevalences, and estimate the effects of demographic, occupational and environmental factors affecting these. We will use occupancy models (*223*) to estimate total viral species and strain diversity and completeness of sampling within the human and wildlife sub-populations, and discrete phylogeographic models to identify taxonomic and geographic centers of viral diversification. All statistical analyses will be performed reproducibly using scripted, programmatic workflows (e.g., the R and Stan languages) and maintained under source code version control (git). As with data management, the DMA team will act as trainers and consultants for exploratory data analysis, power analysis, and study design with project partners, and the EHA computing cluster will be available for partners undertaking additional or expansion studies. Power analyses, current and expansion, are performed via simulation approaches allowing planning for complex, hierarchical variation in study populations. Power analyses and specific analytical components of this study are detailed under each Specific Aim.

7.2. Data Quality Control and Data Harmonization: All data will be are examined at entry by field and lab teams upon data entry, followed by examination by DMA team members at upload and integration, for complete de-identification, completeness, accuracy, and logical consistency. The DMA will provide field and lab teams with reports, produced automatically, of data summaries, including aggregates, distribution, detected outliers and possible mis-entries. On a regular basis (quarterly or as-needed during data collection), DMA team members will review reports with field and lab teams to identify errors and update collection and entry procedures as necessary.

7.3. Statistical Considerations for Behavioral Questionnaires and Clinical Metadata: The data collected from the questionnaire will be analyzed to assess the reported measures of contact for each risk group under study, related to1) occupation and occupational exposures; 2) observed or reported interactions with priority wildlife, especially bats, rodents, and primates in/around house and other livestock animals (e.g. farming, butchering, slaughtering); 3) proximity of residence or workplace to environments of increased risks (e.g. nearby bat roosts); 4) working or regular visitor to animal markets; 5) self-reported ILI/SARI clinical diagnosis or symptoms in the past 12 months and lifetime. Specific measures we are interested in are the proportion of respondents indicating they consume wildlife, where wildlife is obtained for consumption, have hunted wildlife, butchered or slaughtered live animals, seen wildlife in their homes, been bitten or scratched by animals, etc. Comparisons of measures of exposure contacts and types between men and women, children and adults, different study regions will be conducted in order to explore the occupational, environmental, and demographic factors (gender, age, socioeconomic status (SES)) that influence contact with animals and to determine who is

most at-risk. Stat stical analysis will be employed to identify differences between groups with a 95% probably of detecting a difference. Measures of contact related to different activities within specific groups will be compared to determine the activities that put groups at most risk. As appropriate multivariate analysis (e.g ordinary linear regression, logistic regression, non-normal distributions of outcome, least absolute shrinkage and selection operator (LASSO) regression, etc.) will be utilized to evaluate the relationship between the outcome variables, posit ve biological results (PCR or serology) key measures of contact and the factors that influence frequency and types of human-animal contact.

8. Project Milestones and Timelines

8.1 Milestones: **End of Year 1:** **Aim 1:** Sample targeting locations, species (for wildlife), sample size justif cations completed for whole project and reported to in-country teams; Sample testing, viral isolation, NGS, glycoprotein sequencing begun for all archival and some newly-collected samples; *in vitro* work begun; host-pathogen dynamic analyses; animal model work begun. **Aim 2:** Target human community populations identified and sample sizes calculated for some sites in each country; Community data collection, serological testing and RT-PCR testing begun; first epidemiological analyses of data begin in last quarter. **Aim 3:** Clin cal cohort selection underway; clinical enrollment, data collection and sample analysis begun. First Annual meeting in last quarter. First publications submitted by end of year, summary overview papers or reviews.

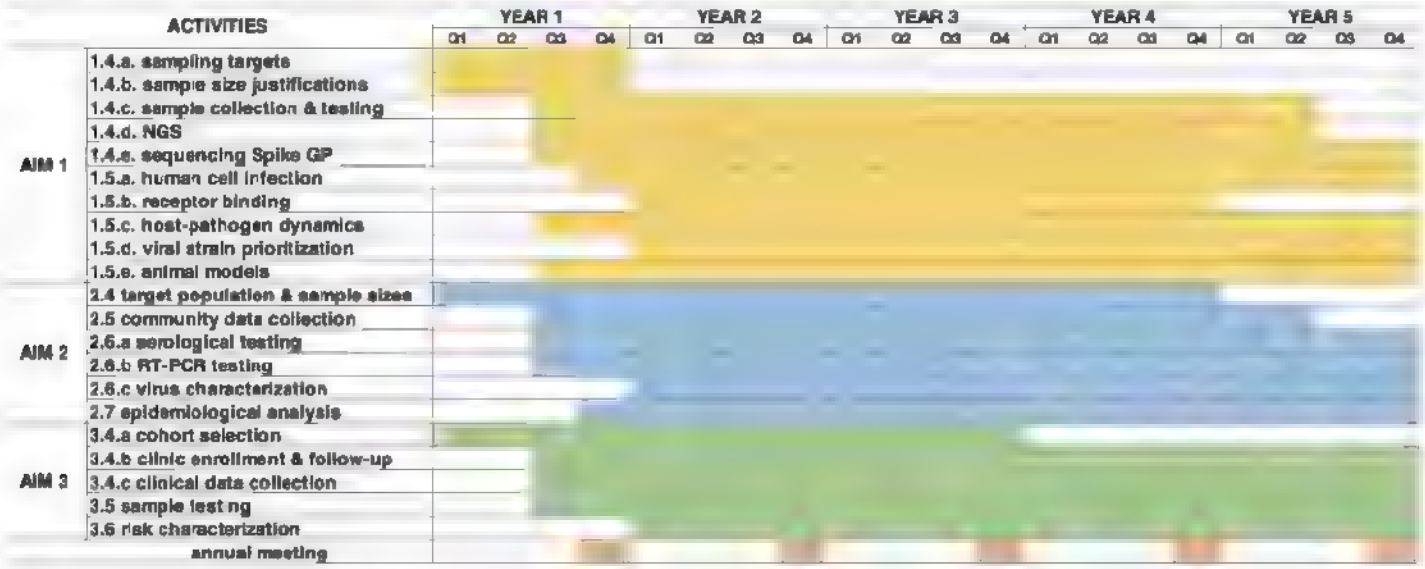
End of Year 2: **Aim 1:** No sample targeting or sample size justification analyses needed. All other aspects underway **Aim 2:** All aspects underway **Aim 3:** All sub-aims underway. Second Annual meeting in last quarter. Further 2 publications submitted by end of year, including first data papers.

End of Year 3: **Aim 1:** No sample targeting or sample size justification analyses needed. All other aspects underway **Aim 2:** All aspects underway **Aim 3:** All sub-aims underway. Third Annual meeting in last quarter. Further 3 publications submitted by end of year, largely data papers.

End of Year 4: **Aim 1:** No sample targeting or sample size justification analyses needed. All other aspects underway **Aim 2:** All aspects underway. Receptor binding work completed. **Aim 3:** No further cohort selection required; all other sub-aims underway. Fourth Annual meeting in last quarter. 3 further publications submitted, including first papers analyzing risk factors, pathogenic potential of novel viruses submitted.

End of Year 5: **Aim 1:** No sample targeting or sample size justification analyses needed. No receptor binding assays continuing. Serological and PCR testing completed end of 2nd quarter. Glycoprotein, *in vitro* and *in vivo* analyses, analysis of viral risk continue to end of project. **Aim 2:** No further community targeting or sample size work. Community data collection completed at end of 2nd quarter. All other aspects continue to end of project **Aim 3:** All sub-aims underway. Final Annual meeting in last quarter. Further 3 publications submitted.

8.2. Timeline:



PHS Human Subjects and Clinical Trials Information

OMB Number 0925-0001 and 0925-0002

Expiration Date 03/31/2020

Are Human Subjects Involved	● Yes ○ No
Is the Project Exempt from Federal regulations?	○ Yes ● No
Exemption Number	☐ 1 ☐ 2 ☐ 3 ☐ 4 ☐ 5 ☐ 6 ☐ 7 ☐ 8
Other Requested Information	

Human Subject Studies

Study#	Study Title	Clinical Trial?
1	Understanding Risk of Zoonotic Virus Emergence in EID Hotspots of Southeast Asia	No

Section 1 - Basic Information (Study 1)

OMB Number 0925-0001 and 0925-0002

Expiration Date 03/31/2020

1.1. Study Title *

Understanding Risk of Zoonotic Virus Emergence in EID Hotspots of Southeast Asia

1.2. Is this study exempt from Federal Regulations * ○ Yes ● No

1.3. Exemption Number ☐ 1 ☐ 2 ☐ 3 ☐ 4 ☐ 5 ☐ 6 ☐ 7 ☐ 8

1.4. Clinical Trial Questionnaire *

1.4.a Does the study involve human participants?	● Yes	○ No
1.4.b. Are the participants prospectively assigned to an intervention?	○ Yes	● No
1.4.c. Is the study designed to evaluate the effect of the intervention on the participants?	○ Yes	● No
1.4.d. Is the effect that will be evaluated a health-related biomedical or behavioral outcome?	○ Yes	● No

1.5. Provide the ClinicalTrials.gov Identifier (e.g. NCT87654321) for this trial, if applicable

Section 2 - Study Population Characteristics (Study 1)

2.1. Conditions or Focus of Study

- Humans living in geographic hotspot areas/close contact with wild animals

2.2. Eligibility Criteria

ELIGIBILITY CRITERIA

Participants to be enrolled in this study will be individuals from Thailand (Ratchaburi and Chonburi provinces), Peninsular Malaysia, Sabah Malaysia, or Sarawak # 12 years old living or working around wildlife habitats (e g bat caves/roosts), those who hunt wildlife, work with wildlife or livestock farming, transportation, selling, or slaughtering wildlife or visiting or working in high-risk sites (e g wildlife markets) who meet the inclusion criteria outlined below. Study sites are prioritized based on the hotspot geographic areas described in Aim 1, according to ecological and epidemiological conditions associated with a high risk for the coronaviruses, henipaviruses, filoviruses spillover.

Research participants will be enrolled in two settings:

1. Community - We aim to enroll and collect biological samples and survey responses individuals' living, working, or visiting targeted high-risk communities (as defined above) who have close contact with wildlife, specifically bats, rodents, non-human primates, with a range of exposures to these animals. Enrolled research participants will be asked to provide biological samples and complete a questionnaire that is designed to obtain detailed information into wildlife contact frequency and exposures related to: 1) occupation and occupational exposures, 2) observed or reported interactions with priority wildlife, especially bats, in/around house and other livestock animals (e.g. farming, butchering, slaughtering), 3) proximity of residence or work place to environments of increased risks, e.g. nearby bat roosts; 4) working or regular visitor to animal markets; 5) self-reported symptoms relating to a) severe/acute respiratory illness (SARI/ARI); b) Influenza-like illness (ILI); c) fever of unknown origin (FUO); d) encephalitis; or e) hemorrhagic fever; or f) diarrhea in combination with any of the previously mentioned illnesses within the 12 months and lifetime.

Additional inclusion criteria:

- Adults (18 years of age or older) who provide informed consent
- Children aged 12-17 years of age who provide assent along with an accompanying parent or guardian who is able to provide informed consent and
- Pregnant women will be considered eligible for inclusion

Exclusion criteria:

- Adults (18 years of age or older) who are unable to provide informed consent, including individuals with physiologically or medically induced cognitive impairments
- Individuals under 12 years of age
- Children without an accompanying parent or guardian who is able to provide informed consent, or a child 12-17 years old unable or unwilling to provide assent or children who are wards of the state
- Prisoners

2. Hospital - Both out-patients and in-patients at clinics or hospitals presenting with clinically defined symptoms of 1) severe/acute respiratory illness (SARI/ARI), 2) Influenza-like illness (ILI); 3) fever of unknown origin (FUO), 4) encephalitis; or 5) hemorrhagic fever; or 6) diarrhea in combination with any of the previously mentioned illnesses of unknown etiology Biological samples will be collected from the patients and the patient, will complete a questionnaire. We will follow up with these participants 35 days after enrollment to collect another biological sample to assess the development of IgG/IgM and collect additional data on the course of symptoms in the interim period.

Additional inclusion criteria:

- Adults (18 years of age or greater) who provide informed consent
- Children aged 12-17 years of age who provide assent along with an accompanying parent or guardian who is able to provide informed consent and
- Pregnant women will be considered eligible for inclusion

Exclusion criteria

- Individuals over the age of 12 years who refuse to provide informed consent
- Adults unable to provide informed consent, including individuals with physiologically or medically induced cognitive impairments
- Children, aged 12-17 years, without an accompanying parent or guardian who is able to provide informed consent, or a child aged 12 to 17 who is unable or unwilling to provide assent
- Children < 12 years of age or children who are wards of the state
- Prisoners

2.3. Age Limits Min Age: 12 Years Max Age: N/A (No limit)

2.4 Inclusion of Women, Minorities, and Children Inclusion_of Women_Min Children_FINAL pdf

2.5. Recruitment and Retention Plan	Section_2_Attm_Recruitment_Retention_Plan_FINAL.pdf	
2.6. Recruitment Status	Not yet recruiting	
2.7. Study Timeline	Section_2_Attm_Study_Timeline_FINAL.pdf	
2.8. Enrollment of First Subject	09/01/2020	Anticipated

INCLUSION OF WOMEN AND MINORITIES:

This study will enroll men and women, including pregnant women, as study participants. Subjects will be enrolled in this study without regard to ethnicity.

Women who volunteer to participate are not at an increased risk based on pregnancy status and are at the same exposure risk as non-pregnant women. Every effort will be made to protect the privacy, dignity, and well-being of all study participants especially special populations who participate in this study.

Individuals in sub-sites in selected geographic hotspot regions will be the primary mechanism for identifying subjects. We will make every effort to have men and women equally represented in this study and no individuals will be excluded based on ethnicity.

- **At community sites,** living or working around wildlife habitats (e.g. bat caves/roosts), who hunt wildlife, work with wildlife or livestock farming, transportation, selling, or slaughtering wildlife in the surveyed areas will be the primary criteria for identifying participants in community.

- **At clinic sites**, only patients who present at the healthcare facility who meet the clinical case definition of 1) severe/acute respiratory illness (SARI/ARI); 2) Influenza-like illness (ILI); 3) fever of unknown origin (FUO); 4) encephalitis; or 5) hemorrhagic fever; or 6) diarrhea in combination with any of the previously mentioned illnesses of unknown etiology will be recruited for this study, and no patients will be excluded based on ethnicity or gender.

INCLUSION OF CHILDREN:

Children aged 12–17 years will be included in this study, and there will be no maximum age restriction for adults, at both community and clinical sites

- Previous clinic-based studies have shown that children are one of the major populations who present to healthcare facilities with severe/acute respiratory illness (SARI/ARI), Influenza-like illness (ILI), or fever of unknown origin (FUO). Our behavioral study in Thailand and Malaysia also suggested the close contact with wild animals among children in the study regions via activities of animal hunting, trade, or butchering.

- Children aged 12 years or older are post-primary school in Thailand and Malaysia and are able to comprehend and respond to the questionnaire autonomously which increases the reliability of responses. We will not enroll children aged 12-17 years without an accompanying parent or guardian who is able to provide informed consent, or a child aged 12-17 who is unable to or unwilling to provide assent.

- Children under age 12 in target communities are mainly school children who have very limited exposures to wild animals under the scenarios of interest to the study, and ethically we do not want to collect or enroll participants without strong scientific need for inclusion. We will not enroll children who are wars of the state

- Every effort will be made to protect the privacy, dignity, and well-being of children who participate in this study. Our in-country human research team are well-trained medical doctors and researchers who have extensive experience working with children, as well as their parents, at both community and clinical settings. Prior to the start of human subject research activities, all research staff will be CITI-trained and further trained on conducting ethical human subject research training including a module on the special considerations for working with children

regarding risk and coercion. Enrollment of children will be monitored and annually reported to the IRB.

RECRUITMENT AND RETENTION PLAN

In order to improve recruitment within target communities, introductory visits will be made by project staff to each of the selected sub-sites. These visits will be advertised through word of mouth and a project description letter to village/town/city leaders and letters that can be posted or shared in a central community location. The letter will inform the community that a team will be coming on a particular day(s) to enroll voluntary participants and after discuss health issues related to animal contact. This letter will be for informational sharing not be used for recruitment purposes. It will only be used to inform the community of the research visits. The project description letter will be written in the local language with a Flesch–Kincaid readability score equivalent to a 7th grade reading level or below (primary school in Thailand and Malaysia), to assure that community leaders and potential community participants understand the study purpose, eligibility, and inclusion guidelines.

Community visits will begin with discussions and meetings with local authorities and community leaders to introduce ourselves and our project, and when appropriate following approval from local authorities, the study team will post flyers to inform the community when the team will be speaking about enrollment and later coming back to enroll interested individuals. Attending this "town hall" style meeting will be completely voluntary and based on our experience, those interested are likely to attend. Although local authorities may be present to introduce the study team members, they will not be involved in the recruitment and/or consent of the participants for the study. Individuals will be clearly informed during the recruitment process that their participation in the study is voluntary. If research visits or recruitment events are held at a workplace individuals choice of involvement will not impact their employment, nor will information discussed be shared with employers. With local permissions and accompanied by local community leaders, district health officers, or authorities the study team members will engage in community town halls and 'walkabouts' during which they will discuss study details, dates, times, and locations for enrollment and participation in the study.

Participation in the study will be strictly voluntary and will require signed informed consent for all participants and signed assent for participants aged 12-17 along with parent or guardian consent. During the enrollment process interested individuals will be given a consent form and research staff will read the consent form to potential participants. Together they will review the consent form and study staff will explain details of the study including: why they were selected, what the study procedures are and what will be expected from them, potential risks and benefits of their participation, that their participation is completely voluntary, and that they can withdraw their participation at any time. After reviewing the consent form individuals will be given as much time as needed to ask questions. At that time if individuals wish to participate they will sign two copies of the consent form and it will be countersigned by the research staff, with a copy given to the participant for their records. Included in the consent form is the contact information for local research staff and a local IRB contact for participants if they have questions in the future. Responses will be kept strictly confidential. Measures will be taken to assure the privacy, dignity, and respect of each participant. Ethical human subjects research methods will be a focus in all training of research staff, we will emphasize the importance of avoiding coercion during enrollment and protecting the privacy of participants.

Community-based recruitment: Participants from the community will be recruited through town hall meetings and community 'walkabouts' as described above. Meeting dates, times, and locations for enrollment and participation will be shared during these activities, and individuals who wish to enroll can volunteer to participate at these times and locations.

Clinic-based recruitment: Patients eligible for enrollment will be identified during standard intake procedures or from overnight intake logs, or in the emergency room, ward, or intensive care unit of each participating clinic or hospital by collaborating clinic staff. Employed staff at each location will identify potential participants meeting the clinical case definition of 1) severe/acute respiratory illness (SARI/ARI); 2) Influenza-like illness (ILI); 3) fever of unknown origin (FUO); 4) encephalitis; 5) hemorrhagic fever; or 6) diarrhea in combination with any of the previously mentioned illnesses of unknown etiology. Patients will be screened for eligibility according to the inclusion/exclusion criteria based on available clinical information and clinical presentation.

We have set a minimum target enrollment sample size to detect live virus in patients at each hospital assuming a population prevalence of 1% with a 95% probability. We will work with the local institution review board to determine the maximum enrollment of patients without undue burden on the population. However, in larger

tertiary healthcare centers where many cases fitting study inclusion are expected or are being enrolled we will regularly evaluate enrollment logs to be sure we are prepared to collect samples throughout the length of the sample collection timeline as to not miss a change in circulating virus. If we need to control the number of patients being enrolled at a hospital interval sampling will be implemented by selecting every Nth case of those individuals who meet enrollment criteria. The interval will be determined in collaboration with the local research staff and implementing partners based on an evaluation of the enrolled participants to date and expected number of cases presenting at the site within a given year in order to best meet study design and sample size criteria and stay IRB compliant. In terms of retention, we will express our gratitude to subjects for their participation and discuss the research importance of the follow-up data collection. Nonetheless, we expect to have an approximate 40% loss to follow up and have included this in our sample size calculations.

STUDY TIMELINE

At each sampling time point, patients/participants will be asked to volunteer approximately 1 hour of their time for participation in the study, including providing biological samples and completing the questionnaire.

This will be an ongoing five-year project from the time of award.

- We anticipate obtaining all required IRB approvals and local permissions in the first 6 months of projects;
- We will start human subject enrollment at community and clinical sites in Year 0.5 at the earliest, and enrollment will continue through Year 5, to be completed by the conclusion of the project;
- Human sample testing will start in Year 0.5 at the earliest, with completion of analyses by the end of the award.

Inclusion Enrollment Reports

IER ID#	Enrollment Location Type	Enrollment Location
Study 1, IER 1	Foreign	Ratchaburi and Chonburi provinces in Thailand; Peninsular Malaysia, Sabah Malaysia, and Sarawak in Malaysia

Inclusion Enrollment Report 1

Using an Existing Dataset or Resource* : ● Yes ○ No

Enrollment Location Type* : ○ Domestic ● Foreign

Enrollment Country(ies): MYS: MALAYSIA, THA: THAILAND

Enrollment Location(s): Ratchaburi and Chonburi provinces in Thailand, Peninsular Malaysia, Sabah Malaysia, and Sarawak in Malaysia

Comments

Planned

Racial Categories	Ethnic Categories				Total
	Not Hispanic or Latino		Hispanic or Latino		
	Female	Male	Female	Male	
American Indian/ Alaska Native	0	0	0	0	0
Asian	4150	4150	0	0	8300
Native Hawaiian or Other Pacific Islander	0	0	0	0	0
Black or African American	0	0	0	0	0
White	0	0	0	0	0
More than One Race	0	0	0	0	0
Total	4150	4150	0	0	8300

Cumulative (Actual)

Racial Categories	Ethnic Categories									Total
	Not Hispanic or Latino			Hispanic or Latino			Unknown/Not Reported Ethnicity			
	Female	Male	Unknown/ Not Reported	Female	Male	Unknown/ Not Reported	Female	Male	Unknown/ Not Reported	
American Indian/ Alaska Native	0	0	0	0	0	0	0	0	0	0
Asian	1217	867	5	0	0	0	0	0	0	2089
Native Hawaiian or Other Pacific Islander	0	0	0	0	0	0	0	0	0	0
Black or African American	0	0	0	0	0	0	0	0	0	0
White	0	0	0	0	0	0	0	0	0	0
More than One Race	0	0	0	0	0	0	0	0	0	0
Unknown or Not Reported	0	0	0	0	0	0	0	0	0	0
Total	1217	867	5	0	0	0	0	0	0	2089

Section 3 - Protection and Monitoring Plans (Study 1)

3.1. Protection of Human Subjects	Section_3_Protection_Human_Subjects_FINAL.pdf
3.2. Is this a multi-site study that will use the same protocol to conduct non-exempt human subjects research at more than one domestic site?	● Yes ○ No ○ N/A
If yes, describe the single IRB plan	Section_3_sIRB_plan_FINAL.pdf
3.3 Data and Safety Monitoring Plan	
3.4. Will a Data and Safety Monitoring Board be appointed for this study?	○ Yes ● No
3.5. Overall structure of the study team	

PROTECTION OF HUMAN SUBJECTS:

1. Risks to Human Subjects

1.1 Human Subjects Involvement, Characteristics, and Design
This project is a study of human spillover and exposure to animal coronaviruses, henipaviruses, and filoviruses in Southeast Asia, with active sample collection in Thailand and Malaysia and testing of archived samples in Singapore. As there is substantial evidence that these viruses likely spillover regularly to people, are often unreported or misdiagnosed and thus underestimated; and this targeted surveillance and detection of spillover and illness in at-risk human populations can be used as an 'early warning system' to conduct public health interventions and disrupt disease emergence Subjects will be enrolled on a voluntary basis and informed consent will be obtained from all participants and assent from all participants aged 12-17. Consenting participants will provide biological samples for PCR or serological testing and complete a questionnaire to collect information on wildlife exposures and frequency. Subjects will be individuals: 1) who are highly exposed to wildlife, specifically bats, rodents, and non-human primates, in community settings, through hunting, butchering, or general handling within the context of their living or working environments (≥ 18 years old); and 2) patients admitted to hospitals and clinics presenting with disease symptoms of clinically-defined 1) severe/acute respiratory illness (SARI/ARI); 2) Influenza-like illness (ILI); 3) fever of unknown origin (FUO); 4) encephalitis; or 5) hemorrhagic fever; or 6) diarrhea in combination with any of the previously mentioned illnesses of unknown etiology.

The study population will be selected from the subnational geographic hotspot regions listed in Aim 1. We will enroll participants from: 1) communities at 4 sub-sites from each of the regions of interest in Ratchaburi (Thailand), Chonburi (Thailand), Peninsular Malaysia, Sabah Malaysia, and Sarawak, 175 individuals from each of sub-site in the 5 regions will be collected and pooled across the region for a total of 700 participants per region, allowing us to make region-level comparisons of differing effects, enrolling a total of 3,500 participants; and 2) patients from the selected 2 town-level level clinics and 2 provincial-level hospitals in each of the geographic regions of Thailand, Peninsular Malaysia, Sabah and Sarawak, we will enroll a minimum of 300 participants per clinic or hospital, for a total of 16 healthcare facilities and 4,800 total clinical participants. This will yield 2,880 participants that will be available for follow-up blood sampling assuming for an estimated 40% loss from follow-up. The community and clinical sites are further defined in Specific Aims 2 and 3.

There are no data to suggest a gender or ethnic bias for coronaviruses, henipaviruses, and filoviruses exposure or infection, therefore individuals will be enrolled based on exposure criteria alone and individuals will not be excluded based on ethnicity or gender. We will also monitor sampling enrollment to ensure equal representation of sex, demographic, and socio-economic factors in each community site.

1.2 Sources of Materials
Biological samples to be collected and tested for coronaviruses, henipaviruses, and filoviruses include whole blood, serum, and nasal/oropharyngeal swabs. Samples will be collected by locally trained medical personnel and a questionnaire will be administered by research or collaborating staff from the local hospitals and clinics.

<u>In community sites</u>, whole blood samples will be collected from participants one time during the data collection period during Years 2-5 of the study. The whole blood samples will be aliquoted into at least one max. 500 µL whole blood and two 500 µL serum samples. Samples will be tested for coronaviruses, henipaviruses, and filoviruses using developed ELISA by consortium partners. For participants who report the symptoms relating to 1) severe/acute respiratory illness (SARI/ARI); 2) Influenza-like illness (ILI); 3) fever of unknown origin (FUO); 4) encephalitis; or 5) hemorrhagic fever; or 6) diarrhea in combination with any of the previously mentioned illnesses of unknown etiology within the last 10 days, an additional sample type will be collected, nasal or oropharyngeal swabs (2x). These samples will be marked for additional PCR-based assays to identify presence of known and novel coronaviruses, henipaviruses and

filoviruses, and for isolation and biological characterization of potential pathogens if PCR results are positive.

In clinic sites, both whole blood samples and nasal/oropharyngeal swabs will be collected at enrollment, whole blood samples will be aliquoted into at least one max. 500 µL whole blood and two 500 µL serum samples. Samples will be tested for coronaviruses, henipaviruses, and filoviruses using consensus PCR (cPCR). We will follow up 35 days after enrollment to collect an additional blood sample of 5mL to be separated and aliquoted into a minimum of two 500 µL serum samples that will be serological tested with the developed ELISA assay.

All blood samples will be kept frozen for future harvesting of Peripheral Blood Mononuclear Cells (PBMCs) for those study participants whose serum tests are positive for emerging viral pathogens. These will be used for harvesting polyclonal and monoclonal antibodies as potential therapeutics.

During data collection a standardized questionnaire will be administered to both community and clinic participants. This survey will collect data on exposure type and frequency with wildlife focusing on: 1) occupation and occupational exposures; 2) observed or reported interactions with wildlife, especially bats, rodents, and non-human primates, in/around house; 3) proximity of residence or workplace to environments of increased risks, e.g. nearby bat roosts; 4) working or regular visitor to animal markets; 5) self-reported ILI/SARI clinical diagnosis or symptoms in the past 12 months. During the follow-up with clinic participants a standardized questionnaire supplement will be administered to collect additional data on the course of symptoms in the interim period. All electronic data will be password protected, and all hardcopy files and biological samples will be stored in secure storage facilities. All consent forms and participant logs will be stored separately from research data in locked filing cabinets.

1.3 Potential Risks

The potential risks to study participants as a result of study participation are minimal. The biological specimen will be collected by locally certified healthcare professionals proficient in phlebotomy techniques, the volume of blood being collected is within normal safety limits and the swab sample is not overly invasive. The questionnaire will be designed to assess exposure risk and may ask personal questions, however, administration will be conducted privately and confidentially to protect individuals' personal health and exposure information. There may be some stress or discomfort for participants who are informed that they have been exposed to a zoonotic virus, to reduce this counseling will be available and options for future medical care will be included in the discussion with the health official or physician reporting results back to individuals.

2. Adequacy of Protection against Risks

2.1 Recruitment and Informed Consent

Potential study participants at each site will be recruited after obtaining local permissions and support from local community leaders, district health officers, and/or authorities the study team members will engage in community town hall meetings and 'walkabouts' during which they will discuss study details, dates, times, and locations for enrollment and participation in the study for individuals who wish volunteer to participate. The team will be trained on conducting ethical human subjects research before the commencement of data collection and enrollment of participants. This will include the importance of avoiding coercion during enrollment, protecting the privacy of participants, how to effectively communicate the research objectives, what is being asked of participants, any risks or benefits to participation, with sufficient support to be able to address any questions that potential participants may have. Training will also include a module on special populations for advanced training on working with minors during human subjects research. During the enrollment process interested individuals will be given a consent form in the local language and research staff will read the consent form to potential participants, via an interpreter in local dialects if necessary. Together they will review the consent form and study staff will explain details of the study including: why they were selected, what the study procedures are and what will be expected from them, potential risks and benefits of their participation, that their participation is completely voluntary, and that they can withdraw their participation at any time. After reviewing the consent form individuals will be given as much time as needed to

ask questions. At that time if individuals wish to participate they will sign two copies of the consent form and it will be countersigned by the research staff, with a copy given to the participant for their records. Contact details for local research staff member, a local IRB contact, and project PI will be provided to all subjects in the consent form to answer any future questions or requests for withdrawal participants may have.

2.2 Protection against Risks

Biological sample collection: collection of whole blood samples and nasal or oropharyngeal swab samples pose minimal risk to subjects. The potential complications associated with whole blood draw include pain and/or hematoma at the site of venipuncture. Nasal or oropharyngeal swab sample collection may cause minor irritation at the time of collection. To protect against and minimize potential complications, all biological sampling will be done by a locally trained and certified healthcare professional and/or clinic staff, and the sample collection sites will be monitored according to existing health facility protocols.

Risk factor questionnaire survey: potential risks associated with the administration of the questionnaire may be discomfort or concern providing responses related to wild animal contact or consumption if practices are taboo or prohibited by local laws. To minimize this risk, questionnaire data will be collected in a strictly confidential manner. The questionnaire will be conducted in private, ensuring that others cannot overhear participant responses and a barrier will be used or created so that no other individuals can view the participants. Depending on the location, this could be a private room, behind a building or fence, or behind a line of trees, obstructing view so that confidentiality may be maintained. The interview team will take care to pair interviewers and participants by sex to the best of their ability to increase the level of comfort of the participant and the team will ensure the privacy and confidentiality of response data. Children aged 12-17 will not be interviewed in the absence of a parent or guardian. Every effort will be made to ensure the privacy, dignity, and well-being of children and adults who participate in this study. In addition, identifying information will not be linked to responses, and data will be stored in secure, password protected files or locked secure storage facilities.

Participants may feel some stress or discomfort if informed that they have been exposed to a known or novel zoonotic virus, to reduce this counseling will be available and options for future medical care will be included in the discussion with the health official or physician reporting results back to individuals. Additionally, we will provide participating hospitals, clinicians, and community leaders with information and background data on relevant zoonotic viruses.

3. Potential Benefits to Subjects and Others

There are no measurable benefits to the individual study participants enrolled in this study. There may be secondary benefits including receiving a physical exam/health check from a medical officer at the time of enrollment or advanced non-diagnostic testing assays that add clarity medical history for clinic participants. There are also benefits to the community and regional healthcare providers understand the risk of zoonotic infections among high-risk populations. At the conclusion of the study, we will deliver an educational workshop reporting study findings that will be open to both study and non-study participants, describing the health benefits of using PPE and hand-washing during animal handling activities throughout the day, as well as to share other prevention interventions that emerge from the research data.

4. The Importance of Knowledge to be Gained

There are valuable potential benefits to the general public from the knowledge to be gained from this study. One key benefit of this study to the community an understanding the risk of zoonotic spillover events among high-risk populations. This strategy for targeted surveillance and detection of spillover and illness in at-risk human populations can be used as an 'early warning system' to conduct public health interventions and disrupt disease emergence. As well as share information with communities on practices that could reduce exposure and related health risks such as the avoidance of particular animals or the need for PPE and extra care when handling wildlife may substantially reduce the risk zoonotic pathogen transmission.

Knowledge gained will also increase understanding of the conditions and human activities associated with the introduction of zoonotic infections into human populations, which may have implications for disease control more broadly.

SINGLE INSTITUIONAL REVIEW BOARD (sIRB)

In compliance with the NIH Policy on the use of a single IRB of record for multi-site research EcoHealth Alliance will prepare, submit, and work the institutional review board that follows the ethical standards set forth by the HHS regulations at 45 CFR 46. Once this single IRB is approved in the US it will functions as the IRB of record and will be relied on at all planned sites and any future sites.

We are currently anticipating working with HummingbirdIRB to serve as the IRB of record for all study sites. All of our local research partners, partner institutions, and study staff will rely on the IRB protocol that is approved at the IRB of record for all planned and future sites where data collection will occur. All data collection (biological and questionnaire) procedures and protocols and consent processes will be conducted using the same protocols outlined in the approved IRB of record and consistent for all location sites. The approved protocol at IRB of record will serve as the foundation for all locally submitted IRB packages in all partner countries, Thailand, Malaysia, and potential Singapore for inclusion of archived samples for testing.

EcoHealth Alliance will submit for IRB approval and maintain all records, and annually manage and submit for continuing review approvals at the IRB of record. Additionally, EcoHealth Alliance will manage the authorization and reliance agreements between partners and implementation the communication plan. Each partner implementing human subjects research in Thailand, Malaysia, and Singapore will maintain regular communication with scheduled updates to the EcoHealth Alliance point of contact on enrollment and recruitment numbers, breakdown of enrollment of special populations and report any adverse events within 8 hours if not sooner.

Prior to commencing study enrollment or sample testing, the partner organization that is managing human subjects enrollment in Thailand, Malaysia, and Singapore will sign a reliance agreement that will acknowledge the role of the IRB of record and responsibilities of the participating institutional partners.

Section 4 - Protocol Synopsis (Study 1)

4.1. Brief Summary

4.2. Study Design

4 2.a. Narrative Study Description

4.2.b. Primary Purpose

4.2.c. Interventions

Type	Name	Description

4.2.d. Study Phase

Is this an NIH-defined Phase III Clinical Trial? ○ Yes ○ No

4 2.e Intervention Model

4.2.f. Masking ○ Yes ○ No

❑ Participant ❑ Care Provider ❑ Investigator ❑ Outcomes Assessor

4.2.g. Allocation

4.3. Outcome Measures

Type	Name	Time Frame	Brief Description

4.4. Statistical Design and Power

4.5. Subject Participation Duration

4.6. Will the study use an FDA-regulated intervention? ○ Yes ○ No

4.6.a. If yes, describe the availability of Investigational Product (IP) and Investigational New Drug (IND)/ Investigational Device Exemption (IDE) status

4.7. Dissemination Plan

Delayed Onset Studies

Delayed Onset Study#	Study Title	Anticipated Clinical Trial?	Justification
The form does not have any delayed onset studies			

VERTEBRATE ANIMALS

1. Detailed description of animal use.

Work with vertebrate animals will be conducted in Thailand and Malaysia for field sampling (collection of diagnostic clinical specimens) of free-ranging mammals; and the University of North Carolina, Chapel Hill, USA and the National Emerging Infectious Diseases Laboratory (NEIDL), Boston, USA for mouse model experimental infections.

Wild animal captures:

Capture and sampling techniques for all wild animals (bats, rodents and non-human primates) described in this study have been previously approved by multiple Institutional Animal Care and Use Committees (IACUCs) for projects led by EcoHealth Alliance. These institutions include: UC Davis IACUC (Mazet and Epstein; UC Davis 15898; current); and The Cummings School of Veterinary Medicine at Tufts University (Olival, Phelps, and Epstein, current), Animal Welfare Assurance (#A4059-01) on file with the Office of Laboratory Animal Welfare at the National Institutes of Health. We have a draft IACUC application for this proposed project, and will submit it within 2 month of the project's start date (to Tufts University) to minimize delays in beginning Year 1 field sampling.

Bats: Free-ranging bats will be captured using either a mist net or harp trap. The net system is manned by two people during the entire capture period, and bats are removed from the net as soon as they become entangled to minimize stress and prevent injury. In the Co-Is Olival experience, a maximum of 20-30 bats can be safely held and processed by a team of three people per trapping period. Duration of trapping will depend on the capture rate. Bats are placed into a pillowcase or small cloth bag and hung from a branch or post in a cool place until samples are collected. Bats are held for a maximum of six hours (typically less than 3 hours), and released after sampling.

Rodents: Free-ranging rodents will be captured through pit traps and box traps. Food, water and shelter will be provided. Traps will be checked a minimum of twice daily, in the morning and in the afternoon. If adverse weather (extreme heat, rain) is expected or researchers are working in areas where predation is common, traps will be checked more frequently, and closed during the adverse weather. Padding, shelter and food and water will be provided in traps.

Non-human primates: Free-ranging and captive non-human primates will be chemically restrained (by darting with anesthetic or through manual chemical injection), and handled only for the duration of sampling. Where possible, small primates (<15 kg) will be captured with nets, using a hoop and mesh size appropriate to the size of the animal. Alternatively, medium sized primates (e.g. free-ranging macaques) will be captured using metal traps placed on flat ground in a secure area or on a pallet constructed on a tree. Trapped animals will be transferred to a transfer cage placed against a sliding door and covered.

Sample Collection from wild animals:

Bats: Bats will be manually restrained during sampling. Depending on the species and size of bat, swabs will be taken from the oropharynx, urogenital tract, and rectum. Fresh feces will be collected if available, in which case a rectal swab will not be collected. Blood will be collected from smaller insectivorous bats (<50g) using a 27g needle to puncture the brachial artery and a 70ul hematocrit tube to collect the blood. For larger bats (>50g) we will collect blood from either the cephalic vein or from the radial artery or vein using a 25 or 23 gauge needle and 3cc syringe.

Rodents: Anesthesia for captive small rodents will be conducted using plastic tubes, with the animals transferred directly from the traps to the tubes containing a cotton swab soaked in ether, isoflurane, or methoxyflurane for anesthetic induction. For larger rodents, chemical restraint and anesthesia (ketamine alone, or ketamine combined with xylazine) will be applied either through the squeeze cages by syringe if applicable. Once anesthetized a small blood sample will be collected using a capillary tube placed into the retro-orbital sinus. Only trained technicians will perform retro-orbital bleeding and it will only be performed on anesthetized rodents.

Femoral or jugular venipuncture may be used for larger rodents (e.g. rats). In all rodents, blood volumes of no more than 1% of body weight will be withdrawn. (example 0.2 ml blood from a 20 gram rodent).

Non-human primates: Chemical immobilization of any small primate species will be preceded by accurate weight determination. For anesthesia, ketamine (8-15 mg/kg depending on animal size) or a combination of tiletamine/zolazepam (7-8mg/kg in smaller animals; 4-6mg/kg in medium sized animals; 3-4mg/kg in larger animals; and 2- 3mg/kg in great apes) or ketamine/medetomidine (3.5 mg/kg ketamine and 0.035 mg/kg of medetomidine), or ketamine/xylazine (100mg/ml each) in a 1:1 ratio at a dose of 10mg/kg IM will be administered, using low doses where possible to allow for relatively rapid sampling. Caution will be taken when administering chemical immobilizing drugs to animals in estrus to prevent against hemorrhage of the tumescent area. Immobilized animals will be allowed to recover in isolation. Sampling procedures for non-human primates will include venipuncture; fecal, urine, and external parasite collection; biopsy of lesions and/or skin samples for genetic testing; oral, nasal, urogenital and anal swabs, plucked hair and milk if/when available. Blood samples from larger primate species will primarily be collected from the forearm veins (cephalic, radial, median, and ulnar veins). In smaller species, the femoral or caudal saphenous veins will be preferred. In very small non-human primates the jugular vein may be the only option. Following handling and when appropriate, benzodiazepine and alfa-2 agonist sedation will be chemically reversed, and the animal returned to its group of con-specifics in the immediate vicinity of their capture, with appropriate observation.

Laboratory animals (mouse models):

The goal of these studies is to identify if novel high risk emerging coronaviruses (CoV), filoviruses (FVs) and henipaviruses that circulate in bats and/or other reservoir species are poised for emergence in human populations, and to assess pathogenicity for selected strains of CoVs, FVs, and henipaviruses. High containment BSL3 and BSL4 pathogens will be recovered from natural infections in reservoir species and/or humans, or recovered from whole genome sequences by reverse genetics using synthetically derived molecular DNA clones. Viruses will be used to infect classic laboratory mouse strains (eg, C57BL6/J), transgenic mice expressing human entry receptors for different coronaviruses, filoviruses or henipaviruses, the Collaborative Cross Genetic Reference populations, or mice reconstituted with the bat immune system designed to identify new mouse models of human disease.

Animal experiments with mice will be performed at the University of North Carolina (UNC), Boston National Emerging Infectious Diseases Laboratory (NEIDL) in dedicated facilities under the direction of the research PIs. Prior to infection studies, the animals will be maintained in Sealsafe™ HEPA-filtered air in/out unit or compatible systems for at least one week prior to virus challenge. In addition, laboratory personnel inspect animals daily and any animal in distress is immediately euthanized (moribund, unresponsive, loss of more than approved percentage of starting weight). Animal care and housing follows IACUC recommendations and all personnel have attended mandatory IACUC training courses. A trained veterinarian is always on call to assist with animal care and husbandry. Below we summarize the description of procedures for each specific Aim, justifications, minimization and pain and distress and methods for euthanasia.

Mice

Species: *Mus musculus*; CC mouse lines and knockout mice

Ages: Adults 6 to 8 weeks of age and C57BL6 mice of 1.5 years of age

Sex: Females and males

Procedures for laboratory animals:

Animal work will be done at the above-mentioned facilities in accordance with the Guide for the Care and Use of Laboratory Animals. The minimum numbers of animals will be used in order to achieve our experimental goals with statistical significance.

Specific Aim 1: Identify, characterize and rank spillover risk of high zoonotic potential viruses from wildlife.

Rationale: The goal of these studies are to use mouse models to assess human disease for novel viruses discoved in wildlife populations. We note that many zoonotic viruses replicate poorly in rodents, requiring adaptation. To circumvent this problem, we will use genetically distinct mouse resources (CC mice), mouse strains expressing human entry receptors and standard laboratory mice to identify mouse models for studying viral pathogenesis, as well as to evaluate vaccine and antiviral treatment regiments.

These studies require tractable experimental model organisms like the CC with sets of defined genetic characteristics (enumerated as follows). Genetically defined and immortal reference populations that allow whole-organism study of natural variation is a powerful approach for modeling human disease susceptibility and cannot be achieved by means other than the use of whole animal genetics. Mice are excellent model systems to study human gene function for the following reasons:

a. The genome has been sequenced and there are many genetic tools available for follow-up and complementary studies.
b. Mice share many aspects of anatomy, physiology, patterns of development, and control of gene expression with humans.
c. The Collaborative Cross (CC) is a large panel of recombinant inbred strains that have been specifically bred to randomize an extraordinarily large amount of genetic variants and has been designed to be an optimal model of the human heterogeneous population while allowing further probing into tissue and cell-type specific responses
d. The CC support integration of data across time, location, demography, and environments.
e. Reference populations of mice provide suitable whole-organism models for human viral infection responses, which to date cannot be replicated faithfully by *in vitro* models.
f. The resource is portable and available worldwide.

Experimental Design and Sample Sizes:

Experiment 1
Mice
Twenty mice (10 males and 10 females) will be infected with six different test viruses/yr.

20 mice x 6 viruses = 120 mice
Total number of mice= 120 mice

Total Animals	# Pain Category C	# Pain Category E
120	100	20

Experiment 2.
Humanized Mice
C57BL6/J-hACE2 Mice
C57BL6/J-hDPP4 288/330 Mice

10 mice (5 female and 5 male) x 4 SARS-like coronaviruses x 2 repeats= 80 mice
10 mice (5 female and 5 male) x 4 MERS-like coronaviruses x 2 repeats= 80 mice
Total numbers of animals for aim 1/yr= 160 mice
Animal Numbers and Pain Categories

Total Animals	# Pain Category C	# Pain Category E
1200	1080	120

Experiment 3
Mice
Six mice (3 males and 3 females) from 6 Collaborative Cross mouse lines (6 to 8 weeks of age) will be infected with six test viruses/yr.

6 mice x 6 lines x 6 viruses= 216 mice
12 mice x 2 lines x 1 virus= 24 mice
Total number of mice for Aim 1 screening/yr: 240 x 5 years= 1200 mice

Animal Numbers and Pain Categories

Total Animals	# Pain Category C	# Pain Category E
1200	1080	120

We note that wild-type EBOV, MARV, NiV, HeV and SARS-CoV causes subclinical infections in standard laboratory strain mice.

Specific Aim 2 and 3. Discovery of Novel Viruses from Human Source Samples. We anticipate discovering one novel virus in focal high-risk human populations/yr.

Rationale: The goal of these studies are to identify novel mouse models of human disease. We note that newly discovered human viruses replicate poorly in rodents, requiring adaptation. To circumvent this problem, we will use genetically distinct mouse resources (CC mice), mouse strains expressing human entry receptors and standard laboratory mice to identify mouse models for studying viral pathogenesis, as well as to evaluate vaccine and antiviral treatment regiments.

Experiment 1
Mice
Twenty mice (10 males and 10 females) will be infected with one different test viruses/yr.

20 mice x 1 viruses x 2 repeats = 40 mice
Total number of mice = 40 mice x 5 years = 200 mice

Total Animals	# Pain Category C	# Pain Category E
200	160	40

Experiment 2.
Humanized Mice
C57BL6/J-hACE2 Mice
C57BL6/J-hDPP4 288/330 Mice

20 hACE2 mice (10 female and 10 male) x 1 SARS-like coronaviruses x 2 repeats= 40 mice
20 hDPP4 mice (10 female and 10 male) x 1 MERS-like coronaviruses x 2 repeats= 40 mice
Total numbers of animals for aim 1/yr= 80 mice x 5 years = 400 mice

Animal Numbers and Pain Categories

Total Animals	# Pain Category C	# Pain Category E
400	300	100

Experiment 3
Mice
Six mice (3 males and 3 females) from 8 Collaborative Cross mouse lines (6 to 8 weeks of age) will be infected with one test viruses/yr.

6 mice x 8 lines = 48 mice
16 mice x 2 lines = 32 mice
Total number of mice for Aim 1 screening/yr: 80 mice x 5 years= 400 mice

Animal Numbers and Pain Categories

Total Animals	# Pain Category C	# Pain Category E
400	320	80

We note that wild-type EBOV, MARV, NiV, HeV and SARS-CoV CoV cause subclinical infections in standard laboratory strain mice. It is anticipated that disease severity will increase in select CC mouse strains.

2. **Justify use of animals, choice of species, numbers to be used**.
Wild animals: Species and number used in study: The purpose of this study is to conduct analyses to geographically- and taxonomically-target testing of samples from wild mammals that are most likely to harbor known high-profile zoonotic pathogens, or close relatives with potential to infect people. We will analyze archived specimens and only collect additional specimens projected from each prioritized taxa to achieve statistically robust sample sizes and to complement our archived specimens. Preliminary analysis indicates that, for all viral target families, we will require ~14,000 new specimens from bats (equating to no more than 7000 individual animals) to identify 80% of remaining bat viral species diversity in our study region, ~5,000 samples from Thailand and ~9,000 samples from Malaysia. Viral strain diversity from a sampling effort this size is expected to number in the hundreds of strains. For example, given ~6% prevalence of CoVs in bat species previously sampled under the PREDICT project, a target of 14,000 individuals would yield ~800 PCR positive individuals, representing, an estimated ~600 novel sequences/strains. Similarly, for PMVs, which have an average PCR detection prevalence of ~1.5%, sampling of 14,000 individuals would yield ~200 positives and an estimated 150 novel strains. The required numbers of specimens to capture 80% of CoV and PMV viral diversity in free-ranging rodents and NHP will be approximately half that of bats given lower levels of viral diversity we expect to capture, for a total of no more than 7,000 specimens (equating to no more than 2300 individuals). Filovirus estimates are not feasible yet due to the small number of positive samples in prior studies, but will be estimated as the project begins.

Laboratory animals: This proposal aims to develop novel mouse models that display human disease phenotypes following infection with phylogenetically unique zoonotic and human strains of these viruses. These studies cannot be done without vertebrate animals. There is no *in vitro* system that accurately mimics virulence of highly pathogenic viruses, or be able to predict disease outcomes following infection. At this time, there is no substitute for *in vivo* efficacy studies. Our studies are designed with the fewest number of animals while retaining statistical significance. The numbers of animals proposed in this study will provide robust statistical confidence of our results.

The Collaborative Cross mice are genetically distinct so infection of these mouse strains can result in wildly different clinical disease outcomes. As such, the CC model will identify unique lines that accurately recapitulate many aspects of the human disease phenotypes and will provide essential information for the testing of vaccines and drugs against these highly pathogenic RNA viruses.

3. **Provide information on veterinary care**. For wild caught animals, veterinary oversight will be provide by EcoHealth Alliance's wildlife veterinarians, led by Senior Veterinarian, Dr. Field. Animals that are injured during the capture or sampling process will be assessed by an experienced team leader, and if the animal is determined to be unlikely to survive if released, it shall be euthanized humanely (see euthanasia section). Animals will be released within hours of capture.

The UNC and NEIDL have veterinary staff and team of experienced animal care technicians who will oversee the housing and care of bats used for experimental infections in their facilities.

4. **Procedures for ensuring animal comfort, lack of distress, pain, or injury**:
Wild animals: Wild animals will not be held longer than 6 hours during the sampling process. Co-Is Olival and Phelps and Dr. Field from EHA, and co-Is Wacharapluesadee and Hughes (from Thailand and Malaysia, respectively) have extensive experience in capture, anesthesia, and sampling wildlife, especially bats and will lead oversight and training of field teams. In our team's experience, wild animals tolerate the described procedure well. Mist nets will be attended continuously during capture periods, and bats will be extracted from the net as soon as they become entangled. This will minimize stress and injury from entanglement. Bats will be placed individually in cotton bags and hung from tree branches while awaiting processing and during recovery. The bags are sufficiently porous as to allow for ventilation and are designed for bat capture. The enclosed

environment seems to calm the bats, as they do not struggle once inside, but they hang quietly – this is a standard and accepted practice in the bat research world and best way to minimize stress to the animal. Rodent traps will be checked a minimum of twice daily, in the morning and in the afternoon. If adverse weather (extreme heat, rain) is expected or researchers are working in areas where predation is common, traps will be checked more frequently, and closed during the adverse weather. Padding, shelter and food and water will be provided in rodent traps. Animals will be monitored by a veterinarian or experienced field team member during all stages of capture, processing, and release. Animals will be kept in a cool place while in the pillowcases.

Laboratory animals: Mouse adapted strains of SARS- and MERS-CoV replicate efficiently in the lungs of mice and may produce significant disease in young and aged animals, including acute onset respiratory distress syndrome, a clinically devastating end stage lung disease with 50% mortality rates. It is unclear whether newly discovered SARS-like or MERS-like coronaviruses or other bat viruses will cause severe disease in mice. Mice will be closely monitored daily for signs of clinical disease. Since analgesics may affect the outcome of infections, analgesics will not be used and we will rely on close monitoring and euthanasia of sick animals to prevent undue pain and suffering. In general, animals will be euthanized if they approach losing >25% of their starting weight; we recognize that this is a significant weight loss, but it is acceptable in these studies as some animals can recover from >25% weight loss after highly pathogenic coronavirus infection. We will euthanize moribund animals, regardless of weight loss criteria. Euthanasia will be performed by overdose with isoflurane. This will immediately be followed by organ harvest/exsanguinations, as prior treatment with these agents ensure that the animals will not suffer during this procedure due to operator error. This approach was chosen because unconsciousness and death occur quickly and the method is consistent with the recommendations of the Panel on Euthanasia of the American Veterinary Medical Association.

5. **Euthanasia**

Wild animals: In the event of injury to a wild animal in the field that results in pain and suffering, and reasonable veterinary care is unavailable, the animal will be euthanized by a veterinarian or trained field team member using ketamine injected intramuscularly 37.5mg/kg and sodium pentobarbital injected intravenously at a dose of 1.0ml per 5kg injected intravenously or intraperitoneally. This protocol is in accordance with the AVMA euthanasia guidelines (2013). Any animal that is euthanized using a chemical agent will be disposed such that it will not be permitted to enter the food supply either through markets or hunting.

Criteria for euthanasia for mice: Mice will be euthanized (isoflurane overdose followed by organ harvest) at the point at which they become moribund, lose over 20 percent of their starting weight (or up to 30 percent of their starting weight if the animals are being maintained under the weight loss exception), reach a clinical score of 4 or higher or reach pre-determined endpoints (ranging from 1 to 7 days post infection), whichever comes first.

0. No clinical signs
1. Ruffled fur.
2. Ruffled fur with hunched posture (only slight or no signs of dehydration)
3. As above with more severe signs of dehydration and some loss of body strength, some loss of spontaneous morbidity
4. Marked loss of spontaneous morbidity and pronounced dehydration
5. Moribund: unresponsive to stimuli and pronounced eye squint

-All scores except 5 can be qualified with a 0.5 for severity
-Any mouse that reaches a clinical score of 4 or more will be euthanized immediately

Criteria for euthanasia for bats: Bats will be euthanized (isoflurane overdose followed by organ harvest) at the point at which they become moribund, lose over 20 percent of their starting weight, reach a clinical score of 4 or higher or reach pre-determined endpoints (ranging from 1 to 7 days post infection), whichever comes first.

0. No clinical signs
1. Decreased activity, behavioral abnormalities.
2. Difficulty flying (only slight or no signs of dehydration)

3. As above with more severe signs of dehydration and some loss of body strength, some loss of spontaneous morbidity.
4. Marked loss of spontaneous morbidity and pronounced dehydration.
5. Moribund: unresponsive to stimuli and pronounced eye squint.

-All scores except 5 can be qualified with a 0.5 for severity.
-Any bat that reaches a clinical score of 4 or more will be euthanized immediately

SELECT AGENT RESEARCH/BIOHAZARDS. Yes

Select Agent Research:

Research on Biological Select Agents and Toxins (BSAT) requires strict compliance with regulations that are primarily overseen by the US Centers for Disease Control and Prevention (CDC) and the Animal and Plant Health Inspection Service (APHIS). These regulations are designed to maintain the safety and security of the materials, personnel and the environment. Per requirements, we outline details of select agent research below for our two EID-SEARCH core laboratory partners, The University of North Carolina at Chapel Hill (UNC) and National Emerging Infectious Diseases Laboratories (NEIDL), who will conduct select agent research.

Identify the Select Agent(s) to be used in the proposed research:

SARS-CoV: We propose using Severe Acute Respiratory Syndrome-associated Coronavirus (SARS-CoV) and SARS-CoV genome RNA (isolated using TriZOL) in this proposal. Derivative viruses encoding 2/3 genome length SARS-CoV are also considered as select agents; consequently, recombinant SARS-CoV encoding various bat SARS-like S glycoproteins will be considered select agents.

Henipaviruses: Wildtype Nipah, Hendra and related bat viruses are select agents and will be used at the Boston NEIDL BSL-4 Laboratories. Nipah virus is an overlap select agent regulated by both HHS and USDA.

Filoviruses: Wildtype Ebola viruses are select agents and will be used at the Boston NEIDL BSL-4 Laboratories.

Provide the registration status of all entities where Select Agent(s) will be used:

The UNC is currently registered with the CDC for select agent use including SARS-CoV as required by select agent regulations (42 CFR 73). The UNC SARS select agent laboratories are routinely inspected by the environmental health and safety department at UNC and by the CDC. Workers receive select agent and BSL3 training focused on SARS-CoV safety, procedures and protective clothing/PAPR training each year.

The NEIDL Environmental Health and Safety (EHS) group to vet, review and approve Standard Operating Procedures, consistent with BU-wide policies and procedures, which meet and/or exceed all applicable federal, state, and local regulations (NIH, BMBL, OSHA, CDC, NRC, MWRA, DEP, BFD, etc.). EHS responsibilities include: biosafety; laboratory and building occupant safety; wastewater management and monitoring; hazardous and non-hazardous solid waste management; biological, chemical, and radioactive waste disposal management; select agent program, medical surveillance program, staff and first responder training programs. For each NEIDL research project which has been approved by the BU Institutional Biosafety Committee (IBC), the EHS Biosafety Manager obtains applicable select agent permits to comply with 7CFR331 and 9CFR121, the Agricultural Bioterrorism Protection act of 2002; *Possession, Use, Transfer of Biological Agents and Toxins: Final Rule.* If an agent-specific immunization is available the EHS Core Biosafety Manager will assist the Research Occupational Health Program physicians to determine whether laboratory personnel will require immunizations for agents handled or present in the laboratory.

Provide a description of all facilities where the Select Agent(s) will be used:

UNC: SARS-CoV and related derivative viruses will be manipulated in research activities (UNC) including establishing growth curves and performing plaque assays in laboratory spaces that meet the operational and procedural criteria for BSL-3 activities as outlined in the CDC/NIH "Biosafety in Microbiological and Biomedical Laboratories", 5th edition, as well as the BL-3 criteria outlined in the NIH Guidelines for Research Involving Recombinant or Synthetic Nucleic Acid Molecules (March 2013). In addition, all mouse work at the University of North Carolina at Chapel Hill will be performed in the approved and registered BSL-3 lab, equipped with Techniplast Sealsafe™ Hepa-filtered animal housing for rodents. All protocols will be approved by the IACUC at the University of North Carolina at Chapel.

At UNC, all BSL-3/ABSL-3/select agent laboratories are equipped with biosafety cabinets, incubators, centrifuges with containment features, cold storage units, an autoclave, sink, eyewash and life safety equipment, as well as mechanical system monitors and alarms to support effective isolation and containment of operations

involving SARS-CoV. The anterooms to the BSL-3 labs house PAPR charging stations, lab and safety supplies, and a changing area. For both the BSL2 and BSL3 select agent spaces, access to the select agents is restricted by the hallway to anteroom door, which requires swipe card and punch codes for entry, the door between the anteroom and the BSL-3 (BL3 only), and freezer locks.

NEIDL: The select agent work to be carried out will be performed in the National Emerging Infectious Diseases Laboratories (NEIDL). The NEIDL is fully permitted for Select Agent work at BSL-3 and ABSL-3, as well as BSL-4 and ABSL-4. We will conduct experimental infection studies using Nipah and Hendra (Henipaviruses) and Ebola and Ebola-related viruses at NEIDL using animal models and cell lines within the biosafety level 4 laboratory at NEIDL. No infectious materials will be moved or handled outside of the BSL 4 facility. All science and animal care staff are fully trained and certified to work under BSL 4 conditions.

At Boston University (BU), research with BSAT is focused to combat infectious diseases caused by the agents, with primary concentration on the development of vaccines, therapeutics and diagnostic tests. Work is conducted in highly specialized containment facilities that are specifically designed, verified and maintained to ensure that the materials are secured, contained and handled safely. Research facilities with BSAT at BU have received prior approval from CDC/USDA and other local regulatory agencies prior to the possession, storage and conducting of research work. All BSAT research proposals are first carefully reviewed by the Institutional Biosafety Committee (IBC) and, together with the Environmental Health and Safety (EHS), checks and verifies that the required safety procedures, personal protective equipment, safety equipment, and trainings are in place and implemented prior to initiation of research work.

A senior Scientific Safety Officer serves as the Select Agent Responsible Official (RO) and has oversight for the implementation of the BSAT program. Under this program, the institution implements and maintains a system of control measures to ensure that all personnel are properly screened for security risks and have passed the required background verification checks by Federal agencies and BU. Personnel complete and meet the medical and health screenings required by the Research Occupational Health Program (ROHP); personnel are appropriately trained on the hazards of the materials, safety procedures and their roles and responsibilities. The RO and the Alternate Responsible Officials (ARO) conduct an annual review of the Security, Biosafety and Incident Response Plans and make necessary changes to the plans.

Describe the procedures that will be used to monitor possession, use and transfer of the Select Agent(s): All personnel who will have access to select agent-regulated materials have been added to the select agent registration following security risk assessments prescribed by the CDC Select Agent Program. Personnel have completed training in all aspects of select agent compliance requirements and have adopted changes to standard operating procedures as applicable to assure that these requirements are met. Personnel will follow all procedures prescribed for accessing and securing the lab, documenting lab activities and materials used, and responding to incidents that could result in theft, loss or release of select agent regulated materials. Transfers of select agent-regulated materials will be coordinated by the Lab Manager and Responsible Official in accordance with standard operating procedure, including obtaining appropriate permits for shipping select agent materials. Lab managers of both facilities are DOT/IATA trained for shipping dangerous goods and will follow all regulations for shipping, both under dangerous goods and select agent regulations. Transfer of select agent RNA in trizol from the BSL3 and BSL2 laboratory is witnessed by UNC and Vanderbilt ARO in a process that has been approved by the CDC.

For NEIDL, all biohazards that are shipped or received for approved projects are mandated to meet the standards of the High Hazard Materials Management policy, which states that BU will meet or exceed all applicable shipping regulations under the requirements of the U.S. Department of Transportation (DOT) and the International Air Transportation Authority (IATA). The RO, the BU Office of Emergency Management and Public Safety have responsibility for overseeing the transportation process for select agents and for contracting appropriate transportation vendors which utilize screened personnel, GPS tracking systems and can provide an all-inclusive chain of custody documentation for each shipment.

Describe plans for appropriate biosafety, biocontainment, and security of the Select Agent(s): Co-I Baric's

laboratories have been operational since 2004 with BSL-3 Core Policies and Procedures documentation in place with lab-specific standard operating procedures. BSL-3 standard operating procedures have been reviewed and approved by the Institutional Biosafety Committees at either the University of North Carolina at Chapel Hill or Vanderbilt and are updated as lab processes change or biosafety procedures evolve. The content of these documents has been reformatted and expanded to conform to the select agent regulations for the biosafety, security and incident response plans. Additionally, lab-specific security risk assessments have been completed and recommendations put in place to ensure that security measures and procedures are sufficient to effectively minimize the possibility of unauthorized access to select agent-regulated materials. Equipment and procedures will be modified if deemed necessary based on this assessment. The facilities at the University of North Carolina at Chapel Hill and Vanderbilt have undergone multiple CDC inspections and are currently in compliance with CDC requirements relating to SARS-CoV and select agent status.

Co-Is Keusch and Corley from NEIDL have endorsed a "safety first" environment which underpin all activities. The NEIDL Public Safety core is responsible for 24 hours a day, 7 days a week facility security and both police-academy highly trained public safety officers and specialized automated building systems are used. Public Safety personnel are well trained in the intricacies of a secure site maintenance, criminal applications with a significant amount of training pertaining to safety, facilities, emergency preparedness and response, biosafety incidents, animal rights activism, insider threats and coordinated notification and response of external local, state and federal responders. Individuals are only granted access to relevant NEIDL facilities based upon their responsibilities in the building. Employees pass through security layers that require identification by a public safety officer, and use a combination of proximity card access and biometric iris readers to gain access to laboratories in which select agent work is carried out. Activities in select agent laboratories can be monitored by closed circuit television, and video recordings can be reviewed. Access is monitored for compliance both electronically and by public safety staff. Variances to authorized access results in notifications of public safety staff within the building which will initiate a response to that variance.

Describe the biocontainment resources available at all performance sites: All BSL-3 and BSL-4 labs are under negative pressure, with redundant systems to ensure negative pressure is maintained. Both facilities have autoclaves to decontaminate all waste materials as well as approved protocols for the treatment or inactivation of any materials leaving the lab. All personnel are extensively trained in basic virology and safety protocols before being approved for select agent work and then undergo extensive training to work with SARS-CoV as a BSL-3 pathogen. In both labs, annual testing is performed to verify that the biosafety cabinets, lab supply/exhaust systems (including alarms), and other laboratory equipment are functioning as designed. The lab is secured at all times and only personnel who have successfully completed select agent clearance and laboratory specific training requirements are permitted to enter without an escort.

OTHER BIOHAZADS

Other Biohazards and Non-Select BSL3 Agents: We will synthesize full length recombinant viruses for MERS-CoV and from a variety of SARS-like, MERS-like and related emerging coronaviruses (e.g., SADS-CoV, HKU2, HKU10, etc.). All of these viruses will be isolated and studied under BSL3 conditions at UNC.

Field Work Biosafety:

Introduction and Background. Many of the novel viruses studied in this proposal have caused or have the potential to cause human outbreaks with significant case fatality rates, and there are no vaccines available for many of these agents. The work proposed in this application will involve two aspects: field work and laboratory work, focusing on distantly coronaviruses, filoviruses and henipaviruses. Fieldwork involves the highest risk of exposure to bat and related human viruses of high pathogenic potential, while working in caves with high bat density overhead and the potential for fecal dust to be inhaled. There is also some risk of exposure to pathogens or physical injury while handling bats, rodents, primates or other animals, their blood samples or their excreta. The Co-PIs and field team have extensive experience and certification working with wildlife species and high-biosecurity pathogens (Nipah virus, ebolavirus, SARS-like CoV, MERS-like CoV etc.), and great care will be taken in the field to limit the risk of accidental exposure to known or unknown animal pathogens. We have strict procedures

for handling bats and working with samples from them as they are secured in the field and transported to the lab. Field team members handling animals will be trained to utilize personal protective equipment and practice proper environmental disinfection techniques. This includes wearing coveralls or dedicated clothing, nitrile gloves, eye protection, and a P95 or P100 respirator, or positive air pressure respirators (PAPRs) in the field. All field clothing and equipment will be disinfected using Virkon disinfectant, and Tyvek suits will be properly disposed of as biohazard. All biological waste from field surveys will be disposed of in the appropriate container (sharps box or an autoclave bag) and will be autoclaved at local hospitals or university labs. All personnel will be vaccinated against rabies and have a neutralizing antibody titer, in accordance with WHO and CDC recommendations. Field teams will carry rabies boosters in the field and will receive a booster in the event of a potential rabies exposure.

Field safety protocol: Our procedures to deal with bites, needle-sticks etc. are as follows: The wound is washed thoroughly with soap and water to clean away dirt and debris, then vigorously scrubbed with a sterile gauze bandage and benzalkonium chloride for 5 minutes. If bleeding, pressure is applied with a sterile bandage for until bleeding has stopped. If the wound continues to bleed, medical attention at the nearest hospital is sought. The bat from which the bite or exposure originated is identified, and the samples collected from it labeled on the data sheet that these were involved in an exposure. Our procedures require that the person potentially exposed reports to a major hospital within 24 hours to have wound examined and receive a rabies booster as per WHO/CDC protocols. The laboratory work is lower risk, as samples placed in lysis buffer will be non-infectious. Samples placed in viral transport medium and frozen will be stored at ultra-low temperatures (-86°C) until viral isolation is required. Serum will be heat inactivated at 56°C for 30 minutes prior to testing.

Available Treatments: No approved treatments are related for MERS-CoV, MERS-like bat CoV, SARS and the SARSr-related and other bat coronavirus infections, however, GS5734 is effective against most coronaviruses, filoviruses and henipaviruses. In addition, therapeutic human antibodies are available against many of the classic high path viruses studied in this proposal, although it is less certain whether these immunotherapeutics will be effective against more phylogenetically distant strains in the family. VSV-EBOV vaccine is used to prevent Ebola infections in humans, having been administered to over 130,000 humans, mostly in the DRC.

P3CO Research. Recognizing the implementation of new gain of function research guidelines under P3CO, SARS-CoV and MERS-CoV are subject to these guidelines, and as such, reverse genetic studies are subject to review. Our group has considerable expertise in interfacing with the appropriate NIH P3CO institutional review boards to review, revise and finalize research designs that have the potential to modify pathogenesis or transmissibility in mammals.

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CONSORTIUM/CONTRACTUAL ARRANGEMENTS:

This project is a multi-institutional collaboration led by EcoHealth Alliance, New York (Daszak, PI), which will subcontract funds to five institutions: Chulalongkorn University's Thai Red Cross Emerging Infectious Disease Research Center (co-I Wacharapluesadee), Conservation Medicine Malaysia (co-I Hughes), the University of North Carolina at Chapel Hill (co-I Baric), the Uniformed Services University (co-I Broder), and Duke-NUS Medical School (co-I Wang). In addition, co-Is Keusch and Corley from Boston University's National Emerging Infectious Diseases Laboratories will provide additional in kind support, using additional funding, to attempt viral isolation on any novel Filoviruses or Henipaviruses we discover over the course of our award. PI Daszak has over 20 years previous experience managing collaborative projects including two R01s on Nipah virus ecology and an R01 on Coronavirus (AI110964) that involve multiple, separate foreign institutions; a 5-year NSF/NIH Ecology of Infectious Disease award on West Nile virus which involved multiple subcontracts, a NIAID R01 on bat viral discovery that involved multiple international contracts, and a multi-million dollar per year contract from USAID that involves 21 international partners. The applicant organization (EcoHealth Alliance) is justified in taking the lead on this project because it specializes in understanding the ecological and virological processes underlying zoonotic disease emergence, and has conducted international, multi-disciplinary and multi-partner research around the world for more than 30 years. The subcontract institutions will work on specific issues and areas in which they have proven expertise. These areas are:

Wildlife and human community surveillance and specimen collection, human clinical or hospital syndromic surveillance, screening and sequencing of specimens using conserved PCR assays for CoV, FV, and PMVs, screening of serum specimens using MMIA (Luminex) assays. (Chulalongkorn University TRC-EID, co-I Wacharapluesadee) and (Conservation Medicine Malaysia, co-I Hughes)

Novel serological and molecular assay development; generation of reagents for novel assays; and training of Thailand and Malaysia laboratory staff for technology transfer for serological and molecular protocol development (Uniformed Services University, co-I Broder) and (Duke-NUS Medical School, co-I Wang).

Small animal models of viral pathogenesis, primary human cell cultures, viral isolation and reverse genetics (University of North Carolina at Chapel Hill, co-I Baric) and (National Emerging Infectious Diseases Laboratories, co-I Keusch)

EcoHealth Alliance (EHA) led by PI Daszak have collaborated with all partners in the EIDRC consortium for 5-20 yrs on NIAID- and USAID-funded research, including more than 10 years each with co-Is Wacharapluesadee, Hughes, Baric, Broder, and Wang.

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June 18, 2019

Peter Daszak, PhD
EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

Reference: Response to RFA-AI-19-028 for grant entitled *Understanding Risk of Zoonotic Virus Emergence in EID Hotspots of Southeast Asia.*

Dear Dr. Daszak

This letter confirms that the appropriate program and administrative personnel at The University of North Carolina at Chapel Hill (UNC-CH) have reviewed the above referenced program announcement and are committed to enter into a subcontract with the EcoHealth Alliance for the performance period of March 1, 2020 to February 28, 2025. The work to be performed by UNC-CH does not include human research subjects but does include animal research subjects. UNC-CH maintains an active and enforced conflict of interest policy meeting the requirements of 42 CFR Part 50, Subpart F and 45CFR Part 94.

The principal investigator at EcoHealth Alliance is Dr. Peter Daszak and he will be collaborating with UNC-CH's Principal Investigator, Dr. Ralph Baric The UNC-CH budget, budget justification and scope of work are provided as separate enclosures to this letter. The total cost of the proposed subcontract for all five years will not exceed $971,975 and this includes appropriate direct and indirect costs.

Furthermore, by submission of this commitment letter UNC-CH and its Principal Investigator (PI) certify (1) that the information submitted within the application is true, complete and accurate to the best of the UNC-CH s and PI's knowledge, (2) that any false, fictitious, or fraudulent statements or claims may subject the UNC-CH and PI to criminal, civil, or administrative penalties; and (3) that the PI agrees to accept responsibility for the scientific conduct of the project and to provide the required progress reports if an award is made as a result of UNC-CH' s application.

If you have any questions, please let us know.

Sincerely,

Terry Magnuson, PhD
Vice Chancellor for Research
Email: [redacted] (b) (6)

Ralph S Baric, PhD
UNC-CH Principal Investigator
Email: [redacted] (b) (6)

06 June 2019

Dr. Peter Daszak
President
EcoHealth Alliance
460 W 34th St. 17th Floor
New York, NY 10001 USA

Dear Dr. Daszak,

This letter expresses the strong interest that staff at Duke-NUS Medical School has in collaborative research with EcoHealth Alliance and other partners on the proposed NIAID Emerging Infectious Diseases Research Center (EIDRC) submission (FOA: RFA-AI-19-028), titled "Understanding risk of zoonotic virus emergence in EID hotspots of Southeast Asia".

The Duke-NUS Medical School recognizes the mutual benefits to be gained through research cooperation and a successful partnership in this center, including sharing of technology, samples, reagents, data and research results. The research proposed will advance our understanding of the ability of wildlife-origin coronaviruses, henipaviruses and filoviruses to spillover into high-risk human populations and cause illnesses that may have been previously unreported, or undiagnosed. We believe the results will be scientifically important, and have great public health value in the region, and globally, by identifying key pandemic threats in an EID hotspot region.

We at Duke-NUS have collaborated successfully with all partners on this proposal, and look forward to continuing our work together. Our work will include managing the test development and sample testing component of this multi-disciplinary project. We will also actively take part in technology transfer and research cross-training with other partners, and are ready, willing and able to work in surge capacity to conduct research during outbreak situations, in collaboration with all other EIDRCs and the EIDCC.

Sincerely,

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Diseases

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June 12, 2019

Dr. Peter Daszak
President
EcoHealth Alliance
460 W 34th St. 17th Floor
New York, NY 10001 USA

Dear Dr. Daszak,

This letter expresses the high interest that I and my laboratory have in continuing and expanding our collaborative research endeavors with EcoHealth Alliance and other partners on the proposed NIAID Emerging Infectious Diseases Research Center (EIDRC) submission (FOA: RFA-AI-19-028), titled "Understanding risk of zoonotic virus emergence in EID hotspots of Southeast Asia".

I and the Uniformed Services University (USU) recognize the mutual benefits to be gained through research cooperation and a successful partnership in this center, including sharing of technology, samples, reagents, data and research results. The research proposed will advance our understanding of the ability of wildlife-origin coronaviruses, henipaviruses and filoviruses to spillover into high-risk human populations and cause illnesses that may have been previously unreported, or undiagnosed. We believe the results will be scientifically important, and have great public health value regionally and globally, by identifying key pandemic threats in an EID hotspot region.

My group at USU has collaborated successfully with all partners on this proposal, and look forward to continuing our work together. Our work will include the serological testing of samples in collaboration with partner laboratories, and we will actively take part in technology transfer and research cross-training in which we are well-experienced. We are ready, willing and able to work in surge capacity to conduct research during outbreak situations, in collaboration with all other EIDRCs and the EIDCC. I look forward to this exciting opportunity to this network in place under the leadership of EcoHealth Alliance!

Sincerely,

Christopher C. Broder, Ph.D.
Professor and Chair
Department of Microbiology and Immunology

Boston University National Emerging Infectious Diseases Laboratories

620 Albany Street
Boston, Massachusetts 02118
bu.edu/neidl

06 June 2019

Dr. Peter Daszak
President, EcoHealth Alliance
460 W 34th St. 17th Floor
New York, NY 10001 USA

Dear Dr. Daszak:

This letter expresses the high interest that faculty and staff at Boston University's National Emerging Infectious Diseases Laboratories (NEIDL) have in collaborative research with EcoHealth Alliance and other partners on the proposed NIAID Emerging Infectious Diseases Research Center (EIDRC) submission (FOA: RFA-AI-19-028), titled "Understanding risk of zoonotic virus emergence in EID hotspots of Southeast Asia".

The NEIDL recognizes the mutual benefits to be gained through research cooperation and a successful partnership in this center, including sharing of technology, samples, reagents, data and research results. The research proposed will advance our understanding of the ability of wildlife-origin coronaviruses, henipaviruses and filoviruses to spill over into high-risk human populations and cause illnesses that may have been previously unreported, or undiagnosed. We believe the results will be scientifically important, and have great public health value in the region, and globally, by identifying key pandemic threats in an EID hotspot region.

We at NEIDL have collaborated successfully with all partners on this proposal, and look forward to continuing our work together. Going from "sequences" to "viruses" is a critical unmet need in surveillance and in assessing spillover potential and we are happy to participate. We are particularly excited about the opportunities to have access to sequences of novel viruses that may need to have 3' or 5' ends "completed", as well as to assess the presence of viruses in samples that are PCR positive for isolation and culture under BSL-4 conditions. We will seek external funding to test these for infectivity in human cells, and make these available to other investigators in the USA. We have a number of investigators that are experienced working with pathogens at maximum containment, have the ability to test viruses for infectivity in a variety of human cell types, and to assess the uptake and receptor usage in these cells. We are already developing small molecule and monoclonal therapeutics with commercial partners, and also hope to receive convalescent sera, PBMCs and other samples from clinical cohorts to further these goals. Finally, we will actively take part in technology transfer and research cross-training with other partners, including externally-funded visiting scholars and are ready, willing and able to work in surge capacity to conduct research during outbreak situations, in collaboration with all other EIDRCs and the EIDRC CC.

Sincerely,

Ronald B. Corley, Ph.D.
Professor and Chair,
Microbiology Director, NEIDL

Gerald T. Keusch, MD
Professor, Medicine and International Health
Boston University Schools of Medicine and Public Health Associate Director, NEIDL

Thai Red Cross Emerging Infectious Diseases Health Science Centre (TRC-EID)
WHO Collaborating Centre for Research and Training on Viral Zoonoses

13 June 2019

Dr Peter Daszak
President
EcoHealth Alliance
460 W 34th St 17th Floor
New York, NY 10001 USA

Dear Dr Daszak,

This letter expresses the high interest that staff at Thai Red Cross Emerging Infectious Diseases Health Science Centre (TRC EID) has in collaborative research with EcoHealth Alliance and other partners on the proposed NIAID Emerging Infectious Diseases Research Center (EIDRC) submission (FOA RFA-AI-19-028), titled "Understanding risk of zoonotic virus emergence in EID hotspots of Southeast Asia".

The TRC EID recognizes the mutual benefits to be gained through research cooperation and a successful partnership in this center, including sharing of technology, samples, reagents, data and research results The research proposed will advance our understanding of the ability of wildlife-origin coronaviruses, henipaviruses and filoviruses to spillover into high-risk human populations and cause illnesses that may have been previously unreported, or undiagnosed We believe the results will be scientifically important, and have great public health value in the region, and globally, by identifying key pandemic threats in an EID hotspot region

We at TRC EID have collaborated successfully with all partners on this proposal, and look forward to continuing our work together Our work will include managing human surveillance, sample collection, testing, and development of laboratory diagnostics We will also actively take part in technology transfer and research cross-training with other partners, and are ready, willing and able to work in surge capacity to conduct research during outbreak situations, in collaboration with all other EIDRCs and the EIDCC

Sincerely,

Thiravat Hemachudha

Prof Thiravat Hemachudha
Director of
Thai Red Cross Emerging Infectious Diseases Health Science Centre and
WHO Collaborating Centre for Research and Training on Viral Zoonoses
Faculty of Medicine, Chulalongkorn University
(b) (6)

Conservation Medicine Ltd,
13H Villamas Condo,
Villamas, Jln Villamas
Off Jalan Sierramas Barat,
Sg Buloh, 47000,
Selangor, Malaysia

Dr. Peter Daszak
President
EcoHealth Alliance
460 W 34th St. 17th Floor
New York, NY 10001 USA

06 June 2019

Dear Dr. Daszak,

This letter expresses the high interest that staff at Conservation Medicine Ltd have in collaborative research with EcoHealth Alliance and other partners on the proposed NIAID Emerging Infectious Diseases Research Center (EIDRC) submission (FOA: RFA-AI-19-028), titled "Understanding risk of zoonotic virus emergence in EID hotspots of Southeast Asia".

I have worked with EcoHealth Alliance as the Project Coordinator for the "Emerging Pandemic Threat PREDICT Program" since 2010, as the Deputy Chief of Party on the USAID funded "Infectious Disease Emergence and Economics of Altered Landscapes" project since 2013 and as Co-PI on the DTRA funded Serological Biosurveillance for Spillover of Henipaviruses and Filoviruses at Agricultural and Hunting Human- Animal Interfaces in Peninsular Malaysia since May 2017. It is with great pleasure that I fully endorse your project and see high value in this work.

Conservation Medicine Ltd recognizes the mutual benefits to be gained through research cooperation and a successful partnership in this center, including sharing of technology, samples, reagents, data and research results. The research proposed will advance our understanding of the ability of wildlife-origin coronaviruses, henipaviruses and filoviruses to spillover into high-risk human populations and cause illnesses that may have been previously unreported, or undiagnosed. We believe the results will be scientifically important, and have great public health value in the region, and globally, by identifying key pandemic threats in an EID hotspot region.

We at Conservation Medicine Ltd have collaborated successfully with all partners on this proposal, and look forward to continuing our work together. Our work will include human and wildlife sample collection, coordination of syndromic surveillance and outbreak response, storage of samples and coordination of all in-country testing, and development of laboratory diagnostics. We will also actively take part in technology transfer and research cross-training with other partners, and are ready, willing and able to work in surge capacity to conduct research during outbreak situations, in collaboration with all other EIDRCs and the EIDCC.

We look forward to collaborating with you and EcoHealth Alliance on this worthwhile project.

Sincerely,

Tom Hughes
Director
Conservation Medicine, Ltd.
(b) (6)
(b) (6) (Mobile)
(b) (6) (Telephone/Fax)

06 June 2019

Dr. Peter Daszak
President
EcoHealth Alliance
460 W 34th St. 17th Floor
New York, NY 10001 USA

Dear Dr. Daszak,

This letter expresses the high interest that staff at Lintang Health Clinic, Sungai Siput, Kuala Kangsar District Health Office has in collaborative research with EcoHealth Alliance and other partners on the proposed NIAID Emerging Infectious Diseases Research Center (EIDRC) submission (FOA: RFA-AI-19-028), titled "Understanding risk of zoonotic virus emergence in EID hotspots of Southeast Asia".

The Lintang Health Clinic, Sungai Siput, Kuala Kangsar District Health Office recognizes the mutual benefits to be gained through research cooperation and a successful partnership in this center, including sharing of technology, samples, reagents, data and research results. The research proposed will advance our understanding of the ability of wildlife-origin coronaviruses, henipaviruses and filoviruses to spillover into high-risk human populations and cause illnesses that may have been previously unreported, or undiagnosed. We believe the results will be scientifically important, and have great public health value in the region, and globally, by identifying key pandemic threats in an EID hotspot region.

We at Lintang Health Clinic, Sungai Siput, Kuala Kangsar District Health Office have collaborated successfully with all partners on this proposal, and look forward to continuing our work together. Our work will include managing human surveillance and sample collection. We will also actively take part in technology transfer and research cross-training with other partners, and are ready, willing and able to work in surge capacity to conduct research during outbreak situations, in collaboration with all other EIDRCs and the EIDCC.

Sincerely,

Dr Jayaseelan Sekaran
Senior Medical Officer of Lintang Health Clinic,
Kuala Kangsar District Health Office,
33000 Kuala Kangsar,
Perak,
Malaysia
Email: [redacted] (b) (6)

06 June 2019

Dr. Peter Daszak
President
EcoHealth Alliance
460 W 34th St. 17th Floor
New York, NY 10001 USA

Dear Dr. Daszak,

This letter expresses the high interest that staff at Pos Betau Health Clinic, Kuala Lipis District Health Office has in collaborative research with EcoHealth Alliance and other partners on the proposed NIAID Emerging Infectious Diseases Research Center (EIDRC) submission (FOA: RFA-AI-19-028), titled "Understanding risk of zoonotic virus emergence in EID hotspots of Southeast Asia".

Pos Betau Health Clinic, Kuala Lipis District Health Office recognizes the mutual benefits to be gained through research cooperation and a successful partnership in this center, including sharing of technology, samples, reagents, data and research results. The research proposed will advance our understanding of the ability of wildlife-origin coronaviruses, henipaviruses and filoviruses to spillover into high-risk human populations and cause illnesses that may have been previously unreported, or undiagnosed. We believe the results will be scientifically important, and have great public health value in the region, and globally, by identifying key pandemic threats in an EID hotspot region.

We at Pos Betau Health Clinic, Kuala Lipis District Health Office have collaborated successfully with all partners on this proposal, and look forward to continuing our work together. Our work will include managing human surveillance and sample collection. We will also actively take part in technology transfer and research cross-training with other partners, and are ready, willing and able to work in surge capacity to conduct research during outbreak situations, in collaboration with all other EIDRCs and the EIDCC.

Sincerely,

Dr Wan Hafizu Nazrin Bin Wan Mohamad Lotfi
Medical Officer of Pos Betau Health Clinic,
Kuala Lipis District Health Office,
27200 Kuala Lipis,
Pahang,
MALAYSIA

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UNIMAS/NC-21.26/03-01 (4)

18 June 2019

Dr. Peter Daszak
President
EcoHealth Alliance
460 W 34th St. 17th Floor
New York, NY 10001 USA

Dear Dr. Daszak,

This letter expresses the high interest that staff at Universiti Malaysia Sarawak has in collaborative research with EcoHealth Alliance and other partners on the proposed NIAID Emerging Infectious Diseases Research Center (EIDRC) submission (FOA: RFA-AI-19-028), titled "Understanding risk of zoonotic virus emergence in EID hotspots of Southeast Asia".

The Universiti Malaysia Sarawak recognizes the mutual benefits to be gained through research cooperation and a successful partnership in this center, including sharing of technology, samples, reagents, data and research results. The research proposed will advance our understanding of the ability of wildlife-origin coronaviruses, henipaviruses and filoviruses to spillover into high-risk human populations and cause illnesses that may have been previously unreported, or undiagnosed. We believe the results will be scientifically important, and have great public health value in the region, and globally, by identifying key pandemic threats in an EID hotspot region.

We at Universiti Malaysia Sarawak have collaborated successfully with all partners on this proposal, and look forward to continuing our work together. Our work will include managing both human and animal surveillance, sample collection testing, and development of laboratory diagnostics". We will also actively take part in technology transfer and research cross-training with other partners, and are ready, willing and able to work in surge capacity to conduct research during outbreak situations, in collaboration with all other EIDRCs and the EIDCC.

Sincerely,

Dr Cheng Siang Tan (PhD, RBP)
Head, Centre for Tropical and Emerging Diseases
Faculty of Medicine and Health Sciences
Universiti Malaysia Sarawak
94300 Kota Samarahan
Sarawak, MALAYSIA
[redacted] (b) (6)

UNIVERSITI MALAYSIA SARAWAK

06 June 2019

Dr. Peter Daszak
Pres dent
EcoHealth Alliance
460 W 34th St. 17th Floor
New York, NY 10001 USA

Dear Dr. Daszak,

This letter expresses the high interest of myself as a staff at Faculty of Resource Science and Technology Universiti Malaysia Sarawak, in a collaborative research with EcoHealth Alliance and other partners on the proposed NIAID Emerging Infectious Diseases Research Center (EIDRC) submission (FOA: RFA-AI-19-028), titled "Understanding risk of zoonotic virus emergence in EID hotspots of Southeast Asia".

I recognize the mutua benefits to be gained through research cooperation and a successful partnership in this center, including sharing of technology, samples, reagents, data and research results. The research proposed will advance our understanding of the ability of wildlife-origin coronaviruses, henipaviruses and filoviruses to spillover into high-risk human populations and cause illnesses that may have been previously unreported, or undiagnosed. We believe the results will be scientifically important, and have great public health value in the region, and globally, by identifying key pandemic threats in an EID hotspot region.

Colleague (Dr Tan Cheng Siang) and I from Universiti Malaysia Sarawak have collaborated successfully with all partners on th s proposal and look forward to continuing our work together. Our work will include managing sample collection and testing. We will also actively take part in technology transfer and research cross-training with other partners, and are ready, willing and able to work in surge capacity to conduct research during outbreak situations, in collaboration with all other EIDRCs and the EIDCC.

Sincerely,

Faisal

Faisal Ali Anwarali Khan
Faculty of Resource Science and Technology
Universiti Malaysia Sarawak
94300 Kota Samarahan, Sarawak
MALAYSIA

(b) (6)

27 June 2019

Dr Peter Daszak
President
EcoHealth Alliance
460 W 34th St. 17th Floor
New York, NY 10001 USA

Dear Dr. Daszak,

This letter expresses the high interest that staff at Klinik Kesihatan Bario has in collaborative research with EcoHealth Alliance and other partners on the proposed NIAID Emerging Infectious Diseases Research Center (EIDRC) submission (FOA: RFA-AI-19-028), titled "Understanding risk of zoonotic virus emergence in EID hotspots of Southeast Asia".

The Klinik Kesihatan Baio recognizes the mutual benefits to be gained through research cooperation and a successful partnership in this center, including sharing of technology, samples, reagents data and research results. The research proposed will advance our understanding of the ability of wildlife-origin coronaviruses, henipaviruses and filoviruses to spillover into high-risk human populations and cause illnesses that may have been previously unreported, or undiagnosed. We believe the results will be scientifically important, and have great public health value in the region, and globally, by identifying key pandemic threats in an EID hotspot region.

We at Klinik Kesihatan Bario have collaborated successfully with all partners on this proposal, and look forward to continuing our work together. Our work will include performing syndromic study by recruiting native patients with respiratory illness We will also actively take part in technology transfer and research cross-training with other partners, and are ready, willing and able to work in surge capacity to conduct research during outbreak situations, in collaboration with all other EIDRCs and the EIDCC.

Sincerely,

DR NADIA DIYANA BT HAMZAH
MEDICAL OFICER
KLINIK KESIHATAN BARIO
NO.10 PEKAN BARIO
98060 BARIO SARAWAK
(b) (6)

28 June 2019

Dr. Peter Daszak
President
EcoHealth Alliance
460 W 34th St. 17th Floor
New York, NY 10001 USA

Dear Dr. Daszak,

This letter expresses the high interest that staff at Hospital Miri, Sarawak has in collaborative research with EcoHealth Alliance and other partners on the proposed NIAID Emerging Infectious Diseases Research Center (EIDRC) submission (FOA: RFA-AI-19-028), titled "Understanding risk of zoonotic virus emergence in EID hotspots of Southeast Asia".

The Hospital Miri, Sarawak recognizes the mutual benefits to be gained through research cooperation and a successful partnership in this center, including sharing of technology, samples, reagents, data and research results. The research proposed will advance our understanding of the ability of wildlife-origin coronaviruses, henipaviruses and filoviruses to spillover into high-risk human populations and cause illnesses that may have been previously unreported, or undiagnosed. We believe the results will be scientifically important, and have great public health value in the region, and globally, by identifying key pandemic threats in an EID hotspot region.

We at Hospital Miri, Sarawak have collaborated successfully with all partners on this proposal, and look forward to continuing our work together. Our work will include managing human surveillance, sample collection, testing, and development of laboratory diagnostics. We will also actively take part in technology transfer and research cross-training with other partners, and are ready, willing and able to work in surge capacity to conduct research during outbreak situations, in collaboration with all other EIDRCs and the EIDCC.

Sincerely,

Dr. Ingrid Ting Hao Lin
Clinical Physician and researcher
Medical Department
Hospital Miri
Jalan Cahaya,
98000 Miri Sarawak
(b) (6)

UMS
UNIVERSITI MALAYSIA SABAH
BORNEO MEDICAL AND HEALTH RESEARCH CENTRE
FACULTY OF MEDICINE AND HEALTH SCIENCES
BLOCK E, LEVEL G
UNIVERSITI MALAYSIA SABAH
88400 KOTA KINABALU, SABAH, MALAYSIA
Tel : +6088-320 000 ext 611051
Faks : +6088-321 377/-321373
Email :

Date : 15 **June 2019**

DR. PETER DASZAK
President
EcoHealth Alliance
460 W 34th St. 17th Floor
New York, NY 10001USA

Dear Dr. Daszak,

This letter expresses the high interest that staff at Borneo Medical and Health Research Centre (BMHRC) has in collaborative research with EcoHealth Alliance and other partners on the proposed NIAID Emerging Infectious Diseases Research Center (EIDRC) submission (FOA: RFA-AI-19-028), titled "Understanding risk of zoonotic virus emergence in EID hotspots of Southeast Asia".

The BMHRC recognizes the mutual benefits to be gained through research cooperation and a successful partnership in this center, including sharing of technology, samples, reagents, data and research results. The research proposed will advance our understanding of the ability of wildlife-origin coronaviruses, henipaviruses and filoviruses to spillover into high-risk human populations and cause illnesses that may have been previously unreported, or undiagnosed. We believe the results will be scientifically important, and have great public health value in the region, and globally, by identifying key pandemic threats in an EID hotspot region.

We at BMHRC have collaborated successfully with all partners on this proposal and look forward to continuing our work together. Our work will include managing human surveillance, sample testing, and development & evaluation of laboratory diagnostics. We will also actively take part in technology transfer and research cross-training with other partners, and are ready, willing and able to work in surge capacity to conduct research during outbreak situations, in collaboration with all other EIDRCs and the EIDCC.

Sincerely,

Kamruddin Ahmed

PROFESSOR DR. KAMRUDDIN AHMED
Director
Borneo Medical and Health Research Centre
Faculty of Medicine and Health Sciences
University Malaysia Sabah
Email: [redacted] (b) (6)

Cc. - File

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Cert No. AF 3081

Gleneagles™
KOTA KINABALU

Gleneagles Kota Kinabalu
A branch of Pantai Medical Centre Sdn Bhd (73056-D)
Riverson@Sembulan, Block A-1, Lorong Riverson@Sembulan
88100 Kota Kinabalu, Sabah
Tel : +6088 518 888 Fax : +6088 518 889
www.gleneagleskk.com.my

20 June 2019

Dr. Peter Daszak
President
EcoHealth Alliance
460 W 34th St. 17th Floor
New York, NY 10001 USA

Dear Dr. Daszak,

LETTER OF SUPPORT FOR THE PROPOSED NIAID EMERGING INFECTIOUS DISEASES RESEARCH CENTER (EIDRC) SUBMISSION (FOA: RFA-AI-19-028) ("Proposed Research")

This letter expresses the high interest that Gleneagles Kota Kinabalu Hospital, Sabah ("GKK") has in the collaborative research with EcoHealth Alliance and other partners on the Proposed Research titled "Understanding risk of zoonotic virus emergence in EID hotspots of Southeast Asia".

2. For your understanding, GKK recognizes the mutual benefits that could be gained through the research cooperation and successful partnership from the Proposed Research, including sharing of technology, samples, reagents, data and research results. The Proposed Research will advance our understanding of the ability of wildlife-origin coronaviruses, henipaviruses and filoviruses to spillover into high-risk human populations and cause illnesses that may have been previously unreported, or undiagnosed. We believe the results will be scientifically important, and have great public health value in the region, and globally, by identifying key pandemic threats in an EID hotspot region.

3. Dr. Timothy Wilham who is the Infectious Disease Consultant accredited by and practicing at GKK has collaborated successfully with all the partners on this Proposed Research, and look forward to continuing our collaboration. The collaboration will include managing patients, human surveillance and sample collection for diagnostic purposes. We will also actively take part in technology transfer and research cross-training with other partners, and are ready, willing and able to work in surge capacity to conduct research during outbreak situations, in collaboration with all other EIDRCs and the EIDCC. Should Dr. William and his colleagues succeed in being awarded the grant, he will work within the bounds of the regulations and ethics governing the conduct of the Proposed Research in Malaysia.

Kindly contact the undersigned should there be any inquiry. Thank you.

Yours sincerely,

Noel Cheah
Chief Executive Officer

HOSPITAL UNIVERSITI MALAYSIA SABAH
Fakulti Perubatan Dan Sains Kesihatan
Pejabat Pentadbiran HUMS, Aras 1, Blok A1,
Universiti Malaysia Sabah, Jalan UMS
88400 Kota Kinabalu, Sabah, Malaysia

Tel : (+6088-320000) samb 611705
Faks : (+6088-320377)
E-mel : hums@ums.edu.my

Our Ref.: UMS/HUMS6.11/100-1/4/249 ( )
Date : 20 June 2019

DR. PETER DASZAK
President
EcoHealth Alliance
460 W 34th St. 17th Floor
New York, NY 10001 USA

Dear Dr. Daszak,

This letter expresses the high interest that staff at Hospital Universiti Malaysia Sabah (HUMS) has in collaborative research with EcoHealth Alliance and other partners on the proposed NIAID Emerging Infectious Diseases Research Center (EIDRC) submission (FOA: RFA-AI-19-028), titled "Understanding risk of zoonotic virus emergence in EID hotspots of Southeast Asia".

Hospital Universiti Malaysia Sabah, a 400 bedded hospital will be completed in June 2020. This hospital will run based on the concept of 'SMART Hospital', focusing on the delivery of high quality evidence based health care, using the latest technology and enhancing effective collaboration between health care providers. Patient centered care and collaboration will be at the centre of our processes. HUMS will also focus on health promotion and maintaining health, wellness and disease prevention

The Hospital UMS recognizes the mutual benefits to be gained through research cooperation and a successful partnership in this center, including sharing of technology, samples, reagents, data and research results. The research proposed will advance our understanding of the ability of wildlife-origin coronaviruses, henipaviruses and filoviruses to spillover into high-risk human populations and cause illnesses that may have been previously unreported, or undiagnosed. We believe the results will be scientifically important, and have great public health value in the region, and globally, by identifying key pandemic threats in an EID hotspot region.

We at HUMS are looking forward to collaborating successfully with all partners on this proposal. Our work will include managing human surveillance, sample collection, testing, and development of laboratory diagnostics. We will also actively take part in technology transfer and research cross-training with other partners, and are ready, willing and able to work in surge capacity to conduct research during outbreak situations, in collaboration with all other EIDRCs and the EIDCC.

Yours faithfully,

PROFESSOR DR HELEN BENEDICT LASIMBANG
Chief Executive Officer

Telephone No. : (b) (6)
Fax No. : 088-321377
e-Mail Address : (b) (6)

HBL/dm

Pusat Penyelidikan Klinikal (CRC)
Hospital Queen Elizabeth
Karung Berkunci No. 2029
88586 Kota Kinabalu
Sabah, Malaysia.
088-517507 / samb 7117, 7468 088-211906 crc.sabah@moh.gov.my

18 June 2019

Dr Peter Daszak
President
EcoHealth Alliance
460 W 34th St. 17th Floor
New York, NY 10001 USA

Dear Dr Daszak,

This letter expresses the high interest that staff at Queen Elizabeth Hospital has in collaborative research with EcoHealth Alliance and other partners on the proposed NIAID Emerging Infectious Diseases Research Center (EIDRC) submission (FOA RFA-AI-19-028) titled "Understanding risk of zoonotic virus emergence in EID hotspots of Southeast Asia".

The Queen Elizabeth Hospital recognizes the mutual benefits to be gained through research cooperation and a successful partnership in this center, including sharing of technology, samples, reagents data and research results The research proposed will advance our understanding of the ability of wildlife-origin coronaviruses henipaviruses and filoviruses to spillover into high-risk human populations and cause illnesses that may have been previously unreported, or undiagnosed We believe the results will be scientifically important and have great public health value in the region, and globally, by identifying key pandemic threats in an EID hotspot region.

We at Queen Elizabeth Hospital have collaborated successfully with all partners on this proposal and look forward to continuing our work together Our work will include managing human surveillance and sample collection We will also actively take part in technology transfer and research cross-training with other partners, and are ready, willing and able to work in surge capacity to conduct research during outbreak situations, in collaboration with all other EIDRCs and the EIDCC.

Sincerely,

DR NAGARAJAN NAGALINGAM
MMC 40081
KETUA UNIT RAWATAN KESAKITAN &
KETUA UNIT CRC
HOSPITAL QUEEN ELIZABETH
KOTA KINABALU, SABAH.
13/7/19

Dr. Nagarajan A/L Nagalingam
Head of Unit
Clinical Research Center (CRC),
Queen Elizabeth Hospital.
Karung Berkunci No 2029.
88586 Kota Kinabalu.
Sabah Malaysia
Email [redacted]

Pusat Penyelidikan Klinikal (CRC)
Hospital Queen Elizabeth
Karung Berkunci No. 2029
88586 Kota Kinabalu
Sabah, Malaysia.
088-517507 / samb. 7117, 7468 088-211906 crc.sabah@moh.gov.my

06 June 2019

Dr. Peter Daszak
Pres dent
EcoHealth Alliance
460 W 34th St. 17th Floor
New York, NY 10001 USA

Dear Dr. Daszak,

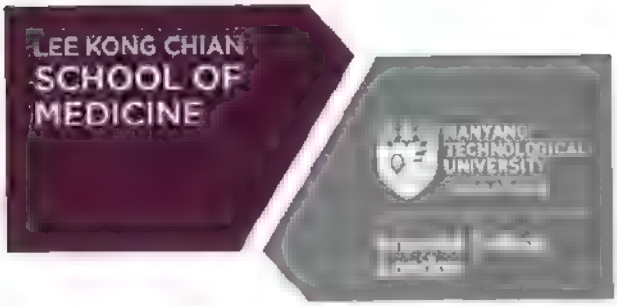
This letter expresses the high interest of myself a staff at Sabah State Health Department has in collaborative research with EcoHealth Alliance and other partners on the proposed NIAID Emerging Infectious Diseases Research Center (EIDRC) submission (FOA: RFA-AI-19-028), titled "Understanding risk of zoonotic virus emergence in EID hotspots of Southeast Asia".

I recognize the mutua benefits to be gained through research cooperation and a successful partnership in this center, including sharing of technology, samples, reagents, data and research results. The research proposed will advance our understanding of the ability of wildlife-origin coronaviruses, henipaviruses and filoviruses to spillover into high-risk human populations and cause illnesses that may have been previously unreported, or undiagnosed. We believe the results will be scientifically important, and have great public health value in the region, and globally, by identifying key pandemic threats in an EID hotspot region.

I and other colleagues from Sabah State Health Department have collaborated successfully with all partners on this proposal, and look forward to continuing our work together. Our work will include managing human surveillance, sample col ection, testing, and development of laboratory diagnostics. We will also actively take part in technology transfer and research cross-training with other partners, and are ready, willing and able to work in surge capacity to conduct research during outbreak situations, in collaboration with all other EIDRCs and the EIDCC.

Sincerely,

Dr Giri Shan Rajahram
Infectious Disease Physician
Queen Elizabeth Hospital
Sabah State Health Department
Locked Bag 2029, 88586,
Kota Kinabalu, Sabah
Malays a
[redacted] (b) (6)



REDEFINING MEDICINE, TRANSFORMING HEALTHCARE

14th June 2019

Dr. Peter Daszak
President
EcoHealth Alliance
460 W 34th St. 17th Floor
New York, NY 10001 USA

Dear Dr. Daszak,

Letter of Support for the Application of NIH NIAID Emerging Infectious Diseases Research Center (EIDRC) – 'Understanding risk of zoonotic virus emergence in EID hotspots of Southeast Asia'

I am pleased to offer the support of the Lee Kong Chian School of Medicine (LKCMedicine), Nanyang Technological University to National Institutes of Health, National Institute of Allergy and Infectious Diseases (NIH NIAID) Emerging Infectious Diseases Research Center (EIDRC) submission (FOA: RFA-AI-19-028), titled 'Understanding risk of zoonotic virus emergence in EID hotspots of Southeast Asia'.

LKCMedicine understands that it will participate officially as a collaborating institution and that A/Prof Yeo Tsin Wen will be listed as a Co-Investigator of the grant. A/Prof Yeo's involvement in the project will be to work with local stakeholders and collaborators to supervise and co-ordinate the clinical field studies in Malaysian Borneo, as well as offering sequencing facilities to detect novel pathogens.

LKCMedicine recognises the mutual benefits to be gained through research cooperation and a successful partnership in this proposed entreprise, including sharing of technology, samples, reagents, data and research results. The research proposed will advance our understanding of the ability of wildlife-origin coronaviruses, henipaviruses and filoviruses to spillover into high-risk human populations and cause illnesses that may have been previously unreported, or undiagnosed. We believe the results will be scientifically important, and have great public health value in the region, and globally, by identifying key pandemic threats in an EID hotspot region.

www.lkcmedicine.ntu.edu.sg

Headquarters and Clinical Sciences Building
11 Mandalay Road
Singapore 308232

Experimental Medicine Building
Nanyang Technological University
Yunnan Garden Campus
59 Nanyang Drive,
Singapore 636921

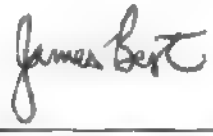
REDEFINING MEDICINE, TRANSFORMING HEALTHCARE

A/Prof Yeo at LKCMedicine has collaborated successfully with partners on previous projects and proposals, and is looking forward to continuing the work together. The work will include clinical studies to establish the risk of crossover zoonotic infections, and development of novel serological and molecular tools to test for viral spillover. A/Prof Yeo will also actively take part in technology transfer and research cross-training with other partners.

LKCMedicine will support A/Prof Yeo's proposed field work in Malaysian Borneo and also has a range of facilities to support the conduct of further experiments to detect novel pathogens, which includes the laboratory space, multiple sequencers and bioinformatic support as well as other research facilities to conduct the project.

Overall, A/Prof Yeo is an independent principal investigator at LKCMedicine and runs a functional laboratory at the School. The School and I fully support his application for the grant.

Yours sincerely,



Professor James D. Best
Dean, Lee Kong Chian School of Medicine
Nanyang Technological University

U.S. CENTERS FOR DISEASE CONTROL AND PREVENTION
SOUTHEAST ASIA REGIONAL OFFICE

Peter Daszak, PhD
President
EcoHealth Alliance
460 West 34th Street, 17th Floor
New York, NY 10001

Ref: RFA-AI-19-028
Title: Understanding Risk of Zoonotic Virus Emergence in EID Hotspots of Southeast Asia

Dear Dr. Daszak:

On behalf of the U.S. Centers for Disease Control and Prevention Southeast Asia Regional Office (CDC-SARO) we would like to offer our enthusiastic support for your application to the National Institutes of Health (NIH) proposing a systematic approach to better understand the diversity and epidemiology emerging viruses from the Coronavirus, Paramyxyovirus, and Filovirus families and commitment and improve laboratory capacity to identify and diagnose these pathogens.

CDC has a long history of collaboration with government organizations, non-governmental organizations, academic institutions including success with the NIH-funded research activities. I believe that CDC's work in Southeast Asia, through CDC-SARO, provides an effective platform to successfully collaborate with you on the proposed "Understanding Risk of Zoonotic Virus Emergence in EID Hotspots of Southeast Asia" project.

I understand that the overall goal of this proposed study is to further understand an important group of emerging zoonotic viruses that threaten global health security. The mission of CDC's global health presence is to protect Americans and people worldwide from public health threats by working with partners to build capacity, advance research, and respond in times of crises. This project will advance CDC's global mission by improving our knowledge of the zoonotic epidemiology of potentially highly-pathogenic emerging viruses, understanding the characteristics of these viruses that may be associated with increased potential for spill over and/or pathogenesis in humans, as well as improving our ability to detect and diagnose these unique pathogens. The emergence of Nipah virus in Malaysia, SARS-CoV, zoonotic influenza viruses (H5N1, H7N9) MERS-CoV, Zika, and finally Ebola in West Africa demonstrates the zoonotic potential of these and other viruses and highlights the critical gaps in knowledge including well-characterized diagnostics and medical countermeasures to stop these public health threats.. Furthermore, the spread of these outbreaks across international borders provides clear evidence of mobility of these pathogens given current trade/movement of animals and extensive networks of international travel.

Should you be successful with your application, CDC SARO is willing to provide technical support, liaise regional Ministries and CDC country offices, and provide general assistance as needed to advance the proposed science.

3rd-5th floor, Building 7, Department of Disease Control, Ministry of Public Health, Tivanon Road, Nonthaburi, Thailand 11000

Telephone : (66-2) 580-0668, 580-0669, Fax (66-2) 591-5443

I wish you all the best for the application and look forward to working together to reduce the threat of emerging viruses in Southeast Asia.

Sincerely yours,

John MacArthur, MD, MPH
Director, Southeast Asia Regional Office
Centers for Disease Control and Prevention
Representative to Thailand, Department of Health and Human Services

THE UNIVERSITY OF QUEENSLAND
AUSTRALIA

05 June 2019

Dr. Peter Daszak
President
EcoHealth Alliance
460 W 34th St. 17th Floor
New York, NY 10001 USA

Dear Peter,

I strongly support the collaborative research proposed by EcoHealth Alliance and other partners on the NIAID EIDRC proposal titled "Understanding risk of zoonotic virus emergence in EID hotspots of Southeast Asia".

As you know, I have long experience with both government and university sectors in researching wildlife-associated EIDs ncluding henipaviruses, coronaviruses and filoviruses in Southeast Asia and China. As an Honorary Professor in the School of Veterinary Science at UQ, the mutual benefits to be gained through research cooperation and partnership in this project, including sharing of technology, samples, reagents, data and research results, are clearly evident. The proposed research will undoubtedly advance our understanding of the ability of wildlife-origin coronaviruses, henipaviruses and filoviruses to spillover into high-risk human populations and cause morbidity and mortality previously unreported or undiagnosed. The results will be scientifically important, and have direct and significant public health value both regionally and globally, by identifying key pandemic threats in an EID hotspot region.

I very much look forward to participating in this new initiative with previous partners with a proven track record in this field. My contribution will include expert input in relevant study design, data collection and analysis, partner meetings, and dissemination and publication, and more broadly, technology transfer and research cross-training with other partners, as well as contribute surge capacity to undertake research during outbreak situations, in collaboration with all other EIDRCs and the EIDCC.

Yours sincerely,

Dr. Hume Field BVSc MSc PhD MACVS

Honorary Professor
The University of Queensland | School of Veterinary Science
Brisbane, Australia
(b) (6)

RESOURCE SHARING PLAN

To share resources with the academic research community, we will use the uniform Material Transfer Agreement (MTA), which acknowledges that the materials are proprietary to Institutions of the Cooperative Agreement and permitting their use in a manner that is consistent with the Bayh-Dole Act and NIH funding requirements. NIH research grants require that research be made available to the scientific community and public. The primary method of data sharing is through peer-reviewed publications in scientific journals and by presentation at scientific meetings. In addition, data and results created from NIH supported research will be submitted to NIH in annual progress reports per the terms and conditions of this award. Recombinant viruses, transgenic mouse models and experimental recombinant protein constructs will be made available upon request following a standard procedure (below). Several viruses isolated and studied in this program are select agents so these viruses will not be shipped unless appropriate documentation demonstrates the existence of approved BSL3/4 facilities, select agent licenses, and shipment using approved CDC and Department of Commerce procedures.

We already have established MTAs between most of our EID-SEARCH, consortium partners and will ensure these agreements are up to date and agreed upon by our consortium at the start of our project and then reviewed annually. Having these agreements in place will further reduce the time needed to share reagents and other resources in the event of an outbreak when time-sensitive sharing of biological resources and diagnostic reagents is most critical. **At the start of the project, we will work with the EIDRC – Coordinating Center to ensure these agreements and resource sharing plans are compliant and aligned with plans created for NIH's other EIDRCs.**

Data Sharing Plan

EcoHealth Alliance (EHA) will house the Data Management and Analysis (DMA) team for EIDRC SEARCH, led by Co-PIs Olival and Zambrana-Toreillo and include Key Personnel Latinne and Mendelsohn. EHA has served as the data and analysis hub for numerous multi-institutional, multi-sectoral, international disease research groups, including acting as the Modeling and Analytics lead institution for the USAID-PREDICT project, the Western Asia Bat Research Network lead by co-I Olival (*1*) and EHA's Rift Valley Fever Consortium (*2*). We will leverage our experience and infrastructure from those projects.

Project Database: We will create a dedicated, centralized EIDRC database to ingest, store, link, and provide for analysis all data associated with the proposed study and other expanded projects associated with the research network. The database will be SQL-based and use encrypted, secure cloud hosting services and enable export to archival and platform-independent formats. It will ensure data and metadata compatibility between project components, track data versioning and annotations. The system will be designed to work with both with both paper- and tablet-based field data entry and with laboratory information management systems in place in individual partner labs. We will design and engineer the systems to be compatible with other NIAID approved data management systems, including those utilized by the EIDRC-CC, by designing secure APIs, and matching data fields and data standards. The database will use existing metadata standards, including NCBI standards for genetic and molecular data and Ecological Metadata Language (EML) for field and wildlife data, as well as other standards and formats designated by the EIRDC CC. This will enable rapid publication and deposition of data. Granular security and privacy controls will be applied so that specific expansion projects undertaken in the network may be managed while maintaining data confidentiality as needed.

Data Identification and Privacy: For human clinical data and questionnaires, data will be identified by a unique identification code assigned to each individual and only this, de-identified code will be accessible in the project database. All questionnaire data and biological samples will be labeled with a unique alphanumeric identification code, assigned to each enrolled, sampled individual that does not identify the individual from whom data are collected. Participants' names and codes, along with other records with identifying information such as informed consent forms, will be stored in a separately secure system accessible to only essential project staff. If participants agree during the consent process, they may be contacted about having their samples or questionnaire data used for future separate studies about new animal infections discovered in the

future, and factors that may affect their chances of getting these animal infections. No data will be released for other purposes without full consent from participants. Upon completion of the project, personal identifying information will be destroyed unless this protocol is extended.

Training. Members of the DMA team will team will develop documentation and provide training for field and laboratory teams at all partner institutions in data management, metadata standards and data hygiene best practices. The DMA team will act as trainers and consultants for partner institutions in experimental design, power analysis, data analysis, and computational and reproducibility issues. DMA trainers will visit each partner institution and/or field team base for training workshops and analysis consultations, and partner institution researchers and students will spend extended time at EHA for collaborative analysis, a model that has been successful in building and maintaining analytical capacity under our NSF EcoHealthNet and PREDICT programs.

Computing Resources: EHA operates a cluster of high-performance servers (System76 20- and 36-core Linux servers with NVIDIA deep-learning GPUs), for data analysis activities, as well as infrastructure to launch cloud-based computing environments of virtual machine with identical software infrastructure. Our servers provide a web-based analysis environment with all necessary software for statistical and bioninformatics work that is available to the DMA and partners anywhere in the world. We use a mixture of cloud services (AWS, Azure, Backblaze, GitHub) to provide redundancy, backup, version control, and rapid post-disaster recovery. The cluster is available to all project partners and can be used use for both high-performance and training-level work (under isolated environments for security and performance).

Data and Code Sharing: Data will be available to the public and researchers without cost or registration, and be released under a CC0 license, as soon as related publications are in press. Data will be deposited for in long-term public scientific repositories. All sequence data will be made publicly available via GenBank. Additional ecological data collected in wildlife sampling will be deposited to the Knowledge Network for Biodiversity, and other data will be deposited in appropriate topic-specific or general repositories. Computer code for modeling and statistical analysis will be made available on a code-hosting site (GitHub), and archived in the Zenodo repository under an open-source, unrestrictive MIT license. Limited human survey and clinical data will be released following anonymization and aggregation per IRB requirements. Publications will be released as open-access via deposition to PubMed commons.

Sharing Model Organisms

Within the program, we will utilize standard laboratory mice as well as different Collaborative Cross mouse strains as well as various transgenic mouse strains, several of which are already available at the NIH-supported Mutant Mouse Regional Resource Center (MMMRC) at UNC. The Collaborative Cross mice are already publicly available from the UNC Systems Genetics Core Facility and the Jackson laboratories, and as such available to the scientific community. All genotyping information generated on these populations will be deposited in the appropriate public repositories (e.g. GEO, ImmPort, ENA). Similarly, all phenotypic data generated within this program from studies with mice will be deposited in the Mouse Phenome Database upon publication, as well as ImmPort to ensure dissemination to the community at large.

In accordance with the NIH/NIAID data sharing and release guidelines, we will coordinate the rapid and unrestricted sharing of all data generated as part of this project.

1. Genotypes generated on the MUGA mouse array, including raw x- and y- intensity data and derived genotype calls will be made available for download from the Mutant Mouse Regional Resource Center at UNC's website (https://www.med.unc.edu/mmrrc/genotypes/publications) and at Zenodo (https://zenodo.org/).

Reagent Sharing

For all other reagents/requests, we have established a consistent process for evaluating requests for samples and reagents from outside scientists. In order of priority, these include: 1) requests for reagents that have been

published in peer-reviewed journals; 2) requests which enhance/promote a specific agenda of the program projects and faculty; 3) requests that promote scientifically valid collaborations between project faculty and outside scientists; and 4) overall research and public health needs. The general format involves: a) establishing a working knowledge of the research agenda and credentials of the requestor, b) group discussion and agreement, 3) MTA agreement with the appropriate institution, or license agreement with a commercial entity, and 4) inventory checking and sending out of reagents. We will work closely with the appropriate institutional Technology Transfer Office and individuals involved in these transactions. The goal will be to provide reagents within a few months of receiving a request for traditional research purposes. In the event of an outbreak or emergency situation, we will communicate with the NIH and EIDRC-CC, and rapidly speed up resource sharing among our EID-SEARCH core partners and our extended network. As documented in the Research Strategy, EHA has successfully provided rapid technical assistance for testing and reagent needs during outbreaks under the USAID-PREDICT project, and has strong existing relationships and existing MTAs with our core EID-SEARCH partners to facilitate this. If needed, we will also acquire appropriate letters from the recipient institutions environmental health and safety officers and help coordinate CDC and/or USDA and Department of Commerce permits. The program faculty will not send reagents to individuals or institutions that do not have appropriate documentation of appropriate containment for the materials, might harbor ill-intentions, or are conducting irresponsible research.

Genomic Data Sharing

We will ensure compliance with NIH's Genomic Data Sharing plans for all viral sequence data generated in this project. We anticipate obtaining genetic sequence data for 100s of novel virus genotypes, including RNA-dependent RNA polymerase (RdRp) sequences for all strains/genotypes and sequences of viral attachment glycoproteins. We will generate full viral genomes for a subset of the viruses and human virus strains that we identify. We will also generate host genetic sequence data for relevant cellular receptor genes of wildlife species. We will deposit all genetic sequences in the NIH data bank, NCBI GenBank as soon as possible after data are generated (including ensurance of quality control), and no later than 6 months, so that they are readily available to the scientific community. We will ensure that all meta-data associated with these sequences, including collection locality lat/long, species-level host identification, date of collection, and sequencing protocols will also submitted. We anticipate sequence generation will occur over the 5 year proposed project period.

All datasets and associated meta-data will be additionally submitted to Virus Pathogen Resource (ViPR, http://www.viprbrc.org). All computational models of biological processes will be made available on the BioModels Database (http://www.ebi.ac.uk/biomodels-main/).

Intellectual Property

Intellectual property agreements, identified during the course of this project, will be accomplished by negotiation in good faith among the institutions and inventors. We will work with the inventors in the production of the necessary documents, working with the particular institutions, legal firms and commercial interests. It is anticipated that companies and institutions will have access to these reagents and viruses by MTA (for research purposes) or by a license agreement to be negotiated in good faith with a company.

Literature Cited

1. K. Phelps *et al.*, Bat Research Networks and Viral Surveillance: Gaps and Opportunities in Western Asia. *Viruses* **11**, (2019).
2. V. Msimang *et al.*, Rift Valley Fever Virus Exposure amongst Farmers, Farm Workers, and Veterinary Professionals in Central South Africa. *Viruses* **11**, (2019).

AUTHENTICATION OF KEY BIOLOGICAL RESOURCES AND SCIENTIFIC RIGOR

EcoHealth Alliance will actively engage with each partner laboratory to ensure that the highest quality of science, public accountability, and social responsibility in the conduct of science is maintained throughout this project. The overall goal is to ensure that the underlying scientific foundation of research conducted under our EID-SEARCH project from conception to completion is scientifically sound. The application is designed to ensure rigor, by using a robust and unbiased experimental design, well defined methodology, large group sizes that ensures statistical rigor and analysis, clearly interpretable endpoints, biological authentication of key biological resources and transparency in the reporting of results. To ensure scientific rigor (e.g., determining group sizes, analyzing anticipated results, reducing bias, ensuring independent and blinded measurements, improving precision and reducing variability including or excluding research subjects, and managing missing data), EcoHealth Alliance will review scientific approaches and statistical justification of study design throughout the duration of the award. We have highlighted our statistical approach to analysis of animal and human data in our Research Strategy and accompanying Statistical Analysis Plan. Whenever possible, multiple experimental approaches are used to demonstrate congruency in data interpretation. We will ensure that experimental designs will include considerations of sex as a "Relevant Biological Variable" in all studies involving human subjects or vertebrate animals. Unless otherwise specified and justified, all sampling and screening will include male and females.

Details below ensure the authentication of key biological resources needed for further biological characterization of viruses in the laboratories of the University of North Carolina, Duke-NUS Medical School, Singapore, and National Emerging Infectious Diseases Laboratories (NEIDL), Boston (Aim 1) as well as authentication of key reagents needed for molecular and serological screening, particularly the multiplex microsphere immunoassay (MMIA) or Luminex assay reagents developed by Uniformed Services University, Bethesda (Aims 2 and 3).

Cell lines. We will purchase cell lines from commercial vendors (e.g., ATCC), which confirm the authentication of the cells they supply using short tandem repeat (STR) profiling (ATCC). For all cell lines, we will create a low-passage (<5 passages) working stock for use across all experiments, and while in use, we will monitor morphology and growth kinetics continuously and perform mycoplasma tests monthly. If cultures exhibit unexpected changes in growth or morphology or test positive for mycoplasma, we will discard them immediately. All genetically modified cell lines will be frozen at low passage and maintained in culture only for 10 passage cycles. Once thawed and placed in culture, each cell line will be re-evaluated for maintenance of gene targeting. Primary cells. Early passage primary lung cells from humans are a key reagent for the proposed studies, including airway epithelial cells and microvascular endothelial cells. Human cells are derived from donors of both sexes and from all ages and ethnic groups and are provided from deidentified donors from the cystic fibrosis center tissue procurement fee for service center (https://www.med.unc.edu/marsicolunginstitute/core-facilities/tissueprocurmentandcellculturecore/). Care is taken during cell isolation to only handle one human organ at a time. Similarly, primary cell populations are handled carefully, only one donor cell type from a single donor at a time to avoid any mixing. The cells are observed to exhibit well-described prototypical characteristics of human primary lung cells in cell type specific medias in culture. For quality control, the cells are cultured in antibiotic free media to test for bacterial and fungal microbial contamination and are subjected to mycoplasma testing. Once the epithelial cells are grown as polarized and differentiated monolayers, a representative sample is subject to quality control histological analysis of cell morphology and Short Terminal Repeat (STR) marker profiling by the UNC Lineberger Cancer Center's Tissue Culture Facility (TCF).

The FreeStyle™ 293-F cell line is used for the development and expression of the viral recombinant proteins. These cells are from Thermo-Fisher Scientific, Inc., and are adapted to suspension culture in FreeStyle™ 293 Expression Medium.

Luminex (MMIA) Serological Reagents. To improve CoV-specific antibody detection, we propose to develop a multiplex microsphere immunoassay (MMIA) to enable serum samples to simultaneously be tested for antibodies reactive to the trimeric S, monomeric S_1 and S_2 subunits, and N. This assay development, being led by Uniformed Services University (USU), will involve some non-standard biological and chemical resources that

require validation and authentication. USU has specialized strategies to oversee the authentication of key biological resources, reagents and chemical resources during assay development and validation. Each purified protein antigen will be tested by protein gel and Western blot analysis to confirm expected protein size and weight. Polyclonal rabbit antisera specific to each purified antigen will be generated and used to test size exclusion and affinity purified proteins with Luminex-based platform. These polyclonal rabbit antisera will act as positive and negative controls for each purified protein and will be used to quantify inter and intra assay variation as well as ensure that each batch of purified protein retains the same level of assay reactivity. This positive and negative control assay standardization will be transferred to both international partner laboratories (JUST, Lugar) and guidelines detailing monthly testing will be included as part of the in-country training. Assay control results between USU and implementing laboratories in Thailand and Malaysia will be compared throughout the project to identify and control of any user or assay errors at each site.

Plasmids. We will sequence all cloned genes after their generation, after each PCR amplification, and after other modifications (such as site-directed mutagenesis). All molecular clones will be synthesized using commercial vendors and sequence verified after receipt. All mutations will be verified prior to assembly of full length clones for recombinant virus recover, which includes SARS-CoV, MERS-CoV, SARS-like and MERS-like CoV, select bat coronaviruses, Ebola and Ebola related filoviruses, Marburg and Marburg related filoviruses, and henipaviruses (Nipah, Hendra and related viruses).

Viruses. We will sequence wildtype and recombinant virus stocks to confirm the absence of unwanted mutations. For experiments in mice, each stock of live virus is deep-sequenced to confirm its authenticity, tested for the absence of mycoplasma, and tested for its lethality in animal models.

Animal Models. We will breed wild-type (WT) C57BL/6J, Collaborative Cross (CC) Recombinant Inbred Mice, and various transgenic C57BL6/J mice expressing the hACE2 receptor and humanized C57Bl6/J 288/330$^{+/+}$ DPP4 mice, which can be used to evaluate pathogenic outcomes following SARS-CoV, bat SARSr-CoV and MERS-CoV and bat MERSr-CoV. Animals will be used at UNC and Duke-NUS or will be shipped to the NEIDL in Boston Biosafety Level 4 (BSL-4) facility for experiments with authentic Ebola, related filoviruses and various henipaviruses. We obtained founder mice for the WT C57BL/6J colony from Jackson Laboratories, which confirms the authenticity of the animals they supply, while all CC mice were obtained from the University of North Carolina CC genetic reference population (https://csbio.unc.edu/CCstatus/index.py).

For assay development at USU, polyclonal rabbit sera specific to the recombinant viral glycoprotein to be generated will be prepared by Noble Life Sciences Inc., Maryland; a fee-for-service and AAALAC accredited, OLAW assured, and USDA licensed company with over 50 years of experience in animal housing and husbandry for large and small animals.

Mouse strain Genetic Validation. Inbred mouse strains and Collaborative Cross Mice are an invaluable tool for biomedical research, and represent a key aspect of this entire program. To ensure that the genetic background of all mice used within this program is known and when applicable they are part of a known inbred strains, we will genotype each mouse strain used within this program on the appropriate MUGA platform (Morgan, AP et.al., G3 2016, Dec 18). The most recent iteration of this state of the art genotyping array contains over 140,000 markers and can be used to precisely determine the genetic background at the substrain level and the precise location (at <1 megabase resolution) of genomic regions derived from different mouse inbred strains. In this way, the identity and genomic integrity of all mice used within these studies will be ensured. As new diagnostic assays become available, we will assess their utility and the cost effectiveness of the different MUGA arrays and implement them as appropriate. Furthermore, for each mutant mouse strain used within the project, positive diagnoses of the mutation will be assessed for each cohort of experimental animals with a diagnostic validated PCR assay or Sanger sequencing diagnostic to ensure proper results.

Mice with novel and interesting phenotypes after infection with different program viruses of interest will be deposited at the MMRRC housed at the University of North Carolina. The MMRRC is the nation's premier national public repository system for mutant mice. Funded by the NIH continuously since 1999, the MMRRC

archives and distributes scientifically valuable spontaneous and induced mutant mouse strains and ES cell lines for use by the biomedical research community. The University of North Carolina is one of the 4 major academic MMRRC centers across the nation.

Genome Sequencing. All PCR assays will be performed using appropriate control materials. Synthetic DNA constructs will be designed and used as universal controls. These DNA plasmids will contain short regions of overlapping viral sequences that act as primer binding sites for different PCR assays. The sequence spanning any two primers binding regions will be unique, allowing for contamination to be readily identified. Contamination control PCR will be used to rule out the possibility of contamination in a sample with universal control when a positive PCR result is obtained. All DNA sequence reads obtained from PCR screening of wildlife and human specimens will be examined by bioinformatic leads in each partner laboratory upon generation and again upon integration into our database system, for completeness, accuracy, and logical consistency. When base calls are uncertain, chromatograms will be reviewed to resolve ambiguities; and cloning and re-sequencing of samples if disagreement is observed. Once all test results (e.g., initial detection by PCR and subsequent sequencing of viruses) are available for a given specimen, the results are interpreted in light of all available and up-to-date scientific literature and previous findings by experienced EID-SEARCH virologists and bioinformaticians. This iterative process ensures the highest quality, most robust, data possible. We will ensure completeness of all existing metadata, meeting NCBI standards for genetic and molecular data.
For authentication of whole genome sequencing using next generation sequencing methods, we will ensure standard QC metrics are met at all points in the process of data generation, including: 1) sample quality control - validation of nucleic acid quality using spectrophotometric methods; 2) QC on base read quality and sequence reads through analysis of quality scores (Q scores); 3) standard methods to ensure quality of assembled/aligned reads by using NCBI and ICTV recognized viral reference sequences.

Following details in our Genomic Data Sharing plans, we will deposit all genetic sequences in the NIH data bank, NCBI GenBank as soon as possible after quality control process is completed, and no later than 6 months after data have been generated, so that they are readily available to the scientific community. All datasets and associated meta-data will be additionally submitted to Virus Pathogen Resource (ViPR, http://www.viprbrc.org) where they can be further authenticated by the scientific research community.

Intellectual Property. Intellectual property agreements, identified during the course of this project, will be accomplished by negotiation in good faith among the institutions and inventors.